Page 226 of 536 Table 4 Single Exon Probas Expressed i

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Table 4
Single Exon Probes Expressed

Probe Express Charles Express Charles Charle						ਨ 	ngle Exon Pro	Single Exon Probes Expressed in Brain
17697 30220 0.92 3.0E-14 AW266354.1 EST_HUMAN 17600 30222 0.97 3.0E-14 AW266354.1 EST_HUMAN 18397 32411 1.49 3.0E-14 AH20786.1 EST_HUMAN 25699 0.62 3.0E-14 AH20786.1 EST_HUMAN 25699 0.67 3.0E-14 AH20786.1 EST_HUMAN 25690 0.67 3.0E-14 AH20786.1 EST_HUMAN 25691 3.0E-14 AH20786.1 EST_HUMAN 17597 30220 7.19 3.0E-14 AH20786.1 EST_HUMAN 13168 25812 3.71 2.0E-14 AL163285.2 NT 13168 25812 3.71 2.0E-14 AL271736.1 NT 15548 26001 3.05 2.0E-14 AL163303.2 NT 15548 26001 3.05 2.0E-14 AL027788.1 NT 15549 27933 1.14 2.0E-14 AL027288.1 EST_HUMAN 15540 2.053 2.0E-14 AL02309.2 NT 15540 3.0550 0.8 2.0E-14 AL02309.2 <t< td=""><td>Probe SEQ ID NO:</td><td></td><td></td><td>Expression Signal</td><td>Most Similar (Top) Hit BLAST E Value</td><td></td><td></td><td>Top Hit Descriptor</td></t<>	Probe SEQ ID NO:			Expression Signal	Most Similar (Top) Hit BLAST E Value			Top Hit Descriptor
17600 30222 0.97 3.0E-14 7666884 INT 18367 32411 1.49 3.0E-14 AL420786.1 EST_HUMAN 25086 0.62 3.0E-14 AL4320786.1 EST_HUMAN 25087 32412 1.49 3.0E-14 AL4320786.1 EST_HUMAN 25088 0.67 3.0E-14 AL4320786.1 EST_HUMAN 17587 30220 7.19 3.0E-14 AL4320786.1 EST_HUMAN 17587 30220 7.19 3.0E-14 AL4320786.1 INT 13168 25811 3.71 2.0E-14 AL4320786.2 INT 1548 26091 9.05 2.0E-14 AL4320786.1 INT 15548 26091 9.05 2.0E-14 AL4320780.1 INT 15548 26091 9.05 2.0E-14 AL4320780.1 INT 15548 26091 9.05 2.0E-14 AL432080.2 INT 15548 27983 1.19 2.0E-14 AL432090.2 INT 15249 27983 1.14 2.0E-14 AL432090.2 INT 15240	4870			0.92		AW265354.1	EST HUMAN	xp45f12x1 NCI_CGAP_HN11 Homo saplens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element:contains element MER9 recetifical element.
19397 32411 1.49 3.0E-14 At20786.1 EST_HUMAN 25099 0.62 3.0E-14 At20786.1 EST_HUMAN 25099 0.62 3.0E-14 At20786.1 EST_HUMAN 23594 38840 1.28 3.0E-14 At20786.1 EST_HUMAN 25594 38222 0.87 3.0E-14 At20786.1 EST_HUMAN 25282 1.68 3.0E-14 At20786.1 EST_HUMAN 25282 1.68 3.0E-14 At20786.1 EST_HUMAN 13108 2.5811 3.71 2.0E-14 At207736.1 NT 14548 2.061 9.05 2.0E-14 At207736.1 NT 15248 2.061 3.01 2.0E-14 At207736.1 NT 15249 2.061 4 At207736.1 NT NT 15248 2.061 3.0E-14 At4077288.1 EST_HUMAN NT 15249 2.0E-14 At4077288.1 EST_HUMAN NT 15240 0.95 2.0E-14 At407320.2 NT 15240 0.95 2.0E-14 At407320.0 NT	4873			0.97		7656884	LN.	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA
19397 32412 1.49 3.0E-14 AL20786.1 EST_HUMAN 25089 0.62 3.0E-14 AL165248.2 NT 21378 3.4522 0.87 3.0E-14 AL165248.2 NT 25584 3.6840 1.28 3.0E-14 AL16528.2 NT 25282 1.68 3.0E-14 AL16528.2 NT 13168 2.5811 3.71 2.0E-14 AL16328.2 NT 15168 2.5812 3.71 2.0E-14 AL163303.2 NT 15185 2.5812 3.71 2.0E-14 AL163303.2 NT 15186 2.061 9.05 2.0E-14 AL163303.2 NT 15245 2.061 4.07 2.0E-14 AL163303.2 NT 15245 2.061 4.06 2.0E-14 AL163303.2 NT 15245 2.061 4.148 2.0E-14 AL163200.2 NT 15380 0.95 2.0E-14 AL163200.2 NT 18236 0.95 2.0E-14 AL163200.1 EST HUMAN 18236 0.95 2.0E-14 BE380681.1 EST HUMAN	9635			1.49		A1420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sepiens cDNA done IMAGE:2094070 3' similar to TR: 000519 000519 FATTY ACID AMIDE HYDROLASE
25099 0.62 3.0E-14 AL163248.2 NT 21378 34522 0.87 3.0E-14 AL163248.2 NT 23564 36840 1.28 3.0E-14 BE88016.1 EST HUMAN 25622 0.87 3.0E-14 AL163285.2 NT 25622 1.68 3.0E-14 AL163285.2 NT 13188 25811 3.71 2.0E-14 AL163285.2 NT 15548 25961 9.05 2.0E-14 AL163286.2 NT 15548 25961 9.05 2.0E-14 AL163286.2 NT 15548 25961 9.05 2.0E-14 AL163280.2 NT 15549 2.061 4.05 2.0E-14 AL163280.2 NT 15245 2.7983 1.18 2.0E-14 AL163280.2 NT 15245 2.7983 1.14 2.0E-14 AL163280.2 NT 15245 2.7983 1.14 2.0E-14 BE322432.1 EST HUMAN 15240 0.95 2.0E-14 BE3206.2 NT 16229 0.91 2.0E-14 BE3806.1 EST HUMAN <	9635			1.49		AI420786.1	EST HUMAN	teg1cf2x1 NCI_CGAP_Pr28 Homo sepiens cDNA done IMAGE:2094070 3' similar to TR:000519 D00519 FATTY ACID AMDE HYDROLASE
2137B 34522 0.87 3.0E-14 N42165.1 EST HUMAN 23504 38840 1.28 3.0E-14 N426536.1 EST HUMAN 25202 1.68 3.0E-14 AL163286.2 NT 25202 1.68 3.0E-14 AL163286.2 NT 13168 25812 3.71 2.0E-14 AL21736.1 NT 1548 26021 9.05 2.0E-14 AL21736.1 NT 15548 26021 9.05 2.0E-14 AL21736.1 NT 15548 26021 9.05 2.0E-14 AL63303.2 NT 15548 26021 9.05 2.0E-14 AL163303.2 NT 1558 2.15 2.0E-14 AL163303.2 NT 1529 1.14 2.0E-14 AL63209.2 NT 1529 0.95 2.0E-14 AL63209.2 NT 1623 3.0E-0 0.95 2.0E-14 AL63209.1 EST HUMAN 1823 3.0E-0 0.95 2.0E-14 AL63209.1 EST HUMAN 1823 3.0E-0 0.95 2.0E-14 AL63209.1 EST HUMAN <	6744			0.62		AL163248.2	Į	Homo sapiens chronosome 21 segment HS2LOAB
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17597 30220 7.19 3.0E-14 AL782854.1 EST_HUMAN 25282 1.68 3.0E-14 AL78285.2 NT 13168 25812 3.71 2.0E-14 AJ271736.1 NT 13168 25812 3.71 2.0E-14 AJ271736.1 NT 15548 26091 9.05 2.0E-14 AJ271736.1 NT 15548 26091 9.05 2.0E-14 AJ271736.1 NT 15548 27081 1.49 2.0E-14 AJ271736.1 NT 15546 27081 1.19 2.0E-14 AJ271736.1 NT 15256 2718 2.15 2.0E-14 AJ271736.1 NT 1526 2718 2.0E-14 AJ271736.1 NT 15290 0.95 2.0E-14 AJ271736.1 NT 16236 0.95 2.0E-14 AJ271736.1 NT 16236 0.97 2.0E-14 BF380691.1 EST_HUMAN 16239 0.91 2.0E-14 BE30691.1 EST_HUMAN 1637 3.342 2.0E-14 BE30650.1 EST_HUMAN 2084	9914			1.28			EST HUMAN	601511530F1 NIH MGC 71 Homo sapiens cDNA clone IMAGE:3913087 F
26282 1.68 3.0E-14 AL163285.2 NT 13168 25812 3.71 2.0E-14 AL71736.1 NT 13168 25812 3.71 2.0E-14 AL71736.1 NT 15548 26081 9.05 2.0E-14 AL763303.2 NT 15185 2.15 2.0E-14 AL763209.2 NT 15245 2.7883 1.19 2.0E-14 AL763209.2 NT 15256 1.14 2.0E-14 AL763209.2 NT 15245 2.7883 0.95 2.0E-14 AL763209.2 NT 15250 0.95 2.0E-14 AL763209.2 NT 15240 0.95 2.0E-14 AL763209.2 NT 15280 0.95 2.0E-14 BE38061.1 EST HUMAN 1633 3.0E-0 0.8 2.0E-14 BE38061.1 EST HUMAN 16420 3.1236 0.91 2.0E-14 BE38061.1 EST HUMAN 16620 3.124 2.0E-14 BE168761.1 EST HUMAN 20084 33167 22.12 2.0E-14 BE168761.1 EST HUMAN 22468	1201	17597	30220	7.19			EST HIMAN	4945f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu
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1508 1.49 2.0E-14 AW372888.1 EST HUMAN 15245 2.7883 1.19 2.0E-14 AL163209.2 NT 15256 1.14 2.0E-14 AL163209.2 NT 15380 0.95 2.0E-14 PD8848 SWISSPROT 18236 0.95 2.0E-14 BF380681.1 EST HUMAN 1823 3.0E50 0.8 2.0E-14 BF380681.1 EST HUMAN 1831 31236 0.92 2.0E-14 BF380681.1 EST HUMAN 16528 31342 3.42 2.0E-14 BE30055.1 EST HUMAN 16628 0.91 2.0E-14 BE000550.1 EST HUMAN 16679 3.724 0.62 2.0E-14 BE168701.1 EST HUMAN 20084 33167 22.12 2.0E-14 BE168701.1 EST HUMAN 20084 33167 22.12 2.0E-14 BE168701.1 EST HUMAN 22468 35671 0.57 2.0E-14 AV741648.1 EST HUMAN	674		26091	9.05	2.0E-14		Į.	Homo saplens chummenane 21 seconds HQ241402
15185 2.15 2.0E-14 7657529 NT 15246 2.7983 1.19 2.0E-14 AL163209.2 NT 15380 0.95 2.0E-14 PD8548 SWISSPROT 18236 3.0650 0.8 2.0E-14 PD8548 SWISSPROT 18231 31236 0.92 2.0E-14 BF380681.1 EST_HUMAN 16528 31342 3.42 2.0E-14 BF380681.1 EST_HUMAN 16528 31342 3.42 2.0E-14 BF380681.1 EST_HUMAN 16529 31342 3.42 2.0E-14 BE300550.1 EST_HUMAN 1657 32724 0.62 2.0E-14 BE168701.1 EST_HUMAN 20084 33167 22.12 2.0E-14 BE168701.1 EST_HUMAN 22488 35671 0.57 2.0E-14 BE168701.1 EST_HUMAN 22864 3671 0.53 2.0E-14 AV741648.1 EST_HUMAN	2387	15108		1.49	2.0E-14	Γ	EST HUMAN	RCS-BT0377-091299-031-01-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-
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18331 31236 0.92 2.0E-14 AB312351.1 EST_HUMAN 18429 31342 2.0E-14 U01317.1 NT 19528 0.91 2.0E-14 BE000550.1 EST_HUMAN 18977 32724 0.62 2.0E-14 BE000550.1 EST_HUMAN 20084 33167 22.12 2.0E-14 BE158761.1 EST_HUMAN 22084 33168 22.12 2.0E-14 BE158761.1 EST_HUMAN 22468 35671 0.57 2.0E-14 AB78795.1 EST_HUMAN 22984 36181 0.53 2.0E-14 AV741648.1 EST_HUMAN	5437	18236	30050	0.8	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Home sabiens cDNA
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22964 36181 0.53 2.0E-14 AV741648.1 EST HUMAN	9817	22468	35671	0.67	2.0E-14			wr59g10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element:
	3317	22964	36181	0.53	2.0E-14	l	Т	AV741648 GB Homo septens cDNA clone CBEBBF04 5:

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Table 4
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Storn ORF SEQ Expression (Top) Hit Acession (Top) Hit Descriptor Signal BLASTE No. Source	21631 34774 1.78 1.0E-15 4507208 NT Homo sapiens spermidthe synthese (SRM) mRNA	21877 35042 0.87 1.0E-15 Q39575 SWISSPROT DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM		35370 0.94 1.0E-15 AA864653.1 EST_HUMAN		25148 30898 4.72 1.0E-15 A1783944.1 EST HUMAN element;	03168	23595 38841 2.04 9.0E-16 F08889.1 EST HUMAN HSC23F061 normalized trifant brain cDNA Homo sapiens cDNA clone p-2305	37615 1.46 8.0E-16 A1244341.1 EST HUMAN	EST HUMAN	31324 0.71 7.0E-16 4885120 NT	TOGGGG BY DO F	SWISSPROI	33002 1.49 7.0E-16 088807 SWISSPROT	25237 1.08 7.0E-16 T94149.1 EST_HUMAN 19e28c12.r1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:119062.5	8.38 6.0E-16 AW972811.1 EST_HUMAN	20009 1.08 5.0E-18 AJ251154.1 NT		25134 2.17 5.0E-16 AA992178.1 EST HUMAN	OTTO CONTRACTOR OF THE CONTRAC	3/418 3.6 5.0E-16/BF21/368.1 EST HUMAN	14.19 5.0E-16 11418127 NT	1.81 4.0E-16 AB001523.1 NT	27839 1.77 4.0E-18 AW797168.1 EST_HUMAN	27840 1.77 4.0E-16 AW797168.1 EST_HUMAN	28856 3.58 4.0E-16 Q16653 SWISSPROT	29489 5.02 4.0E-16 BE083875.1 EST_HUMAN	29490 5.02 4.0E-16 BE083875.1 EST_HUMAN	33386 46.62 4.0E-16 AL163284.2 NT
											L				7	7				l	1								
Exan D SEQ ID NO:								. :	24291		5 18411	l				37 14867	76 14223		2260	1			- 1					_	2 20278
Probe SEQ ID NO:	8940	9146	1	9032	10720	12722	4469	10915	11606	11696	5615	7244	7	7241	12675	2137	1476	ŝ	7007		11304	/6/21	2233	প্ত	2378	3450	4121	4121	7612

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Top Hit Descriptor	7/82h09.x1 NCL_CGAP_Pr28 Homo septems cDNA clone IMAGE:3303521 3'	CM4-PT0034-180200-506-e01 PT0034 Homo septens cDNA	CM4-PT0034-180200-508-e01 PT0034 Homo sapiens cDNA	Homo sapiens pitultary tumor transforming gene protein (PTTG) gene, complete cds	ef39g11.s1 Soeres_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:1034084 3' similar to	contains OFR, t2 OFR, repetitive element;	CVC-5INC146-U/O/UC-XXX-410 BN0148 Home septens CUNA	Homo saplens SNCA isoform (SNCA) gene, complete cds, alternatively spliced	Homo sapiens CGR8 chemokine receptor (CMRBR8) gene, complete cds	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)	Homo sepiens COR8 chemokine receptor (CMKBR8) gene, complete cds	QV2-PT0012-040400-124-e06 PT0012 Homo sepiens cDNA	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA	1922c11.XI NCI_CGAP_CLL1 Homo sepiens cDNA done IMAGE:2109524.3' similar to contains MER28.12 MFR28 persettine alement:	xq49q12x1 NCI CGAP Ut1 Homo sapiens cDNA clone (IMAGE:2630950 3' similar to contains OFR to OFR	repetitive element;	Homo sapiens pituitary fumor transforming gene protein (PTTG) gene, complete cds	QV0-OT0032-080300-155-d01 OT0032 Hamo saplens cDNA	Homo saplens chromosome 21 segment HS21C080	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA	AV730759 HTF Homo sepiens cDNA done HTFAQB07 5'	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane	Des HINDONS SOOM ON 171 Years and 171 Years	NO IT INVOICES NET TO DO STATE AND THE STATE OF THE STATE	Li repetitive element;	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)	ycodhoa.r1 Stratagene kung (#837210) Homo sapiens cDNA clone IMAGE:79839 5'	yd28604.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:109327 5'
Top Hit Databese Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	1 LN		Т	HOMAN		TN	SWISSPROT	Т	EST HUMAN	Г	TOT HIMAN	1	EST_HUMAN I	Г	EST_HUMAN (TN	EST_HUMAN	EST_HUMAN /	EN L	LN.	<u> </u>	14444	TOWAN TO THE PARTY OF THE PARTY	EST_HUMAN	П	EST_HUMAN V	EST HUMAN
Top Hit Acession No.	2.0E-16 BE858026.1	2.0E-16 AW877214.1		1.0E-16 AF200719.1				7.				1.0E-16 AW875851.1		9 NE-47 A 1392084 1		_	9.0E-17 AF200719.1	8.0E-17 AW880701.1	8.0E-17 AL163280.2	8.0E-17 BE172081.1	8.0E-17 AV730759.1	6753097	7.0E-17 AF216650.1	7 05.47 & 5220843 4	Ī,	0.0E-17 AVI 802000.1	8.0E-17 AW682772.1			
Most Similar (Top) Hit BLAST E Value	20E-16	2.0E-16	20E-16	1.0E-16	07 20 7	1.0E-16/	1.0E-18	1.0E-16	1.0E-16 U45983.1	1.0E-16 Q02779	1.0E-16 U45983.	1.0E-16	9.0E-17	9 OF-47		9.0E-17	9.0E-17	8.0E-17	8.0E-17	8.0E-17	8.0E-17	7.0E-17	7.0E-17	7 05 47	20.00	0.00	8.0E-17	6.0E-17 P20138	5.0E-17 T64110.1	5.0E-17 T81043.1
Expression Signal	0.57	0.81	0.81	1.84	3	29.66	23/	0.75	27.85	3.39	7.15	1.07	2.11	66		4.75	2.47	1.77	0.87	3.7	1.94	3.44	3.3	a a	3	٥	29.1	0.48	2.97	2.09
ORF SEQ ID NO:	33884	34256		25630		3,5,6	2/414	31343		32246		35018	29112							31183				3736E	S S S S S S S S S S S S S S S S S S S	33	31971	36053	25436	33250
Exan SEQ ID NO:	20752	21118	21118	12992		1	14098	18430	19111	19246	1911	21853	16475	19386		20702	22772	13757	16622	25069	19861	14188	18046	10354	1	3	18995	22838	12823	20158
Probe SEQ ID NO:	8028	8425	8425	180		2 2	3	2835	6341	0479	7453	9183	3722	8624		8007	10124	997	3872	5496	7175	1441	5240	8288	3 3	8	6221	10190	412	7486

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Most Similar Top Hit Acession (Top) Hit Acession Database ID NO: Signal BLASTE No. Source Source	34188 1 2.0E-17 AA300640.1	35628 2.81 2.0E-17 BE299888.1 EST HUMAN	35857 3.22 2.0E-17 AL163247.2 NT	2455 35658 3.22 2.0E-17 AL163247.2 NT Homo sapiens chromosome 21 segment HS21C047	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)	36138 0.73 2.0E-17 P98063 SWISSPROT	36139 0.73 2.0E-17 P98063 SWISSPROT	36169 0.49 2.0E-17 AI798902.1 EST HUMAN	36170 0.49 2.0E-17 AI708002.1 EST_HUMAN	26164 3.66 1.0E-17 P08183 SWISSPROT	1.26 1.0E-17 AJ271736.1 NT	27204 2.73 1.0E-17 AL163207.2 NT	27571 2.35 1.0E-17 P02481 SWISSPROT	27795 2.06 1.0E-17 U79410.1	13 10E-17 AE224880 4 NT	7.37 1.0E-17 R09942.1 EST HUMAN	0 60 1 0E-17 AWARRARE 1 ECT LI MAAN	32327 2.04 1.0E-17 A185842.1 EST HIMAN	32328 2.04 1.0E-17 A185642.1 EST HUMAN	32730 0.93 1.0E-17 Q16831 SWISSPROT	182 34324 1.33 1.0E-17 BE062744.1 EST_HUMAN QV0-BT0263-101289-072-407 BT0263 Homo sapiens cDNA	35751 0.88 1.0E-17 AW998538.1 EST_HUMAN	37304 2.09 1.0E-17 Q28824 SWISSPROT	225 37849 2.47 1.0E-17 AA453647 1 IEST HIMAN IG1283081 MARINER TRANSPOSASE .	27932 0.95 9.0E-18 AA174078.1 EST HUMAN	3.31 9.0E-18/A/472167.1 EST HUMAN	29156 1.52 8.0E-18 4758977 NT	25778 16.92 7.0E-18 AW316976.1 EST_HUMAN
SEQ ID ORF SE NO:		22420 356	22455 356	22455 358	22807 360		22926 361			13507 261	14446	14503 272	14840 275	15059 277	16309	16858	19136						24000 3730	24325 3764	l	22060	16518 2915	13140 2577
Probe E. SEQ ID SEQ NO:				9804 2	10159	L	Ш	Ш		733 13		1761 14		2335 16	3554		6366						11394 24	11732 24	2474 15	8398 22	3766 16	339 13

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qoo1e02x1 NCI_CGAP_Kid5 Home saplens cDNA done IMAGE:1915898 3' similer to TR:Q69386 Q69386 OKFZp762F192_r1 762 (synonym: hmel2) Homo septens cDNA clone DKFZp762F192 5' ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 x87b02x1 Sceres_NFL_T_GBC_S1 Homo septens cDNA done IMAGE:26841713' similar to contains Homo sapiens DEAD/H (Asp-Gkt-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX8) mRNA Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) z80b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE.435145 3' PM0-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA th01c08.x1 NCI_CGAP_Lu26 Homo septens cDNA clone IMAGE:2052302 3 802130910F1 NIH_MGC_56 Homo seplens cDNA clone IMAGE:4287674 5' Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14 Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501 AV708136 ADC Homo saplens cDNA clone ADCAMA11 5' Homo saplens NPD008 protein (NPD008) mRNA, complete cds Top Hit Descriptor LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 6) LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6) Homo sepiens phorbolin I protein (PBI) mRNA, complete cds AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5 Homo sapiens Xq pseudoeutosomai region; segment 1/2 Homo sepiens chromosome 21 segment HS21C00 Rattus norvegicus cp151 mRNA, partial cds M.musculus mRNA for TPCR33 protein (UBE2D3) genes, complete ods BETA-2 ADRENERGIC RECEPTOR BETA-2 ADRENERGIC RECEPTOR OLFACTORY RECEPTOR 6 (M50) OLFACTORY RECEPTOR 6 (M50) element MSR1 repetitive element Single Exon Probes Expressed in Brain (LOC63222), mRNA POL/ENV GENE; ZP-X) (RC55) EST_HUMAN EST_HUMAN EST_HUMAN NT EST_HUMAN EST HUMAN EST_HUMAN SWISSPROT SWISSPROT EST HUMAN **EST_HUMAN** EST_HUMAN SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT SWISSPROT Database Top I∷it Source z Ż 눋 눋 4758139 NT F 11432214 NT 눋 LN Top Hit Acession 6.0E-19 AW852930.1 5.0E-19 AW 183725.1 4.0E-19 AB007970.1 4.0E-19 BF697362.1 3.0E-19 AF165620.1 2.0E-19 AI311783.1 2.0E-19 AV731382.1 AF092090.1 2.0E-19 AL163201.2 7.0E-19 AA 705684.1 6.0E-19 AL120817.1 3.0E-19 AV708136.1 3.0E-19 AF223467.1 4.0E-19 AF224069.1 6.0E-19 AJ271735.1 5.0E-19 AJ297699.1 7.0E-19 AI344951. 3.0E-19 X89685.1 5.0E-19|Q00193 3.0E-19 043900 3.0E-19 043900 7.0E-19|P26444 6.0E-19 P34986 6.0E-19 P34986 3.0E-19 Q28997 3.0E-19 Q28997 7.0E-19 3.0E-19 Most Similar (Top) H# BLASTE Value 1.34 1.36 5.36 1.68 1.02 1.04 0.99 0.99 0.9 0.51 9 9.64 23.34 21.33 8. 0.57 1.03 40. Expression Signal 27708 32969 35758 32129 29795 29796 31485 37431 25958 28136 30773 29219 29622 29623 33548 31706 ORF SEQ 30301 36191 29220 29777 28017 ÖΝΩ 16513 17166 24125 18115 19885 22560 17186 17470 18558 17148 18745 SEQ ID 14970 19134 13324 16004 17150 17692 15398 16584 16994 18006 19966 20430 24709 15279 25397 16584 22071 E E 8384 7189 SEQ ID 824 **4**430 11525 3833 4253 7283 5963 198 3781 4747 5767 10324 2889 5311 3833 4413 9359 2565 4411 12036 4253 5198 12264 4987 ĝ

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8394	21087	34223	12.48		7.0E-20 AA557657.1	EST HUMAN	nI46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element:
11714	24308		1.95	7.0E-20	6912633 NT	۲	Homo saplens ribosomal protein L13a (RPL13A), mRNA
3543	16298	28949	3.52	6.0E-20 P39188		SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4239		29605	3.33	6.0E-20	6.0E-20 BE622434.1	EST_HUMAN	601441231F1 NIH MGC 72 Homo sapiers cDNA clone IMAGE:3916231 5
4556	_l		1.18		5.0E-20 AV725123.1	EST_HUMAN	AV725123 HTC Homo sepiens cDNA clone HTCBTA01 5
7015	19707	32763	1.07	5.0E-20	5.0E-20 AF075301.1	EST HUMAN	AF075301 Human fetal liver cDNA library Homo saplens cDNA clone HA0250
7848	20541	33668	5.28	5.0E-20	5.0E-20 W90525.1	EST HUMAN	zh78d08.s1 Scares_feta_liwer_spieen_1NFLS_S1 Home sapiens cDNA cione iMAGE:418191.3' similar to contains MER30,11 MER30 repetitive element:
7846	20541	33669	5.28	5.0E-20	5.0E-20 W90525.1	EST HUMAN	zh/8d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:418191 3' similar to conteins MER30.t1 MER30 nepetitive element
8002	20697	33825	0.7	5.0E-20	5.0E-20 BE165980.1	Г	MR3-H10487-150200-113-001 H10487 Homo sanients aDNA
8734	21428	34672	2.54	5.0E-20		Ţ	Mus musculus MMAN-a mRNA, complete cds
8734	21426	34573	2.54	5.0E-20		LN	Mus musculus MMAN-a mRNA, complete cds
9345			0.94	5.0E-20 O60809		SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
1616		27054	1.34	4.0E-20	4.0E-20 AL163247.2	K	Homo sapiens chromosome 21 segment HS21C047
22	18359		8.0	4.0E-20 Q99880	Q99880	SWISSPROT	HISTONE H2B C (H2B/C)
7828	20521		5.15	4.0E-20	4.0E-20 AI874352.1	EST_HUMAN	t284g03.x1 NCI_CGAP_Ov35 Homo sepiens cDNA clone IMAGE:2293396.3
10398	23042	36259	1.33	4.0E-20	4.0E-20 AW937469.1		QV3-DT0043-090200-080-c04 DT0043 Homo saplens cDNA
2135	14865	27595	1.02	3.0E-20	3.0E-20 U03888.1		Human BXP21 gene
4185	16926	29557	1.29	3.0E-20 P23273		SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4582	17317	29944	1.05	3.0E-20	3.0E-20 AA037616.1		2k36b12.s1 Sceres_pregnent_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895.3' similar to contains L1.12 L1 recetitive element:
8833	21525		2.95	3.0E-20	3.0E-20 D14547.1	N	Human DNA, SINE repeditive element
10219	22867	36078	0.63	3.0E-20	3.0E-20 BF185264.1	EST HUMAN	601843561F1 NIH MGC 54 Homo saplens cDNA clone IMAGE: 4064343 51
10501	23257		1.87	3.0E-20 P11369		SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE)
11496	24097	37408	1.6	3.0E-20	3.0E-20 AI284244.1	EST HUMAN	q70d02.x1 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11496	24097	37409	1.5	3.0E-20	3.0E-20 A(284244.1		q70d02.x1 NCI_CGAP_Kid3 Homo saplens dDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
12051	24569	31118	2.65	3.0E-201	3.0E-20 BE888422.1	П	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5
811	13582		3.12	2.0E-20	2.0E-20 AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo septens cDNA done IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.;

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Defebase Source	Top Hit Descriptor
1089	13847	26505	3.37	2.0E-20	2.0E-20 AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_LIp2 Hamo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224068 ORF2: FUNCTION UNKNOWN.;
1089	13847	26506	3.37	2.0E-20	2.0E-20 AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Hamo sepiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224086 ORF2: FUNCTION UNKNOWN.;
2820	13582		2.38	2.0E-20	2.0E-20 AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_Ut4 Homo septens cDNA clone IMAGE:2781098 3' similar to SW.RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.;
£887	17620	30238	76.4	2.0E-20 Q28983	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4893	17820	30239	4.97	2.0E-20 Q28983	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2009	17786			2.0E-20	5174538 NT	NT	Homo sapiens maiate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
8017	20712	33843	0.81	2.0E-20	2.0E-20 AA309457.1	EST_HUMAN	EST180326 Liver III Homo septens cDNA 6' end
6806	21778	34942		2.0E-20	2.0E-20 D10083.1	NT	Homo saplens RGH1 gene, retrovirus-like element
6806	21778	34043			2.0E-20 D10083.1	NT	Homo sepiens RGH1 gene, retrowns-like element
12426	25141	30895	. 2.03		2.0E-20 H66371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo septens cDNA done C22_391 5'
12815	25057		1.39	2.0E-20	11437152 NT	NT	Homo sapiens heparin-binding growth factor binding protein (HBP17), mRNA
2002	45500	27,000	. 0	10		ŀ	211d08.r1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:712811 5 similar to contains MER19.t2
3	1302	2/468	3.71	1.0E-20	1.0E-20 AA281961.1	EST_HUMAN	MEK'I 9 repetitive element;
4408	17143	28772		1.0E-20	1.0E-20 BF115158.1	EST HUMAN	hr84b08.x1 NCL_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3135155 3' similar to contains L1.t2 L1 repetitive element;
8704	19538	32588	0.75	1.0E-20,	1.0E-20 AF049567.1	EST HUMAN	AF049567 Human activated dendriftic cell mRNA Home sapiens cDNA clone GA05
1906	21750	34909	2.04	1.0E-20	11418491 NT	Į.	Hamo sepiens Autosamel Highly Conserved Protein (AHCP), mRNA
11541	24141	37450	2.62	1.0E-20,	1.0E-20 AF2Z3391.1	Į.	Homo sepiens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial ods, attennatively soliced
							nc60g08.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.t3 L1
12171	24051		1.73	1.05-20	1.0E-20 AA420453.1	EST_HUMAN	repetitive element;
2913	15679		96.0	9.05-21	9.0E-21 AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpt12-8J21
11904	24469		2.52	9.0E-21	9.0E-21 AW898189.1	EST_HUMAN	RC3-NN0068-090600-021-b03 NN0068 Homo septens cDNA
8711	21403		2.15	8.0E-21	8.0E-21 AW674891.1	EST_HUMAN	bb30e02.y1 NIH_MGC_10 Homo septens dDNA done IMAGE:2884714.6' similar to SW:NIAM_HUMAN 095169 NADH-UBKQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR
11528	24128	37432	3.52	8.0E-21	8.0E-21 AA800411.1	EST_HUMAN	ob71f08.s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1336835.3
12084	24679		4.49	8.0E-21 O21330	021330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2061	14793	27518		7.0E-21 P15800	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2061	14703	27519	1.62	7.0E-21 P15800		SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3689	16442	29083	0.69	7.0E-21			Homo saplens chromosome 21 segment HS21C100
4228	16969		5.58	7.0E-21	7.0E-21 AA046502.1	EST_HUMAN	2407.806.r1 Sceres_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE:487858 5'

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Probe SEQ ID NO:	_ თ	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detebase Source	Top Hit Descriptor
6340	19110	32100	62'0		7.0E-21 AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8287		34121	1.53		7.0E-21 AJ277557.1	ΙΝ	Homo sapiens dNT-2 gene for mitochondrial 5(3")-decoynibonucleotidase (dNT-2 gene), exons 1-5
9258		1	10.78		7.0E-21 D14718.1	N	Human chromosomal protein HMG1 related gene
10013		35877	0.86		7.0E-21 AW856922.1	EST_HUMAN	RC0-CT0301-271199-031-F03 CT0301 Homo sepiens cDNA
10594	23288	36525	2.19		7.0E-21 AA723404.1	EST HUMAN	zg73d03.s1 Soeres_fetal_heart_NbHH19W Homo septens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.t3 OFR repetitive element;
11234	23897	37184	1.75		7706668 NT	NT	Homo saplens PTD013 protein (PTD013), mRNA
4083	16827	29454	0.83		6.0E-21 BE408611.1	EST HUMAN	601304125F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3638310 5
9034	21724		9.0	6.0E-21	BE162737.1	EST_HUMAN	PM1+HT0454-080100-002-h09 HT0454 Hamo sepiens cDNA
903	13670		0.7	12-30.3	TN 1502031	M	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4330			2.91	€.0E-21	BE968839.1	EST_HUMAN	601649871F1 NIH_MGC_74 Hamo sapiens cDNA clane IMAGE:3933880 5
4749	17481	30112	5.56	5.0E-21	4885474 NT	N	Homo septens melanoma antigen, family C, 1 (MAGEC1), mRNA
6665	19582		6.0		5.0E-21 AW440864.1	EST_HUMAN	he05e10.x1 NCI_CGAP_CML1 Hamo saplens cDNA clone IMAGE:2918154 3'
7	1005	002.00	Ġ C		7 30203010	100 H	7783411 x1 NCI_CGAP_Pr28 Homo sapiens cDNA done IMAGE:3303573 3' similer to contains OFR.t1
10474	24.3	36240	30.0		3.0E-Z1 DE6303U3.1	EN HUMAN	OTR (Specials General)
76,50	1	2002		0.0L-21 G91G90	00160	SWISSTROI	ZINO TINGEN FROITING GLI (GEF!)
44004	-		4 6	5.0E-Z1 (191690	080180	SWISSPROI	ZINC FINGER PROTEIN GLT1 (GLF1)
006	772677		2.83	5.05-21	5.0E-21 AA393574.1	EST HUMAN	ZI/ZG04,11 Scenes_testis_NHT Hamp septens CDNA done IMAGE:727878 5
1727	14460	27168	1.81	4.05-21	4.0E-21 AA970713.1	EST_HUMAN	0086608.s1 NCL_CGAP_Kid5 Homo saplens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains OFR.t1 OFR repetitive element;
6772	19516		3.27	4.0E-21	4.0E-21 AB019576.1	NT	Rattus nonegicus mRNA for rTIM, complete cds
0896	22332	35527	8.0	4.0E-24	4.0E-27 U91328.1	, F	Human hereditary heemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphete transporter (NPT3) gene, complete cds.
9705	22356	35552	0.7	4.0E-21	4.0E-21 AL163202.2	LN L	Homo sablens chromosome 21 segment HS21C002
1829	14568	27280	49.0	3.0E-21		T HUMAN	2415406.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE 629771 3'
2272	14908	27736	1.24	3.0E-21		Į.	Homo sapiens chromosome 21 segment HS21C001
3078	15843	28485	4.31	3.0E-21		TN	Homo sapiens LGMD2B gene
5412	18211	30919	0.68	3.05-21	3.0E-21 AJ277557.1	TN	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5412	18211	30820	89.0	3.0E-21	3.0E-21 A.1277557 1	Į.	Homo sapiens dNT-2 name for mitro-handrial 5//30-de-warbonir-la-didese (JNT-2 name)
							and appropriate the control intercentage of a control and control

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Table 4
Single Exon Probes Expressed

Single Exon Pression Top Hit Detabase Source	nelanoma antigen family A12 nily A3 (MAGEA3), caltractin	8		yme E2D 3	ne E2D 3								1	24.6	Y .	1				1							9				
Single Exon Pression Top Hit Detabase Source	NAMEA12), melanoma Aq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), catractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHII), and i 15	9939603.X1 Soeres_bests_NHT Hamo sepiens cDNA clone IMAGE:1839460 3' simile SW:MV10_MOUSE P23249 PROTEIN MOV-10.;	(UBEZIA) genes, complete cds	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enz	Homo sapiens mannosidase, beta A, lysosomai (MANBA) gene, and ubiquitin-conjugating enzyn (UBE2D3) genes, complete cds	Homo saplens chromosome 21 segment HS21C049	I Natura norwegicus KIM1B (Rim1B) mRNA, complete cds	Rethie house (u. meterogester) Hike protein (NOT68L) mRNA	Homo sapiens Not56 (D. melenomeden III/a modelia (NOTEGA). Print	AV647246 GLC Hamo sepiens cDNA clane GLCAWC073'	Wants parite Decre Decre Decre many complete cds	Gallie radius Device Victoria in Orivota de CONA	IL2-UM0078-070400-061-F11 UM0078 Homo explain CDNA	gaugotyti NCI_CGAP_CGL1 Homo sapiens cDNA clone IMAGE:2020981 3' similer to contains MER2 MER29 repetitive element;	MERZ9 repetitive element;	q209b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone INA GE: 2020c81 31 similar to contact the contact to the contact the contact the contact to the contact the conta	MR0-8T0659-220200-002-h07 BT0659 Homo saniens c/NA	Human DNA, SINE repetitive element	Human familial Abheimer's disease (STM2) cene complete of	PM4-SN0020-010400-009-h02 SN0020 Homo serviers CNNA	Homo saplens chromosome 21 segment H2910mm	he24f04x1 NCI CGAP Kid12 Home services CONA Alone IMA CE 2027 April 2	InvO4h11.s1 NCI CGAP Pro Home Septemble CDNA clone IMAGE:1219269 3'	MANA STAIR COAR DOOL	q178h06.x1 Soares_NhHMPu_S1 Home septens cONA clone IMAGE:1878299 3' struiter to conteins	RCO-TN0079-150800-025-112 TN0079 Home section 2014	220101.r1 Scares_senescent_fibroblasts_NbHSF Homo septems cDNA done IMAGE:322873 5 similar	PM1-ST0282-261199-001-412 ST0262 Home seniors COMA	Homo seniens protein knose. AND activated	Top Hit Descriptor	bes Expressed in Brain
0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0										HOMAN	1	-	ST_HUMAN	ST_HUMAN	HOMAN		ST HUMAN	누	5	ST_HUMAN	5		EST HUMAN	FST HIMAN	EST HUMAN	EST HUMAN	MAN H FRE	EST_HUMAN	Į.	Top Hit Database Source	gle Exon Pro
	82671.2 NT				6.0E-23 AF224669.1 N				31952	T										7.1					2.0E-22 AI276522.1	-	20E-22 W39456 1	2.0E-22 AW817794.1		Top Hit Acession No.	Sin
Most Similar Top Hit Ac BLAST E No. Value Value 2.0E-22 AW817794 2.0E-22 AW817794 2.0E-22 AW817794 2.0E-22 AW116315.1 2.0E-22 AW116315.1 2.0E-22 AW116315.1 2.0E-22 AW116315.1 2.0E-22 AW116315.1 1.0E-22 AW865517.1 1.0E-22 AW865517.1 1.0E-22 AW805801.1 3.0E-22 AW802801.1 3.0E-22 AW802801.1 3.0E-23 AF198349.1 7.0E-23 AF198349.1 7.0E-23 AF198349.1 6.0E-23 AF224689.1 6.0E-23 AF224689.1 6.0E-23 AF224689.1	6.0E-23 U82671.2	6.0E-23 A		6.0E-23 A	6.0E-23 A	200	8 0E-23 A	6.0E-23 A	7.0E-23	1.05-20.7	7.0F-23.A	8.0E-23	9.0E-23 /	1.0E-22	1.00	L	1.0E-22	1.0E-22	1.0E-22	1.0E-22,	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2.0E-22	2.0E-22	Most Similar (Top) Hit BLAST E Value	
Expression Signal 1.18 1.17 1.18 3.68 3.74 1.17 1.17 1.17 1.17 1.17 1.17 1.17 1	4.09	3.28		1.5	1.5	+	1 39	1.72	4.16	2007	2.55	0.79	98.c	0.79		F	38.	1.37	1.1	1.79	3.71	1.88	0.69	09.0	1.53	3.58	1.18	1.17	4.41	Expression Signal	
ORF SEQ ID NO: 28821 29567 29567 31476 31828 35440 35540 35684 36895 38328 38328 38328 38328 38328 38328 31106 31106	30844	31067		31106	31105		29601		36895	36805	-	28959		36329		36328	01400	20014	20030	27320			35541							S O	
Exan SEQ ID NO: NO: 16941 16941 16942 16975 22347 22347 22347 22347 22347 22347 23346 16163 23097 2309	18160	24663		24540	24540		16976	16184	23042	23842	16065	18312	500	23007		23097	3300	3 20	10002	14605	0	24352	22347	_1				_]			
Probe SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	5358	12192	-	12005	12005		4235	3427	200	10068	3305	3557		10451		10451		78.4	3405	10/1	7/01	10/11	9696	9696	9602	8084	5781	4200	3414	Probe SEQ ID NO:	

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Single Lyong Lypressed in plain	Top Hit Descriptor	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds	Hamo saplens chromosome 21 segment HS21C027	Homo sapiens chromosome 21 segment HS21C027	z/35g09.r1 Sceres, pregnant, uterus, NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.t2 MER29 repetitive element;	Human endogenous retroviral element HC2	Human endogenous retroviral element HC2	T	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	Human metrix Gle protein (MGP) gene, complete cds	TENASCIN-X PREGURSOR (TN-X) (HEXABRACHION-LIKE)	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	qs73f11.x1 NCI_CGAP_Pr28 Home septens cDNA clone IMAGE:1943757 3's similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.	T	Г		Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450	polypeptide 5 (CYP3A5) gene, pertial cds	Homo sapiens chromosome 21 segment HS21C103	Human alcohol dehydrogenase gamma subunit (ADH3) gene, excn 1	Homo sepiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	Homo saplens chromosome 21 segment HS21C052	Homo sapiens chromosome 21 segment HS21C010	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'	-			601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'	ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similer to TR:E19822 E19822 CA PROTEIN ;	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
מום דייטון בו	Top Hit Detabase Source	NT	TN	TN	٦	EST HUMAN	F	LN LN	EST_HUMAN	N	N L	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN		뉟	N	LΝ	⊥N	LN	Ę	EST_HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT
5	Top Hit Acession No.	5.0E-23 AF179818.1	5.0E-23 AF179818.1	3.0E-23 AL163227.2	3.0E-23 AL163227.2	3.0E-23 AA130165.1	3.0E-23 Z70664.1	3.0E-23 Z70664.1	3.0E-23 AW897927.1	2.0E-23 AJ289880.1	2.0E-23 M55270.1	P22105	P22105	2.0E-23 Al201458.1	2.0E-23 BE165980.1	20E-23 H59931.1	2.0E-23 H59931.1		2.0E-23 AF280107.1	20E-23 AL163303.2	2.0E-23 M32658.1	2.0E-23 AF009660.1	1.0E-23 AL163252.2	1.0E-23 AL163210.2	1.0E-23 BE378471.1		1.0E-23 AA448097.1	1.0E-23 BE409643.1	1.0E-23 BE409643.1	9.0E-24 AA663213.1	11422027 NT
	Most Similar (Top) Hit BLAST E Value	5.0E-23	5.0E-23	3.0E-23	3.0E-23	3.0E-23	3.0E-23	3.0E-23	3.0E-23	2.0E-23	20E-23	20E-23 P22105	2.0E-23 P22105	2.0E-23	20E-23	20E-23	2.0E-23		20E-23	20E-23	2.0E-23	2.0E-23	1.0E-23	1.0E-23	1.0E-23		1.0E-23	1.0E-23	1.0E-23	9.0E-24	8.0E-24
	Expression Signal	3.93	3.37	1.34	1.34	4.1	2.96	2.98	1.18	4.25	3.87	1.98	1.98	1.46	3.35	3.65	3.65		4.3	1.21	2.45	2.87	1.1	5.56	3.28		4.6	2.05	2.05	1.84	1.53
f	ORF SEQ ID NO:	31893	31893	32106	32107	33556	35045	35046		26068		28243	28244		-	29346	28347			34579			29857	-			34085	36503	36504		32121
	Exen SEQ ID NO:	25086	25086	19117	19117	20434	21879	21879	22863	13420	15520	15503	15503	16123	16458	16707	16707		20408	21434	24530	24960	17228	17448	19382		20048	23285	23265	13322	19127
	Probe SEQ ID NO:	6145	7337	6347	6347	7738	9148	9148	10215	651	1120	2798	2798	3364	3705	3968	3958		7772	8742	11991	12508	4492	4714	0820		8	10570	10570	539	6357

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						200	
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signet	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
3853	16603		1.49	7.0E-24	7.0E-24 AW837954.1	EST_HUMAN	QV0-DT0047-170200-122-e06 DT0047 Homo sepiens cDNA
5087	17805		96.0	7.0E-24	7.0E-24 AL039498.1	EST_HUMAN	DKFZp434A2311_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 5
							xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
10536			1.33	7.0E-24	7.0E-24 AW303317.1	EST HUMAN	repetitive element,contains MER19.t2 MER19 repetitive element;
990			2.72	6.0E-24		L	Macaca fuscala mRNA for Testis-Specific Protein Y (TSPY), complete cds
818		26256	11.74	6.0E-24	6.0E-24 AL163249.2	INT	Homo sapiens chromosome 21 segment HS210049
3953	16703	. 29342	7.9	5.0E-24	5.0E-24 AJ229043.1	LN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, excns 7-49, and partial cds, alternatively
7857	20321	33430	0.58	5.0E-24	5.0E-24 AF223391.1	LN	display
11595	24194	37513	1.45	5.0E-24	5.0E-24 AW514229.1	EST_HUMAN	hd24b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910413.3' similar to TR:094861 094851 KIAA0750 PROTEIN.;
2040	10600	24582	20 0	10.1	4 05 24 44 5044 78 4	MALATIN TOD	nn31h05.s1 NCI_CGAP_Gas1 Homo sepiens cDNA done IMAGE:1085529 3' similar to SW:POL_MLVRK
8584	L	2444	2000	4.0E-24	4.0E-24 AWA43744 4	EST HIMAN	RCASTOLIANO CANA STATE CONTRACTOR
11133		37078	1.95	4.0E-24	4.0E-24 BE544822.1	EST HUMAN	801078812F1 NIH MGC 12 Homo sapiens cDNA clone IMAGE:348498 5'
12361	L	31062	4.89	4.0E-24		I LN	Homo saplens mRNA for KIAA1093 protein, partial cds
12595		30986	1.77	4.0E-24	18318	TN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
							hh68c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2
8322			2.85	3.0E-24		EST_HUMAN	WER29 repetitive element;
8377			1.57	3.0E-24	_	EST HUMAN	EST374149 MAGE resequences, MAGG Homo sapiens cDNA
9385		35114	4.33	3.0E-24		NT	Homo saplens chromosome 21 segment HS21C052
12438		31045	1.41	3.0E-24	3.0E-24 BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_46 Homo septens cDNA clone IMAGE:4053396 5'
2346		27806	2.72	2.0E-24	2.0E-24 AA167539.1	EST HUMAN	zp11f09.r1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:609161 5'
3778	16531		1.01	2.0E-24	2.0E-24 AW898189.1	EST_HUMAN	RC3-NN0088-090500-021-b03 NN0088 Home sapiens cDNA
7374		33135	0.81	20E-24		L	Mus musculus rho/rac-interacting citron kinase (Crit) mRNA, complete cds
7379		33138	0.65	2.0E-24	3	EST HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPip12-5H13
8639	21331	34476	3.28	20E-24	20E-24 AL119158.1	EST_HUMAN	DKFZp761L1712_r1 781 (syncnym: hamy2) Homo saplens cDNA clone DKFZp781L1712 5'
							yr92b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains
8876			0.98	2.0E-24	2.0E-24 H69214.1	EST_HUMAN	MER28 repetitive element ;
9754		35611	0.94	20E-24		EST_HUMAN	#77409x1 NCI_CGAP_Kid11 Homo septens cDNA done IMAGE:2138008 3'
9754		35612	16.0	2.0E-24	2.0E-24 AI521759.1	EST_HUMAN	ti77809.x1 NCI_CGAP_Kid11 Hamo sepiens cDNA done IMAGE:2138008 3'
11825		37744	1.31	2.0E-24		EST_HUMAN	MR1-SN0063-040500-001-e06 SN0063 Homo sapiens cDNA
11825		37745	1.31	20E-24	2.1	EST HUMAN	MR1-SN0063-040500-001-e06 SN0063 Hamo sapiens cDNA
12281	25377		7.44	2.0E-24	2.0E-24 M28877.1	NT	Human O family dispersed repeat element

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	ORF SEQ Expression (Top) Hit Top Hit Acession (Top) Hit Top Hit Acession (Top) Hit Top Hit Acession (Top) Hit Top Hit Descriptor Signal BLASTE No. Source Source	27131 2.69 1.0E-24 7706340 NT Homo sapiens CGI-127 protein (LOC51646), mRNA	1.63 1.0E-24 AW820194.1 EST_HUMAN QV0-ST0294-100400-185-c10 ST0294 Homo septens cDNA	28433 1.49 1.0E-24 D86423.1 NT Mus musculus mRNA for HGT keratin, partial cds	1.71 1.0E-24 AF143313.1 NT Homo sapiens PTEN (PTEN) gene, exon 2	33214 4.32 1.0E-24 AL163303.2 NT Homo sepiens chromosome 21 segment HS21C103	33404 0.81 1.0E-24 BE144526.1 EST_HUMAN MR0-HT0166-271199-005-d09 HT0166 Homo sepiens cDNA	33687 2.09 1.0E-24 AW901164.1 EST_HUMAN CM0-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA	37619 1.31 9.0E-25 7706707 NT Homo saplens putative secreted protein (SIG11), mRNA		30275 Z.33 7.0E-25 AA483944.1 EST HUMAN MERT repeative element;	33946 6.59 7.0E-25 AA468846.1 EST HUMAN repetitive element;	37822 3.28 7.0E-25 A 583540.1 JEST HUMAN POSIGE PROBABLE 60S RIBOSOMAL PROTEIN 14FA	4.9 6.0E-25 W87623.1 EST_HUMAN	6.0E-25 7305360 NT	1.18 6.0E-25 AW850271.1 EST_HUMAN	2.44 5.0E-25 AW979107.1 EST_HUMAN	2.25 4.0E-25 T98107.1 EST_HUMAN ye56h04.r1 Sogres fetal liver spleen 1NFLS Homo septens cDNA clone IMAGE:121783 5'	4.0E-25 AW887671.1 EST_HUMAN	2.83 4.0E-25 BE170957.1 EST_HUMAN	3.98 3.0E-25 8923321 NT	3.98 3.0E-25 8923321 NT	30190 0.75 3.0E-25 P29622 SWISSPROT KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)	32288 0.6 3.0E-25 AA603590.1 EST HUMAN FINGER PROTEIN 85 (HUMAN);	34065 4.86 3.0E-25/AL163210.2 NT Horno septems chromosome 21 segment HS21C010	1.99 3.0E-25 AA579013.1 EST_HUMAN	2.94 2.0E-25 5032158 NT	27768 6.42 2.0E-25 BE889016.1 EST_HUMAN 601511530F1 NIH_MGC_71 Homo septens cDNA clone IMAGE:3913087 5	3.67 2.0E-25 P17008 SWISSPROT	1.76 2.0E-25 P17008 SWISSPROT	29536 1.76 2.0E-25 P17008 SWISSPROT 40S RIBOSOMAL PROTEIN S16
		27131		28433		33214	33404	33667	37619	2000	302/5	33946	37822		33397	27083	37242	26861			28724	28725	30190	32288	34065	 36886	28749	27.768	27997	29535	29536
ŀ		14435	15388	15786	16978	20123	20206	20540	24294	1007	1/88/	20811	24296	17969	20288	14393	23947	14176	16155	17021	16074	16074	17568	19284	20929	 23635	14075	15031	15259	16907	16907
	Probe Exon SEQ ID SEQ ID NO: NO:	1691			4237	7447 24	7630 2	7845 2	11699 2		4638	8117	11701	L		1847	11286						4837	6518	8235			2306	2835 1		4167

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	AL449573 Homo sapiens Testis (Starrides GS) Homo sapiens cDNA	DKFZp434H0313_r1 434 (synonym: https3) Homo septems o'DNA clone DKFZp424H0313 R'	Human endogenous retrovirus, complete genome	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (S) IBI INIT C)	PM1+HT0454-080100-002-h09 HT0454 Homo sapiens cDNA	245b06.s1 Stratagens NNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu receitifue element.	m54h11.s1 NCI CGAP Kid6 Home sepiens cDNA clone IMAGE-10877403	298004.s.1 Scares fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822.3' similar to contains PTR5.t3 PTR5 repetitive element:	R.rattus RY2G5 mRNA for a potential linand-hinding portein	R. rettus RY265 mRNA for a notamital brand-binding protein	Hamo saptens WAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) peres, complete ods	Human lambda-immunodobulin constant radon complay (garmilina)	Homo sapiens chromosome 21 segment HS21(0)8	Human DNA, SINE repetitive element	Homo saplens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	H.sapiens DNA for endogenous retroviral like element	hd02e12.x1 Source NFL T GBC S1 Homo septens cDNA clone IMAGE-2909366.3"	Homo sapiens chromosome 21 segment HS21C002	2030d08.11 Stratagene neurospithelium NT2RAMI 937234 Homo sepiens cDNA clone IMAGE:548943 5' similar to db:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECY IPSOR ALL 13AAN.	EST36629 MAGE resequences. MAGC Homo seniens chiNA	Homo sactions chromosome 9 dimilianities of the T and sections chromosome 9.	205/204 Stratonena merroacility emploatered in the 1 centrocapus total richard and trypsingen gene families	Homo saplens chromosome 21 cerment HOM 700	Homo sablens chromosome 21 secment HS21Cn02	Homo saplens chromosome 21 segment HS21C010	as38h08.x1 Barsbead eorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' simiter to WP:F49C12.11 CE03371;
Jie Exon Prob	Top Hit Database Source	EST HUMAN	Ι		SWISSPROT	EST_HUMAN		Т		Т						Ę	Į.	EST_HUMAN H		EST HUMAN 8	Г	L	T HUMAN	T			EST_HUMAN W
Sin	Top Hit Acession No.	2.0E-25 AL449573.1	1.0E-25 AL040229.1	35487		1.0E-25 BE162737.1	1.0E-25 AA189080.1	1.0E-25 AA582890.1						22		2		7.0E-28 AW340153.1	7.0E-28 AL163202.2	7.0E-26 AA115895.1	7.0E-26 AW954559.1	6.0E-26 AF028308.1		T			
	Most Similar (Top) Hit BLAST E Value	2.0E-25	1.0E-25	1.0E-25	1.0E-25 Q06055	1.0E-25	1.0E-25	1.0E-25/	1.0E-25/	1.0E-25 X60660.1	1.0E-25 X60660.1	1.0E-25 U93163.1	1.0E-25 X51755.1	9.0E-28	8.0E-26 D14547.1	7.0E-26	7.0E-26 X89211.1	7.0E-28	7.0E-28	7.0E-26	7.0E-26 A	6.0E-26 A	6.0E-28	6.0E-26	6.0E-26	6.0E-26 A	6.0E-26 AI708235.1
	Expression Signal	1.94	1.03	2.02	1.03	2.84	0.79	3.14	4.03	0.75	0.75	3.08	2.18	1.41	1.99	1.72	1.23	2.27	0.62	8.45	1.64	2.04	0.95	0.68	0.68	2.03	3.61
	ORF SEQ ID NO:		25794			30160		32657	33633	35302	35303	36821	-	27945		27003	28351	28508	31257			27689	28752	36301	36302	37900	28572
	Exon SEQ ID NO:		_		- 1	17537	19230	25100	20509	22123	22123	23570	25024	15204	18403	14318	18711	16880	18348	24284	24885	14960	16100	23078	23078	24278	13000
	Probe SEQ ID NO:	9865	355	1226	2435	4808	6472	6696	7814	9446	9446	10890	12788	2487	2907	1571	3000	4138	3551	11980	12547	2222	3341	10432	10432	11683	1154

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Oligio LAVIII I IODOS LAPIOSSOU III DI BIIII	Top Hit Descriptor	MR3-HT0487-150200-113-g01 HT0487 Homo saplens cDNA	DKFZp56802146_r1 588 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp588C2148 5'	CHR220032 Chramosome 22 exan Homo sepiens cDNA dane C22 45 5'	RC8-FN0138-110800-022-A02 FN0138 Homo saplens cDNA	Homo septiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds	nee03c07x1 NCI_CGAP_Pr28 Homo seplens cDNA clone IMAGE:3253844 3' similar to contains OFR.rt	OFR repetitive element;	w/49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA done IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;	Homo sapiens chromosome 21 segment HS21C027	eu87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN):	au87h08.x1 Schneider fetal brain 00004 Homo septens cDNA clone IMAGE.2783295 3' stmller to gb:K00558	TUBULIN ALPHA-1 CHAIN (HUMAN);	PM2-SN0018-220300-002-e07 SN0018 Homo sepiens cDNA	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)	Homo septems WRN (WRN) gene, complete cds	AV732214 HTF Homo sapiens cDNA clone HTFBC806 67	MR4-BT0398-250800-204-d06 BT0398 Homo sepiens cDNA	11751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE FI FAMENT L1	CM1-CT0315-091299-063-d07 CT0315 Hamo seciens cDNA	CM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA	Human endogenous retroviral element HC2	hi51h12xf Soerse, NFL, T_GBC_S1 Homo sepiens cDNA dane IMAGE;2975879 3' similar to TR:076040 078040 ORF2: FUNCTION UNKNOWN.	Human mRNA for KIAA0231 gene, pertiel cds	Homo sapiens Xq pseudoautosomal region; segment 1/2	AV723365 HTB Homo sepiens cDNA clone HTBAHE02 5'	Human nucleolar protein (B23) mRNA, complete cds	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
or From Diff	Top Hit Database Source	EST_HUMAN M	EST_HUMAN D	EST_HUMAN C	Г	Ĭ Č	Г	EST_HUMAN O	EST_HUMAN T	Г	EST HUMAN TO	T	EST_HUMAN T	EST_HUMAN P	SWISSPROT NO	Ĭ	EST_HUMAN A	EST HUMAN MI	JA FST HIMAN RE	Т	EST_HUMAN C		EST HUMAN 07	Г		EST_HUMAN AV		NT TN
	Top Hit Acession No.	1.0E-26 BE165980.1	1.0E-26 AL038487.1	1.0E-26 H55093.1	9.0E-27 BF371227.1	9.0E-27 U93163.1		9.0E-27 BF445558.1	8.0E-27 AI831462.1	8.0E-27 AL163227.2	8.0E-27 AW162737.1		1	8.0E-27 AW864776.1			8.0E-27 AV732214.1			10.1	8.0E-27 AW857579.1		7.0E-27 AW629172.1		7.0E-27 AJ271735.1			
	Most Similar (Top) Hit BLAST E Value	1.0E-26	1.0E-28	1.0E-26	9.0E-27	9.0E-27		9.0E-27	8.0E-27	8.0E-27	8.0E-27		8.0E-27	8.0E-27	8.0E-27 P12236	8.0E-27	8.0E-27	8.0E-27	8 0E-27 N84970 1	8.0E-27	8.0E-27	7.0E-27 Z70664.1	7.0E-27	7.0E-27 D86984.1	7.0E-27	7.0E-27	6.0E-27 M26697.1	6.0E-27 U93163.1
	Expression Signal	3.05	2.21	3.53	1.11	4.14		5.72	3.83	4.33	59.39		59.39	1.37	1.81	0.81	1.02	2.53	2.29	1.51	1.51	1.23	2.25	1.19	4.26	2.12	2.76	1.57
-	ORF SEQ ID NO:								25450		28819		26820	27629	28584	28762	31317		32444	34961	34962						36558	37728
	Exen SEQ ID NO:	19574		25395	20156	22082	l	24454	12837	13327	14142		14142	14893	15943	16107	18404	17957	19429	21797	21797	13444	17750	21448	23341	24843	23320	24394
	Probe SEQ ID NO:	6740	10809	12348	7484	8203		11875	10	544	1395		38	2164	3180	3348	2608	6881	6947	9109	8109	888	2030	8756	10850	12484	10627	11804

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Single Exon Probes Expressed in Brain

hi61h12x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975679 3' similar to TR:076040 076040 ORF2: FUNCTION UNKNOWN.; nk01b10.s1 NCI_CGAP_Pr11 Hamo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886 60S nh08h05.s1 NCI_CGAP_Thy1 Homo sepiens cDNA clone IMAGE:943737 similar to contains L1.t3 L1 NO110.81 NOT_CGAP_Pr11 Hamo septiens aDNA clane IMAGE:1000669 similar to gb:M17886 80S Homo sapiens jun dimerization protein gene, pertial cds; cfos gene, complete cds; and unknown gene Home saplens jun dimerization protein gene, partial cds; cros gene, complete cds; and unknown gene y38e01,r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to 7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08 EST00738 Fetal brain, Stratagene (cat#036206) Homo sapiens cDNA clone HFBCF07 EST00738 Fetal brain, Stratagene (cat/838206) Homo sepiens cDNA clone HFBCF07 7e33f02.x1 NCI_CGAP_Lu24 Homo septems cDNA clane IMAGE:3284283 3' 602121491F1 NIH_MGC_56 Hamo sapiens cDNA clone IMAGE:4278527 5' 602121491F1 NIH_MGC_56 Hamo sapiens cDNA clone IMAGE:4278527 5' 601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5' W28g07x1 NCI_CGAP_Ut1 Homo septens cDNA clone IMAGE:2426268 3 Rattus norvegicus putative four repeat ion channel mRNA, complete cds Rattus norvegicus voltage-gated sodium channel mRNA, complete cds AU121685 MAMMA1 Homo septens cDNA clone MAMMA1000746 5 Top Hit Descriptor QV0-OT0033-070300-152-b10 OT0033 Homo sepiens cDNA R.rettus RYA3 mRNA for a potential ligand-binding protein PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA Mus musculus sperm tail associated protein (Stap), mRNA Rrattus RYA3 mRNA for a potential ligand-binding protein SP:HIMGC_MOUSE Q02891 HOMEOBOX PROTEIN; H.sepiens DNA for endogenous retroviral like element Homo sapiens chromosome 21 segment HS21C046 Homo sapiens chromosome 21 segment HS21C009 Homo sapiens alpha NAC mRNA, complete cds ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); repetitive element; EST_HUMAN **EST HUMAN** EST_HUMAN EST HUMAN EST_HUMAN EST HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN **EST_HUMAN** EST_HUMAN Database Top I Source 눋 눋 ¥ 눋 9910569 NT Top Hit Acession 4.0E-27 AW880859.1 20E-27 AW629172.1 5.0E-27 BF666614.1 2.0E-27 AF111167.2 BF666614.1 4.0E-27 AL163209.2 4.0E-27 AF078779.1 3.0E-27 BE071924.1 2.0E-27 AA565345.1 2.0E-27 AF111167.2 2.0E-27 AU121685.1 2.0E-27 AA565345.1 1.0E-27 AL163246.2 3.0E-27 BE670351.1 2.0E-27 AF054187.1 2.0E-27 AA551527.1 20E-27 AF000368. AA077705. BF035327. 2.0E-27 AI868347. 4.0E-27 X89211.1 2.0E-27 M78590.1 X60658.1 2.0E-27 H02655.1 2.0E-27 X60658.1 20E-27 M78590. 5.0E-27 3.0E-27 3.0E-27 3.0E-27 **Most Similar** BLASTE 世(成) Value 1.65 8. 2.82 1.07 1.54 1.06 6.24 5.12 1.96 0.76 1.28 0.7 4.61 0.63 14.84 10.39 1.96 1.36 0.61 1.65 23 4.1 3.31 1.51 Expression Signal 37525 27489 29604 33475 35996 35258 25487 28633 32353 35997 32421 29385 35782 ORF SEQ 35491 30697 28632 33810 35536 35783 36802 ΘNO 22785 20578 24203 14769 22342 SEQ ID 22785 19407 20535 22296 16979 14625 19340 22583 13212 22084 12868 15981 15981 20684 22583 23555 14625 18068 15872 21839 20351 16755 E E 6645 7840 7883 11604 2034 1888 3218 3218 426 SEO ID 10137 5262 7698 9205 5 3107 7989 9168 9935 11469 10137 6577 10875 9691 9935 4009

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	Top Hit Descriptor	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	hingent of NCI CGAP Kid13 Homo sapiens cONA clone IMAGE:3146256 3' similar to contains MER29.b3	MER29 repetitive element;	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA	HSPD20461 HM3 Homo seplens cDNA clone s4000095C10	HSPD20461 HM3 Homo sepiens cDNA clone s4000095C10	Homo sapiens mRNA for KIAA0454 protein, partial cds	RC8-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA	Human mRNA for KIAA0260 gene, partial cds	Bos teurus letrophilin 3 spiloe varient bbah mRNA, complete cds	hw17c11x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3183188 3' similiar to TR:Q07314 Q0/314 SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ;	AU128260 NT2RP1 Homo septents cDNA clone NT2RP1000443.5	21 Stratacene fetal retina 837202 Homo saplens cDNA clone IMAGE:609602 3	CAST TRIADA OF COMMUNICATION CONTRACTOR CONT	AMAZ-INOTAGOU-SIZ-SUL INOTAGORIO CONTRO	au83h08.x1 Schneider fetat brain 00004 Homo sapiens cDNA cione INACE2/oz911 3 similar to TR:0e0302 060302 KIAA0555 PROTEIN, ;contains element MER22 repetitive element;	AU142750 Y79AA1 Hamo septens cDNA clane Y79AA1000824 5'	Homo sapiens gamme glutamytiransferase-like activity 1 (GGTLA1), mRNA	AV735348 CB Homo sepiens cDNA clone CBFAKA12 5'	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds	as80e03.r1 NCI_CGAP_GC81 Homo espiens cDNA clone IMAGE:825340 5' similar to contains Aku	Topound of the Contract of the	WOLDSOLX INCLUDED A SECOND SOLD SOLD SOLD SOLD SOLD SOLD SOLD SOL	V800/10 r1 Shares placents Nb2HP Homo sabiens cDNA clone IMAGE:146443 5'	AND COAP KIA11 Home series CDNA clone IMAGE 2695504 3' similar to SW 3095 HUMAN	Q08379 GOLGIN-85.;	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA	601300703F1 NIH_MGC_21 Homo septens cDNA clone IMAGE:3636305 5'	qf86f10.x1 Sogres_tests_NHT Homo sepiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
חמסו ו וומעדו פול	Top Hit Detabese Source	<u> </u>		EST_HUMAN N		T_HUMAN	EST_HUMAN I		EST HUMAN F	INT TN	NT	FST HUMAN	T	T	Т	EST_HUMAN	EST HUMAN	HUMAN		HUMAN			NOW TO	NOT TOO	Т	Τ	1 EST HUMAN	Г	T	EST_HUMAN
2	Top Hit Acession No.		1.0E-2/ ADV20090.1	1.0E-27 BE350127.1	M 9005855 NT				1.0E-27 BE079780.1	1.0E-27 D87449.1	1.0E-27 AF111093.1	0 NE. 28 BF348300 1	8.01-20 DLW-00-8.1	9.0E-20 A0120200.1	AA1/40/0.1	9.0E-28 BF377859.1	8.0E-28 AW157571.1	7.0E-28 AU142750.1	11417888 NT	7.0E-28 AV736348.1	6.0E-28 AF016052.1		6.0E-28 AA504562.1	7 000 700 7	5.0E-28 AIGZ1003.1	0.0E-20 IN 81 02.1	4.0E-28 AW195086.1	4505318	4.0E-28 BE409100.1	4.0E-28 A1198941.1
	Most Similar (Top) Hit BLAST E Value	10.4	1.05-27	1.0E-27	1.0E-27	1.0E-27 F30158.1	1.0E-27 F30158.1	1.0E-27	1.0E-27	1.0E-27	1.0E-27	8C 110 0	00.00	8.0E-20	S.UE-ZB	9.0E-28	8.0E-28	7.0E-28	7.0E-28	7.0E-28	8.0E-28	1	6.0E-28	i I	5.05-28	0.0E-20	4.0E-28	4 0F-28	4.0E-28	4.0E-28
-	Expression Signal		40.	0.98	6.26	1.96	1.96	0.98	2.26	2.55	3.51	200	1000	10.0	0.03	4.85	2.48	7.80	3.36	2.78	76.0		2.35	,	4.19	‡.	89	0.78	2.52	1.93
	ORF SEQ ID NO:		20404	_	32215			34346		35463	37825	İ		75/4/				26576								7/977	28087			
	Exan SEQ ID NO:		13741	16806	19217	19515	19515	21200	21575	22275	24299	42064	1087	ŀ		24504	25245					Ι.	24873			16/38	15343			<u> </u>
	Probe SEQ ID NO:		976	4061	6449	67771	6771	8208	8884	9822	11704	107	13/	303	10289	11951	12266	1158	44442	11910	8817		12526		310	3990	2631	207A	3406	7230

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Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tryosimosen gene families	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds	qf86f10.x1 Soeres, bestis, NHT Homo septiens cDNA clone IMAGE:1755019.3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN):	RC3-CT0254-240400-210-f12 CT0254 Homo sepiens cDNA	Homo sapiens metalloprotease-lika, disimbagrin-lika, cystaine-rich protein 2 epsilon (ADAM22) mRNA,	Hamo sapiens T cell receptor beta locus TCRRV7S3A2 to TCRRV42S2 region	MR3-HT0713-280500-013-f09 HT0713 Homo saplens cDNA	Hamo seplens MHC class 1 region	wj98f07.xt NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Aku	PCL PTOSA 22020 040 AG PTOSA LATA AND AND AND AND AND AND AND AND AND AN	Homo sepiens a disintentin and metallicanderines domain 23 (ADAM23) mRNA	Homo sapiens ITGB4 gene for integrin beta 4 subunit earns 3-41	4935b06.x1 NCI_CGAP_Lu5 Homo eaplens oDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element:	hr76c03x1 NCL CGAP (Xd11 Homo septens cDNA clone IMAGE:3134404 3' similar to contains (OR1 b1	LOR1 repetitive element;	801814198F1 NIH_MGC_54 Homo sepiens oDNA clone IMAGE:4048751 5'	Sus scrofia domestica submeedilary apomucin mRNA, complete cds	EST384394 MAGE resequences, MAGL Homo sepiens cDNA	Homo sepiens mennosidese, beta A, Iysosomal (WANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete, cas	W79509.rf Soares Infant brain 1NIB Homo seplens cDNA clone IMAGF.44300 5	Human gene for Ah-receptor, expn 7-9	QV1-BT0821-120900-360-b03 BT0821 Homo sepiens cDNA	Homo sablens similar to ribosomal protein 1.12 (H. saplens) (1.00x3091) mRNA	Homo septens hypothetical protein FLJ10968 (FLJ10968), mRNA	EST178615 HCC cell line (matestasis to liver in mouse) II Homo septens cDNA 5' end similar to similar to	TOTOMICAL L.I.K.	Homo sapiens gamma-giutamytransferase-like activity 1 (GGTLA1), mRNA	Homo saplens gamme-glutemythensferase-like activity 1 (GGTLA1), mRNA
gie Exon Proc	Top Hit Database Source	۲	L	EST HUMAN	EST_HUMAN	TN	L	EST HUMAN	TN	TOT LIMAN	EST HIMAN	-1	NT.	HUMAN		EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	Į.	T HUMAN		EST HUMAN				HOMAN		
	Top Hit Acession No.	4.0E-28 AF029308.1	4.0E-28 AB038241.1	4.0E-28 Al198941.1	4.0E-28 AW854244.1	3.0E-28 AF155382.1				3 0F.28 A 1831004 1		1912		-		2.0E-28 BF224402.1			1	2.0E-28 AF224889.1		-	1.0E-28 BF33236.1	29885	8922793 NT		1.0E-20 AMSUB/44.1	4768431 N1	4758431 NT
	Most Similar (Top) Hit BLAST E Value	4.0E-28	4.0E-28	4.0E-28	4.0E-28	3.0E-28	3.0E-28	3.0E-28	3.0E-28 U53588.1	2 DE 28	2 OF 28	2.06-28	2.0E-28 Y11107.3	2.0E-28		2.0E-28	2.0E-28	2.0E-28	2.0E-28	2.0E-28	2.0E-28 H06378.1	1.0E-28 D38044.1	1.0E-28 B	1.0E-28	1.0E-28	4 ac 10 4	1.05-20.4	1.05-28	1.0E-28
	Expression Signal	3.08	17.24	4.75	1.84	2.88	1.05	1.89	2.09	3.83	10.6	0.86	16.03	2.1		1.33	5.07	0.71	5.54	1.84	222	2.84	2.37	3.2	3.3	7	40.4	8.03	8.73
	ORF SEQ ID NO:			32988		-		34562	36778		25551	28444	28558	27839		31966		33766		37536	-	26895	27685			26044	\$1000 \$5693	30033	32034
	Exon SEQ ID NO:	23457	23608	19915	24734	14009	17770	21418	23533	24751	12913	13783	13897	15199		18989	19012	20638	22137	24212	24741	14208	14945	20455	20612	24848	2017	77 5	77477
	Probe SEQ ID NO:	10774	10928	10850	12312	1288	5051	8726	10853	12344	8	1023	1142	2481		6215	6238	7943	9484	11614	12322	1461	22/17	7759	1161	04.78	0770	0//8	9//8

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Single Expressed in Brain	Most Similar Top Hit Acession (Top) Hit Top Hit Acession (Top) Hit Descriptor Signal BLASTE No. Source	0.63 1.0E-28 AU146356.1 EST_HUMAN AU146356 NT2RM4 Homo sapiens cDNA clone NT2RM4002146 3'	478 7.79 1.0E-28 AA054182.1 EST_HUMAN 2/51c01.r1 Sogres retine N2b4HR Homo sepiens cDNA clone IMAGE:380448 5'	1.88 1.0E-28 AL163247.2 NT	30603 3.18 9.0E-29 AW 663987.1 EST_HUMAN	3.32 8.0E-29 Q00130 SWISSPROT	27034 1.37 7.0E-29 AW968447.1	7.13 7.0E-29 AJ132352.1 NT	25989 16.68 6.0E-20 Alg36748.1 EST HUMAN	8.09 8.0E-29 BE940436.1 EST HUMAN	1.72 6.0E-29 BF568097.1 EST_HUMAN	5.36 5.0E-29 AW887541.1 EST_HUMAN	1.84 4.0E-29 AI752367.1 EST_HUMAN	7.91 4.0E-29 BE164930.1 EST_HUMAN	33797 0.55 4.0E-29 AI678101.1 EST HUMAN	33798 0.55 4.0E-29 AI678101.1 EST HUMAN	34480 6.21 4.0E-29 J04988.1 NT	29751 1.4 3.0E-29 AB042297.1 NT	30054 1.07 3.0E-29 BF333236.1 EST_HUMAN	31564	34465 2.87 3.0E-29 D38044.1 NT	35034 1.69 3.0E-29 AW303317.1 EST HUMAN repetitive element, contains MER19 repetitive element, contains MER19 repetitive element.	1.87 3.0E-29 AL163246.2 NT	0.81 3.0E-29 BE350127.1 EST HUMAN	37185 1.47 3.0E-29 AA403053.1	1.53 3.0E-29 D63882.1 NT	7.53 3.0E-29 AA016177.1 EST_HUMAN	25900 1.72 2.0E-29 AF084869.1 NT
	ORF SEQ ID NO:								25989							33798	34480		30054	31564	34465	36034			37185			25900
	Exen SEQ ID NO:	2 23068	5 24478		3 25346	3 24806	3 14344	25045	13361	24869	3 24717	21322	15989	18704	20674	20874	21336	17118			21324		22109	22509	23898	L	25376	13285
	Probe SEQ ID NO:	10422	11915	12651	12749	12436	1598	12794	581	12201	12286	8630	3226	5919	7979	2797	8644	4381	4684	684	8632	9200	9431	9859	11235	12102	12799	480

Page 257 of 536 Table 4 Single Exon Probes Expressed In Brain

Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo seplens envelope protein RIC-6 (erv) gene, complete cds	wr05d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:015546 015546 HERV-E ENVELOPE GLYCOPROTEIN;	wr85d10.x1 NCI_CGAP_UtI Homo sepiens cDNA done IMAGE.2492563 3' similar to TR:015546 015546 HERV-E ENVELOPE QLYCOPROTEIN;	Homo sapiens chromosome 21 segment HS21C068	os71e04.x1 NCI_CGAP_GC2 Hamo septens cDNA clone IMAGE:1610814 3' similar to contains L1.t2 L1 repetitive element;	wt27g07x1 Soares_NF_T_GBC_S1 Homo sepiens cDNA done IMAGE:2356880 3' similar to contains element MER6 repetitive element;	wt27g07x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA done IMAGE:2356890 3' sfmiller to contains element MFR6 reporting element.	601442206F1 NIH MGC 65 Homo sapiens cDNA clone IMAGE:3846648 5'	Homo sapiens DNA-binding protein (LOC56242), mRNA	Homo sapiens DNA-binding protein (LOC56242), mRNA	Hamo sepiens chromosome 21 segment HS21 C048	Homo sapiens chromosome 21 segment HS21C048	Hamo sapiens chromosome 21 segment HS21C048	Homo saplens chromosome 21 segment HS21C048	601669634F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3952833 5'	Homo sepiens spiiding factor similar to dnaJ (SPF31), mRNA	QV0-OT0032-080300-155-d01 OT0032 Homo sepiens cDNA	RC1-HN0003-220300-021-b04 HN0003 Homo saplens cDNA	R.rettus RYA3 mRNA for a potential ligand-binding protein	nz20c07.s1 NCI_CGAP_GCB1 Homo seplens cDNA done IMAGE:1288332 3' similar to contains MER4.b1 MER4 recettive element:	Homo sapiens zincfron regulated transporter-like (ZRTL), mRNA	HSC23F051 normalized fritent brain cDNA Home septens cDNA clone c-23f05	EST97317 Thymus I Homo saplens cDNA 5' end similar to EST containing O family repeat	PT2.1_13_B11.r tumor2 Homo sepiens oDNA 3'	PM4-BT0724-150400-004-d11 BT0724 Homo sepiens cDNA	Human mRNA for integrin alpha subunit, complete cds	QV0-BN0147-280400-214-f12 BN0147 Homo saplens cDNA	Homo sepiens CTCL tumor entigen se20-10 mRNA, partial cds
gle Exon Probe	Top Hit Database Source	TN	EST_HUMAN H	EST_HUMAN F	Г	EST HUMAN			Т			FA FA				HUMAN		EST_HUMAN C	EST_HUMAN F	NT TN		11422745 NT	Т	EST_HUMAN E	EST_HUMAN P	Г		EST HUMAN C	
Sily	Top Hit Acession No.	2.0E-29 AF084869.1	2.0E-29 Al063604.1	2.0E-29 Al963604.1	~	2.0E-29 Al082459.1	2.0E-29 AI806418.1	2 0F-29 A 1906418 1		87821	10567821 NT	2.0E-29 AL163248.2	2.0E-29 AL163248.2	2.0E-29 AL163248.2	2.0E-29 AL163248.2	2.0E-29 BF025947.1	11425108 NT	1	10.1	1.0E-29 X60658.1	9 0F-30 AA761215 1	11422745	-08688.1	8.0E-30 AA383873.1	8.0E-30 AI557072.1	7.0E-30 BE091133.1		6.0E-30 BE008026.1	
	Most Similar (Top) Hit BLAST E Value	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2 OF-20	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	2.0E-29	1.0E-29	1.0E-29	9 0E-30	9.0E-30	8.0E-30 F08688.1	8.0E-30	8.0E-30 /	7.0E-30	6.0E-30 D25303.1	6.0E-30	6.0E-30/
	Expression Signal	1.72	6.62	6.62	1.63	66:0	1.48	8	1.16	0.63	30.0 30.0	3.61	3.61	3.61	3.61	1.31	2.04	1.73	7.37	0.85	2.97	1.78	8.94	3.72	3.1	1.03	1.73	2.3	0.48
	ORF SEQ ID NO:	25901	26955	26958	29610	31449	31830	31830	33608	34313	34314	35241	35242	32866	36000	36804			34527	36391	32255			33994	34412		27209	28598	36310
	Exen SEQ ID NO:	13265	14270	14270	16987	18527	18885	18865	20571	21169	21169	22070	22070	22787	22787	23567	24063	24100	21383	23164	19254	24531	19001	20862	21275	14251	14508	15948	23083
	Probe SEQ ID NO:	480	1523	1623	4248	5735	6087	7459	7876	8477	8477	90408	9408	10139	10139	10877	11459	11499	8691	10518	6487	11992	6227	8168	8283	1505	1768	3185	10437

Page 258 of 536 Table 4 e Exon Probes Expressed in

Single Exon Probes Expressed in Brain	Top Hit Descriptor	Human lambda-immunoglobulin constant region complex (germline)	tg92g03x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;	Human aconitate hydratase (ACO2) gene, exon 7	Homo sapiens chromosome 21 segment HS21C078	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosome 21 segment HS21C010	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]	CM1-ST0181-091199-035-f08 ST0181 Homo saplens cDNA	qq63c05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to	contains MER29.b2 MER29 repetitive element;	Homo sapiens belomerase reverse transcriptase (TERT) gene, exons 1-6	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	Rettus norvegicus putative four repeat ion channel mRNA, complete cds	ht09g01x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;	Homo saplens mRNA for KIAA1143 protein, partial cds	Homo sapiens mRNA for KIAA1143 protein, partial cds	TRANSCRIPTION FACTOR AP-2	CM0-CT0307-310100-158-h03 CT0307 Home sapiens cDNA	HSC23F051 normalized Infant brain cDNA Homo sapiens cDNA clone c-23f05	RC5+HT0582-110400-013-H08 HT0582 Homo saplens dDNA	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds	UI-H-BI1-efo-o-12-0-UI.s1 NOI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 57	601119860F1 NIH_MCC_17 Homo sapiens cDNA clone IMAGE:3029438 5	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138983 5'	za58c10.r1 Soares retina N2b4HR Homo saplens cDNA clone IMAGE: 363186 5	C18939 Human placenta cUNA (1 Fujiwara) Homo sapens cUNA cione CEN-5/0001 5
le Exon Probe	Top Hit Database Source	H F	EST HUMAN R	Т			F	EST_HUMAN Q	EST_HUMAN C	SWISSPROT E	EST HUMAN C	Г	EST_HUMAN o	F	F	FN	EST HUMAN A			SWISSPROT 1	EST_HUMAN C	\Box		T_HUMAN			EST_HUMAN 6		П	П	EST_HUMAN
Sing	Top Hit Acession No.	6.0E-30 X51755.1	,		2	Γ		4.0E-30 AW937471.1	4.0E-30 AW937471.1	P11369	4.0E-30 AW812488.1		3.0E-30 Al338551.1	_		3.0E-30 AF078779.1	3 0E-30 BE350127 1	3 0F-30 AB032969.1	3.0E-30 AB032989.1	P34056	2.0E-30 AW857315.1	2.0E-30 F08688.1	2.0E-30 BE175877.1	2.0E-30 BE785232.1	2.0E-30 AF114156.1	AW206581.1	2.0E-30 BE298945.1	2.0E-30 BE298945.1	2.0E-30 BF306337.1	2.0E-30 AA019103.1	2.0E-30 C18939.1
•	Most Similar (Top) Hit BLAST E Value	6.0E-30	A 0E-30	5.0E.30	5.0E-30	5.0E-30	5.0E-30	4.0E-30	4.0E-30	4.0E-30 P11369	4.0E-30		3.0E-30	3.0E-30	3.0E-30	3.0E-30	3 DF-30	3 0F-30	3.0E-30	3.0E-30 P34056	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30	2.0E-30
	Expression Signal	3.38	8, 0, 8,	5.44	1.95	2.47	2.47	1.72	1.72	0.63	282		2.11	0.93	0.58	0.48	17	0 53	0.53	248	0.02	3.11	5.31	8	6:39	2.26	1.51	1.51	0.55	0.45	4.66
	ORF SEQ ID NO:		87,5000		-	37047								29128			36200		36343				26896	28165	28331			30008	32435	34208	34265
	Exen SEQ ID NO:	17897	48740	25178	23485	23773	23773	14869	1_			1	13885	1_	20547	L	L			L		13820	14209	١.	1_	L	_	L		21068	21128
	Probe SEQ ID NO:	12769	7000	5150	10807	11103	11103	2139	2139	6758	8803	3	128	3740	7852	8385	40333	40485	10465	11168	88	1062	1462	2720	2820	3769	4727	4727	0000	8375	8435

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	7e37c12x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3284662 3' similar to suv. Duca unitaras	P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR; 7837c12.x1 NCI CQAP Lu24 Home semiens CDNA Alexa MAAGE 2016 (2016)	P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR:	ES 138303/ MAGE resequences, MAGL Homo sepiens cDNA he33406.x1 NCI_CGAP_Kid12 Homo sepiens cDNA clone IMAGE:2875499 3' similer to contains THR b3	Classes Himman alement;	hd30b04x1 Soares, NR_T_GBC_S1 Homo septens cDNA clone GEN-570C01 5*	MENTIL MENT MENT repetitive element;	AND STATE OF THE S	SCT (bus; s1 Stratagene lung (#63/210) Homo sepiens cDNA clone IMAGE:868599 3'	CALVAZZOUT I INCLUDAR DINO HOMO SEDENS CONA CIONE IMAGE: 4157991 5	6018000254 MILL 1100 2011 TITLE COUNTY TO MOUSE IN HOMO Septems CDNA 5° end	CHROMESS Character in Figure 84 piece CLYNA Clark IMAGE: 4040694 5'	VERSON IN SERVICE AND HOUR SQUERS CLINA clone C22, 728 5'	yeo5506.r1 Strategiere liver (#63/72/4) Home septients cDNA clone IMAGE:85570 5/	VISSIOBLIT Scenes Infert brain 1/118 Homo septens CDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN PAR-2 (4 HAAA).	y/99b08.rf Scares infant band 1/18 Homo saplens cDNA clone IMAGE:30666 6' similar to gb:X12963 RAS-	SCOREGIST ROOM LEGISTATION AND SCORE OF THE	Portion to the interface of the first control of the control of th	Homo series a hundred four repeat for channel mRNA, complete cds	Homo septemb characters of the CL20420 (FLJ20420), mRNA	OF FACTORY BECEDADO 45 (Aga)	OLFACTORY RECEDENCE 15 (OR3)	05e11 x1 NCI OSAP 124 L	hw05a11 of NCI COAD 1.24 D	Homo seniens V1-westuler wassers:	Homo sapiens V1-vascular vascynessin receptor AVPR1A gene, promoter region and partial cds Homo sapiens V1-vascular vascynessin receptor AVPR1A gene, promoter region and partial cds
gle Exon Prob	Top Hit Detabase Source		EST HUMAN	\Box	TOWAN TO THE	7	T	T	T LIMIN	Т	Т	Т	Т	Т	Т		T	T	Т			ISSPROT	Т	I	T		
Sin	Top Hit Acession No.		2.0E-30 BEG(1011.1	2.0E-30 BE670617.1	2 0F-30 AW-Am704 1					1.0E-30 BF347728 1									į	23389				17.1			
	Most Similar (Top) Hit BLAST E Value		Z-0E-30	2.0E-30	2.05-30	1.0E-30	1.0F-30	1.0E-30	1.0F-30	1.0E-30	1.0E-30/	1.0E-30	1.0E-30 H55593.1	9.0E-31 T73025.1	9.0E-31 T73025.1	9.0E-31 R18214.1	9.0E-31 R18214.1	9.0E-31 Z38293.1	9.0E-31 A		8.0E-31 A	8.0E-31 P23275	8.0E-31 P23275	7.0E-31 B	7.0E-31 B	7.0E-31 AF208541.1	7.0E-31 AF208541.1
	Expression Signal	, a		3.67	7.37	16.33	2.34	2.62	7.16	2.01	0.94	2.48	6.95	0.81	0.81	0.81	0.81	1.63	0.48	2.41	4.6	1.43	1.43	3.29	3.20	96.0	0.96
	ORF SEQ ID NO:	34388		35741	35839	25729	25942	26122	27675	27921	28461	33399		29135	29136	34053	34054		34369	26473		30213	30214	28123	28124	34130	34131
	Exan SEQ ID NO:	21225		22547	22630	13087	13309	13474	14937	15182	15816	20230	25288	16501	16501	20917	20917	21214	21218	13813	15135	17500	17590	15383	15383	20894	20994
	Probe SEQ ID NO:	8533	00000	7686	9982	280	525	88	2209	2464	30.20	7624	12581	3748	3748	8228	8223	8522	8524	1054	2414	4881	\$8 <u>\$</u>	2874	2674	88	8300

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Table 4
Single Exon Purbes Exonogen

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	ONA DALLA CONTRACTOR OF THE CO	UNISUATIZE I NIH MGC_21 Homo sepiens cDNA clone IMAGE:3638310 5	Trunisan samoda-immunoglobulin constant region complex (germine) Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds. alternatively	Hymn seriors	https://www.capiets.minc.caps.iregion https://www.caps.iregion.com/all-sepiers	WILLY POPULO GENERIT;	OU 145308 / F1 NIH _MGC_72 Homo saplens cDNA clone IMAGE:3918524 5	Homo sapiens type i UNA topoisomerase gene, expr 8	700604.XI NCLCGAP_GC8 Homo septens cDNA clone IMAGE:3443479 3' similar to TR-013537 013537	SIMILAR TO POGO ELEMENT, contains L1.ff L1 repetitive element;	Florito septens Xq pseudosutbsornal region; segment 1/2	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (IIDD OAINAGOG) VALLED	ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)	Hamo saplens chromosome 21 segment HS21C080	Homo sapiens SET domain and mariner transposase fusion cene (SETMAR) mRNA	Homo saplens GGT1 gene, exon 1	Hamo saplens KIAA0569 gene product (KIAA0569), mRNA	Home and the MANAGE LANGE	Homo seniens hardware for a 1400 mRNA Homo seniens hardware for the feature fo	Home captains characters from 11042 (FLJ10842), mRNA	Horse many for foreign 1 segment NSZ1COOG	THE OF THE STATE AND THE STATE OF THE STATE	AGO BIDGO AM DESCRIPTION SEPTEMBER CON CONTRACTOR STATEMENT OF THE SEPTEMBER OF THE SEPTEMB	ANTARARASE NILL MODE SO I	Horne Section - This Action September CDNA clone IMAGE:3862086 5	i ronino equenta intaka for ILAAL protein, pertial cds	MAZADE S.	DKF7-203X 30M es_NFL_I_GBC_ST Hamo sapiens cDNA clone IMAGE:2111672 3	ae88f112. Strategere feder refine 937202 Homo sapiens cDNA clone DKFZp761Q1513 5: THR.tz. THR reporting elements:	ייייי בייייי בייייי בייייי בייייי ביייייי
gle Exon Pro	Top Hit Detabase Source	TOT	ESI DOMAN		I L	FOT CHRISK	EST LINKS	ESI JOMAIN	Į Z		EST HUMAN			SWISSPROT	LN	5	LN.	Ę		-	Z	LN.	T HIMAN	Т	Т		T LIMAN	Т	Т	T	1
Sin	Top Hit Acession No.	RF408811 1	7.0E-31 X51755 1	6.0E-31 AF223301 1	6.0E-31 AF055066 1	6.0E-31 BE350127 1	6 0F-31 BF804488 4								4.0E-31 AL163280.2	88	4.0E-31 AJZ30125.1	11430273 NT	4826853 NT	11420329 NT	3.0E-31 AL163206.2		7	Γ	27.1	Ī	_	Τ	T		1
	Most Similar (Top) Hit BLAST E Value	7.0F-34	7.0E-31	6.0E-31	6.0E-31	6.0E-34	6.0F-31	5.0E-31	6.0E-31	5 OF 34	4.0E.31			4.0E-31 Q10473	100.0	4.0F-61	4.01.01	4.05-31	3.0E-31	3.0E-31	3.0E-31 A	3.0E-31 D14523.1	3.0E-31 A	3.0E-31 P11174	3.0E-31 B	3.0E-31 A	20E-31 A	20E-31 Al393388.1	2.0E-31 AL119245.1	2.0E-31 A	
	Expression Signal	0.94	228	2.88	4.37	99.0	8	3.58	3.58	ς, ξ,	5.18	-		0.91	10.	3	200,	86.	12.23	1.26	2	3.7	0.54	2.04	3.65	1.66	1.37	1.09	1.89	4.01	
	ORF SEQ ID NO:		31044			34062		25640	25641					27240		1			32999	33151		35312	36371	36459			27358	27677	27800	27898	
	SEQ ID	21836	24805	16420	20747	20923	25195	13000	13000	21037	13362		64.0	14550	15407	1	1		19924	20072	20755	22132	23144	23224	23771	25050	14847	14939	15062	15161	
	Probe SEQ ID NO:	9166	12434	3867	8053	8228	12169	187	187	8344	582		100	1810	2012	12205	12457		7239	7303	8	2	10408	10527	1101	12810	198	221	2330	2442	
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Single	

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	UI-H-BI3-akb-f-09-0-UI.st NCI CGAP Sub5 Homo sanians cDNA class IMAGE 27232833 31	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:	Inf08f04.s1 NCI_CGAP_Co10 Home saplens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MFR37 TRANSPOSABILE EL ENENT CONTRACTOR CONTRACT	Homo sanians Ro mytain (RO) THOUS A CONSENSUS SEQUENCE;	AV710948 Ct. Home series CDNA class CT. & N Doz E	Т	Т	601304125F1 NIH MGC 21 Home septeme CNA April 14A OF 2000012 F1	Homo sepiens herokinese il nene promoter rector	HA1110 Human fetal liver cDNA library Home series cONA	Hamo sepiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1	(MAYOR-B.) ganes, complete as	O EACTORY RECEPTOR SCI	OF ACTORY BENEFIT OF ACT	DKF76478335 H Ad / (sepantim: beat) United	DKF7-647B235 of 647 (Sprintipin: night) morns septems clone DKF2p547B235 5	MR3-ST0/20-451200-028 - 08 4 ST0/201 U. Tromo Beptens CLNA clone DKF 255478235 5	Homo saniens minisatellitte cekt repeat regions	Bos trurus xenobiotic/medium-chain fatty ecid: CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, comblete cits	Homo sapiens MAGE-B2 (NAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete acts	qf21h03 x1 NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:1750709 3' similer to TR:Q16595 Q16595 FRATAXIN	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV1SS1, TCRBV15S1, TCRBV16S1P, T	ICRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>	AV723976 HIB Homo sepiens cDNA clone HTBAAG01 57	oz15808.x1 Soares fetal liver soleen 1NFLS S1 Homo saniems cINA close MACE 4675284 21
gie Exuli Pi	Top Hit Database Source	EST HUMAN	EST_HUMAN	FST HIMAN	TN - IN	EST HUMAN	EST HIMAN	EST HUMAN	EST HUMAN	N L	EST HUMAN	H LA	SWISSPROT	TOGGSSIWIS	SWISSPROT	EST HIMAN	EST HIMAN	EST HUMAN	L	N FN	Į	EST HUMAN		IN LOL	ESI HUMAN	EST_HUMAN
	Top Hit Acession No.	2.0E-31 AW444496.1	2.0E-31 BE350127.1	20E-31 AA877764 1	7861535 NT	2.0E-31 AV710948.1			_	2.0E-31 AF148512.1		1 0F.31 [103163 1				26.1		2		1.0E-31 AF128145.1	1.0E-31 U93163.1	1.0E-31 Al086434.1		T	9.0E-32 AV / 239/0.1 ES	2200
	Most Simifar (Top) Hit BLAST E Value	2.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	2.0E-31	1 0E-34	1.0E-31 095371	1.0E-31 095374	1.0E-31 O95374	1.0E-31	1.0E-31	1.0E-31	1.0E-31	1.0E-31	1.0E-31	1.0E-31	i c	1.0E-31 UGGUGT.1	9.0E-32	8.0E-32
	Expression Signal	0.81	3.57	2.05	3.64	0.94	0.94	2.35	2.35	1.58	1.75	11.09	1.35	1.35	1.35	1.15	1.15	3.79	2.2	1	0.51	2.7	Q	0 28	0.66	2.48
	ORF SEQ ID NO:	30624	31334			35661	32002	35829	35830			25456	27092	27093	27094	28952	29953	30640	31782	32948	35995	36757	37752	32312		27530
	Exan SEQ ID NO:	18001	18421		21795		22457	22623	22623	24632	25413	12842	14404	1404	14404	17327	17327	18018	18822	19875	22784	23515	24414	19307	20164	14802
	Probe SEQ ID NO:	5193	5624	8975	9107	9086	9086	9975	2002	1214	12279	13	1658	1658	1668	4592	4592	5210	6042	7189	10136	10833	11830	8542	7492	2070

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	RC2-BN0048-200300-015-604 BN0048 Homo sabiens cDNA	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)	Human chromosome 22 immunoglobulin V(K)I gene, part. with 5' breakpoint between orphon and neighbouring non-emplified region	Im34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994 3' similar to contains MER29.t3 IMER29 repetitive element:	801511530F1 NIH MGC 71 Home seniers cinvla close IMAGE 3043087 E1	Homo saplens PRO1181 mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C046	ws08h12.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2496647 3' similar to contains MER18.b3 MER18 reportitive element:	Homo sepiens AT-binding franscription factor 1 (ATRE1) mRN a	Homo sapiens AT-binding transcription factor 1 (ATRE1) mRNA	RC4-BT0311-141199-011-h06 BT0311 Homo seriens cDNA	Homo sapiens FLH gene, pertial	AV731500 HTF Homo saciens cDNA clone HTFAKC07 6	AV758634 BM Homo sepiens cDNA clone BMFBBH12 51	AV758634 BM Homo sapiens cDNA clone BMFBBH125	295s07.s1 Scares_feta_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:448500 3' similar to contains THR tis THR resettive element:	601156285F1 NIH MGC 21 Homo sabiens cDNA clone IMAGE:3139701 5:	Homo sapiens myeloid/lymphold or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLT4) mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (Ali I TA) mena	601156286F1 NIH MGC 21 Homo canians a DNA alone IMAGE 3420244 ET	Human cell 12-liboxycenese mRNA complete of	H. sapiens mRNA for myosin	H. sepiens mRNA for myosin	27986008.rf Stratagene HeLa cell s3 837216 Homo saniens cDNA clone IMA DE Resuso E	Zn00c08.r1 Stratagene Hella cell s3 937216 Homo septems cDNA close INAACE-563450 FT	b12056t Testis 1 Homo sapiens cONA clone b12056	AV736449 CB Hamo sepiens aDNA dane CBFBIA08 5'
gie Exon Pro	Top Hit Database Source	EST_HUMAN	SWISSPROT	F	EST HUMAN	EST HUMAN	NT.	NT.	EST HUMAN	N IN	Į.	EST HUMAN	LN LN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	FA	Į.	EST HUMAN	N	L	¥	EST HUMAN	EST HUMAN	Π	П
	Top Hit Acession No.	8.0E-32 AW997214.1	P52591	7.0E-32 X17283.1	6.0E-32 AI478104.1	6.0E-32 BE888016,1	5.0E-32 AF116627.1	4.0E-32 AL163246.2	4.0E-32 AI985583.1	11432574 NT	11432574 NT	4.0E-32 BE064410.1		3.0E-32 AV731500,1	3.0E-32 AV758634.1	3.0E-32 AV758634.1	VA777621.1	3.0E-32 BE279086.1	8174574 NT	5174574 NT	3.0E-32 BE279086.1				_	-		
	Most Similar (Top) Hit BLAST E Value	8.0E-32	7.0E-32 P52591	7.0E-32	6.0E-32	6.0E-32	5.0E-32	4.0E-32	4.0E-32	4.0E-32	4.0E-32	4.0E-32	3.0E-32 Y17293.1	3.0E-32/	3.0E-32	3.0E-32/	3.0E-32 AA777621	3.0E-32	3.0E-32	3.0E-32	3.0E-32 E	20E-32 M35418.1	20E-32 Z38133.1	20E-32 Z38133.1	2.0E-32 AA114294	2.0E-32 AA114294	2.0E-32 T18862.1	2.0E-32 AV736449.
	Expression Signel	0.97	0.98	8.19	1.01	1.47	16.78	1.76	0.91	2.94	2.94	1.2	3.7	8.08	8.38	8.38	3.57	3.51	2.97	2.97	2.27	0.81	5.32	5.32	2.28	2.26	2.96	242
	ORF SEQ ID NO:	30887	30161		28180		28431			33266	33267		25872	26870	35135	35136	36788		30586	30587		31902	32155	32156	34003	34004	37784	30961
	Exon SEQ ID NO:	18194	17538	24614	15442	19950	13771	13677	17867	20174	20174	20951	13229	14184	21961	21961	23525	24634	17890	17890	24956	18935	19156	19156	20870	20870	24443	25022
	Probe SEQ ID NO:	6394	4807	12122	2735	7266	1011	940	5148	203	2092	8257	4 43	1437	928	8294	10843	12146	12507	12607	12656	6158	6387	6387	9178	8178	11859	12763

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READ Exam Weat Smile Top-lit T	- 1		T		_		T.		_		_		_																	
Expn NO: OFF SEQ ID NO: Expression Signal Most Smiller Agine Top Hit Agine Top Hit Agine Top Hit Agine Top Hit Agine Top Hit Agine Top Hit Agine 25022 30862 2.42 2.0E-32 AV738449.1 EST_HUMAN 16855 1.0F.3 1.0E-32 AV738449.1 EST_HUMAN 21186 3.4229 8.0B 1.0E-32 AV738449.1 EST_HUMAN 21186 3.4523 8.0B 1.0E-32 AV738449.1 EST_HUMAN 16230 4.6B 8.0E-33 BE327112.1 EST_HUMAN 16230 4.6B 8.0E-33 BE37712.1 EST_HUMAN 16280 2.6E-17 3.14 7.0E-33 AV183280.1 IT 16280 2.6E-18 8.0E-33 BE37712.1 EST_HUMAN IT 1580 3.14 7.0E-33 AV8971307.1 IT IT 1580 3.14 7.0E-33 AV8971307.1 IT IT 24619 3.1020 2.4 7.0E-33 AV8971307.1		Top Hit Descriptor	AV738449 CB Homo septens cDNA clone CBFBIA08 5'	801573207F1 NIH MGC 9 Homo sabiens cDNA clone IMAGE:3834433 5	Homo sapiens chromosome 11open reading frame 9 (C110RF9), mRNA	mw21g02.s1 NCI_CGAP_GCB0 Homo sapiens dDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element:	hw07c05x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:088539 088539 WW DOMAIN BINDING PROTEIN 11.:	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively soliced	302021164F1 NCI CGAP Bm67 Home seriens CONA Agre INTAGE 4158870 F	domo sabiens chromosome 21 segment HS21Ch80	Homo saplens short-chain alcohol dehydrogenese family member (HED27) mRNA	Homo sapiens short-chain stochol dehydrogenese family member (HEP27) mRNA	1209x1 NCI_CGAP_Utz Homo sapiens cDNA done IMAGE:2178809 3' similar to contains OFR.11 OFR	Speciality adminity	S7383396 MAGE resonuences, MAGI Homo seniore, CNA	Human hLRP mRNA for feukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 5.1.3.48)	302021164F1 NCI CGAP BINGT Homo sepiens abna done IMAGE:4159870 5	5ST383657 MAGE resequences, MAGL Homo sepiens cDNA	1016h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 epetitive element:	damo sapiens chromosome 21 segment H321C085	-ISPD21201 HM3 Homo saplens cDNA clane s4000107H06	4SPD21201 HM3 Homo saplens cDNA clane e4000107H06	furnen giyceraidehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds	tomo saplens similar to RAD23 (S. cerevisiae) homolog B (H. saplens) (I, CC63777) mRNA	Aus musculus SRY-box containing gene 6 (Sax6), mRNA	ilus musculus SRY-box containing gene 6 (SaxB), mRNA	2V1-FT0169-100700-271-a02 FT0169 Homo saplens cDNA	tomo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA	komo sapiens spermidine synthase (SRM) mRNA	domo sapiens spermidine synthase (SRM) mRNA
Exon NO: ORF SEQ Signel 1D NO: Expression Signel Signel 1D NO: Most Smiler Crop Hit Value Top Hit Acession Place Availer Most Smiler Place Availer Top Hit Acession Value 25022 30662 2.42 2.0E-32 ER7432841 16855 1.0F-32 BE743289.1 11439789 21186 34328 8.08 1.0E-32 BR742289.1 21379 34523 7.02 1.0E-32 BR742289.1 22387 25518 4.05 8.0E-33 BF327112.1 12887 25518 4.05 8.0E-33 BR327112.1 12887 25518 4.05 8.0E-33 BR327112.1 12887 25518 3.14 7.0E-33 BR327112.1 12887 25518 3.14 7.0E-33 AV730066.1 15888 27622 2.2 0.0E-33 AV730066.1 15889 3.7162 1.34 7.0E-33 AV890115.1 23419 31050 4.34 7.0E-33 AA601416.1 21589 31721 0.96		Top Hit Database Source	EST HUMAN	EST_HUMAN	LN	EST_HUMAN	EST HUMAN		HUMAN		F	L'N		T	Т		T HUMAN	Π			Г	HUMAN					T_HUMAN			
Exen NO: ORF SEQ ID NO: Expression Signal Mos Mos 25022 30862 2.42 15865 1.67 19437 32453 7.02 2186 34329 8.08 2187 34523 4.68 19096 4.05 2.22 23392 25517 3.14 12887 25517 3.14 12887 25517 3.14 12887 25517 3.14 12887 25517 3.14 12887 25517 3.14 12887 25517 3.14 12887 25517 3.14 12887 25517 3.14 15888 27622 2.29 16385 8.36 8.36 16386 2.41 3.14 16588 3.14 3.16 224619 31720 0.94 18758 3431 9.33 21770 34438 3.09 2		Top Hit Acession No.	-	_	139789	AA720574.1	_	_			5031736	5031736			-			L						11429198	6099549	6755809		1884	4507208[h	4507208 N
Expn NO: ORF SEQ ID NO: Express Signs 25022 30862 Signs 25022 30862 Signs 16856 19437 32453 19096 21186 34523 23392 25517 12887 25517 12887 25517 12887 25517 12887 25517 12887 25518 12887 25518 12888 27622 15598 27622 15598 27624 15698 37162 22419 31090 16473 3438 2170 34315 2170 34315 2170 34316 22569 35754 14612 14612 14623 27337 14628 27338		Most Similer (Top) Hit BLAST E Value	20E-32	1.0E-32	1.0E-32	1.0E-32	9.0E-33	9.0E-33	9.0E-33	9.0E-33	7.0E-33	7.0E-33	7 05 99	7 OF 33 /	7.0E-33/	7.0E-33	7.0E-33	7.0E-33	7.0E-33	6.0E-33 /	6.0E-33 F	6.0E-33 F	€.0E-33	8.0E-33	6.0E-33	6.0E-33		5.0E-33	5.0E-33	5.0E-33
Exan SEQ 1D ORI 25022		_	2.42	1.67	7.02	8.08	4.58	4.05	1.95	5.22	3.14	3.14	2,00	8 45	9.3	1.56	2.41	1.93	4.34	0.94	96.0	96.0	9.33	3.09	1.12	1.12	1.46	1.19	1.43	1.43
		ORF SEQ ID NO:	30862		32453	34329			34623		25517	25518	27822	7	-		36680	37162	31090		31720	31721	34315	34438	35754	35755			27337	27338
Probe SEQ ID NO: NO: NO: 3090 6055 6055 6887 10701 10732 11213 112		Ø						19096	21379	23392	12887	12887	14888	16365	15998	21537	23419	23876	24619	16473	18758	18758	21170	21295	22569	22559	14512	14612	14628	14628
		Probe SEQ ID NO:	12763	3090	6055	8494	3474	6326	8687	10701	58	83	2158	2656	3236	8845	10732	11213	12127	3720	5976	5978	8478	8803	9910	9910	1770	1874	1891	1891

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo sapiens calcium/calmodulin-denandant profain Unices IV / CAMAA - DAVA	Homo sepiens F-box profein FRI 4 (FRI 4) mRNA American Action	Homo saplens protein kinasa C beta-II tone (PRKCB1) mRNA commissional	Human dystrochin (DMD) none agains 7.8 and 0. and analysis of the control of the	QV3-BN0047-230200-102-b03 BN0047 Homo seniene c.DNA	Human dystrochin (DMD) cene econs 7. 8 and 6 and ecological colo	we8806x1 NCI CGAP Kid11 Home sapiens cDNA clone IMAGE-2462410 2	Homo sapiens X-linked anhidaotitic ectodermal dysplasia protein gene (EDA), excn 2 and flanking repeat	regions	AV727809 HTC Hamo septens aDNA clone HTCCNC12 5	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo eaplens hypothetical protein FLJ10900 (FLJ10900), mRNA	MR4-BT0399-200100-001-h03 BT0399 Homo sapiens cDNA	yd15e05.r1 Soeres fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE 108320 F	yd15e05.r1 Sceres fetal liver spleen 1NFLS Homo saciens cDNA clane IMAGE 108320 5	M14c10.r1 Source placenta ND2HP Homo saplens cONA Home IMA GE - 148772 5.	Human G2 protein mRNA, partial cds	Human G2 protein mRNA, pertial cds	Mus musculus DAB/2J hair-specific (hacl-1) gene	Homo sapiens Npw38-binding protein Npw8P (LOC5/1729) mRNA	Human splicing factor SRp66-1 (SRp-66) mRNA, complete cds	Rattus novegicus putative four repeat fon channel mRNA, complete cds	Homo septens mRNA for KIAA1435 protein, partial cds	Homo explens chromosome 21 segment HS21 Coop	#84c06.xt NCI CGAP Pr28 Homo septems CDNA class IMACE: 224c4c4.2	8K35c01.81 Sogres feets NHT Home seniors of the PAGE-1407008 of	601874950F1 NIH MGC 54 Homo september CDNA Alone IMAGE 4402312 5	Human id germine H-chain D-region genes nartiel ode	901458531F1 NIH MGC 66 Home septents of the IMAGE 3862018 A	wd35g08.xf Source_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2330170 3' similar to contains MER29.t2 MER29 repetitive element:	
gie Exon Pro	Top Hit Database Source	F	N.	¥	TN	μ	EST HUMAN		EST HUMAN			EST HUMAN	Z	۲.	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	LN FN	NT	Z	NT	NT	ΙΝ	LN FN	EST HUMAN	EST HUMAN	EST HUMAN	L	EST_HUMAN	EST HUMAN	
	Top Hit Acession No.	1.0E-33 AF003528.1	4502556 NT	1.0E-33 AF199420.1		1.0E-33 U60822.1	8.1	1.0E-33 U60822.1	+	4 AF 93 A FAASEAN 4		1.0E-33 AV /2/809.1		22751	2.1			7.0E-34 H12866.1			6.0E-34 U03686.1	TN06500 NT		1		5.0E-34 AL163209.2	4.0E-34 Al804867.1		_		5		
	Most Similar (Top) Hit BLAST E Value	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	1.0E-33	7 10 80	30.7	1.0E-33	8.0E-34	8.0E-34	8.05-34	7.0E-34	7.0E-34	7.0E-34	6.0E-34	6.0E-34	6.0E-34	5.0E-34	6.0E-34	5.0E-34	5.0E-34	5.0E-34/	4.0E-34/	4.0E-34	4.0E-34	3.0E-34 M37277.1	3.0E-34 E	2.0E-34	
	Expression Signal	1.16	2.46	93.0	1.04	0.84	1.83	3.32	221	207		4. 4.	5 6	96.0	80.0	2.27	0.56	3.05	2.3	2.3	2.13	2.9	3.61	1.37	2.24	1.79	1.64	0.64	1.28	0.78	3.14	1.16	
	ORF SEQ ID NO:		30485	31198	23067		37251	37581			31005	200	07001	27631	20400	26858	26858		25884	25885	31107		30328	34607	36482		27449	31488	34760	31886		34687	
	Exan SEQ ID NO:	12835	17873	18299		25432		24259	24790	12835	24014	25034	4 4007	70353	3	14173	14173	24962	13243	13243	24544	14811	17725	21457	23248	2882	14727	18561	21627	18916	23770	21541	
	Probe SEQ ID NO:	8	5156	5501	7307	9920	11292	11663	12407	12570	12002	12780	2468	8 8 2		8	88	12191	88	₹	12011	1873	2002	8/62	19550	11210	<u>ğ</u>	5773	9838	9138	11100	8850	

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Table 4
Single Exon Probes Expressed in Brain

Most Similar Top Hit Acession Top Hit Descriptor Top Hit Descriptor Source Value Value Source Value Value	wd35g06.x1 Soeres NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2330170 3' similer to contains 1.18 2.0E-34 Ai678101.1 EST_HUMAN MER29.t2 MER29 repetitive element;	1.34 2.0E-34 P51805 SWISSPROT	1.34 2.0E-34 P51805 SWISSPROT	928 6.53 1.0E-34 P12236 SWISSPROT NUCLEOTIDE TRANSLOCATOR 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3)	137 10F-34 AFD03528 1 NT	0.97 1.0E-34 AY009397.1 NT	0.97 1.0E-34 AYD08397.1 NT	3.44 1.0E-34 BE071414.1 EST_HUMAN	2.05 1.0E-34 BE874052.1 EST_HUMAN	2.05 1.0E-34 BE874052.1 EST_HUMAN	0.45 1.0E-34 P23266 SWISSPROT	7.1 1.0E-34 AL036635.1 EST_HUMAN	1.39 1.0E-34 BE781790.1 EST_HUMAN	1.39 1.0E-34 BE781780.1 EST_HUMAN	1.82 1.0E-34 11439599 NT	1.0E-34 AAB07097.1 EST_HUMAN TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);	4.22 1.0E-34 AL163210.2 NT	1.2 9.0E-35 AW663302.1 EST_HUMAN		171 3.43 8.0E-36 BF589937.1 EST_HUMAN O75912 DIACYLGLYCEROL KINASE IOTA.;	11111 1 102 1 1 10000000 N 20 80 80 80 80 80 80 80 80 80 80 80 80 80	2.69 8.0E-35 BF183195.1	2.42 8.0E-36 BE378480.1 EST HUMAN	1 EST HUMAN	2.05 7.0E-35 11425417 NT	1.83 8.0E-36 AA767115.1 EST_HUMAN	2.09 6.0E-35 6005975 NT	0.84 6.0E-35 AW 297191.1 EST_HUMAN
	1.18	1.34	1.34	6.53	132	0.97	76.0	3.44	2.05	2.05	0.45	7.1	1.39	1.39	1.82	39.1	422	1.2	7.71	3,43	27.	2.88	2.42	3.9%	205	1.83	2.09	0.84
Exam ORF SEQ SEQ ID ID NO: NO:	21541 34688		23783 37058	14241 26928	16416 29055						_			23805 37084	23820 37100	25350		16389 29029	13029	14472 27171	27716 27777		23283 36522	24611	19162 32163		14696 Z7409	16775 29406
Probe Ex SEQ ID SEC NO: N	8850 21	L.	11113 23	1494 14	3683 16	L					_		\perp		11153 23	12372 25			218 13	1730 14	1730	1	10589 23	12119 24	63 93 19			4030 16

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Top Hit Acession Top Hit Descriptor No. Source	6005921 NT Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA	232.1 NT H.sapiens mRNA for novel T-cell activation protein	TN	02364.1 NT Human mRNA for KIAA0386 gene, partial cds	37786.1 NT Homo sapiens mRNA for KIAA1365 protein, partial cds	392.1 NT H.sapiens immunoglobulin kappa light chain variable region 1.14	07866.2 NT Homo sapiens mRNA for KIAA0406 protein, partial cds	6912639 NT Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA	Homo sapiens cit. Kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete	ods; metazin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial 23288 1 NT lods	FST HUMAN	EST HUMAN	EST HUMAN	1 EST HUMAN	1 EST HUMAN	EST HUMAN	ļ.	htt09g01.xt NCL_CGAP_Ktd13 Homo sepiens cDNA clone IMAGE:3146256 3' similar to contains MER29 to S0127 1 FST_H IMAN MER29 recettive element:	EST HUMAN	EST HUMAN	1 EST HUMAN	N N	7n25a09.x1 NCI_CGAP_Lu24 Homo sepiens cDNA done IMAGE:3565361 3' similer to TR:Q9QZH7 33100.1 EST_HUMAN Q9QZH7 F-BOX PROTEIN FBL2.;	7n25e09 x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3565361 3' similer to TR:09QZH7
Top Hit Acess No.	9009	6.0E-35 X94232.1	6.0E-35 X94232.1	6.0E-35 AB002364.1	6.0E-35 AB037786.1	5.0E-35 X63392.1	5.0E-35 AB007866.2	6912		5.0F-35 AF023268 1	5.0F-35 BER90992.1	5.0E-35 A 208765.1	5.0E-35 AI208765.1	5.0E-35 AA001786.1	4.0E-35 BE257907.1	4.0E-35 H91193.1	4.0E-35 AF003528.1	4.0E-35 BE350127.1	4.0E-35 AL046596.1	4.0E-35 AW303317.1	3.0E-35 BE268182.1	3.0E-35 AF224492.1	3.0E-35 BF433100.1	3.0E-35 BF433100.1
Most Similer (Top) Hit BLAST E Value	6.0E-35	6.0E-35	6.0E-35	6.0E-35	6.0E-35	5.0E-35	5.0E-35	5.0E-35		5.0E-35	5.0F-35	5.0E-35	5.0E-35	5.0E-35	4.0E-35	4.0E-35	4.0E-35	4.0E-35	4.0E-35	4.0E-35	3.0E-35	3.0E-35,	3.0E-35	3.0E-35
Expression Signal	3.84	0.93	0.93	98'0	3.17	1.36	1.07	1.7		17	3 99	2.35	2.35	2.46	16.86	4.87	0.72	181	8.88	1.38	7.78	1.5	31.47	31.47
ORF SEQ ID NO:	33615	34445	34446	35403	32928	27146	28232	28424		29746		33936	33937		26845	27265			34248	37646	27008		30690	30691
Exan SEQ ID NO:	20493		21302		22454		15492	15775		17413	20778	20803	20803	23798	14161	14551	17485	19796	21109	24322	14320	15055	18062	18062
Probe SEQ ID NO:	27798	8610	8610	9565	8803	1704	2787	3008		4378	8084	8100	8100	11130	1413	1811	4753	7108	8418	11720	1573	2330	5256	5258

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	partial cds, alternatively	** SW:POL1_HUMAN	5' similar to						ct=TCBA Homo saplens	ct=TCBA Homo saplens	70 6'													5' similar to		12.1	
Top Hit Descriptor	Homo saplens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	WT03e05.X1 NCI_CGAP_GC6 Homo sepiens cDNA clone IMACE:2480432 3' similar to SW:POL1_HUMAN P10286 RETROVIRUS-RELATED POL POLYPROTEIN ICONTAINS: REVERSE TRANSCRIPTASE:	K6832F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT	A971F Heart Homo sablens cDNA done A971	Homo sepiens mRNA for Gab2, complete cots	Homo sapiens Grb2-essocieted binder 2 (KIAA0571), mRNA	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	Homo sepiens mRNA for KIAA0895 protein, partiel cds	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukernia Baylor-HGSC project≂TCBA Homo saplens	WOT 9812 IT Some field live sales 1NFIS Home seriens CONA close MARCE 274070 F	OV0-8T0701-210400-198-b04 RT0701 Homo seniens cDNA	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA	CM2-MT0125-280700-297-G02 MT0125 Homo septens cDNA	AV723718 HTB Homo saplens cDNA clone HTBAYA10 5"	AV723718 HTB Hamo sepiens aDNA done HTBAYA10 5"	H.seplens PROS-27 mRNA	QV0-BT0701-210400-159-b04 BT0701 Hamo saplens cDNA	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	Homo sapiens Grb2-essociated binder 2 (KIAA0571), mRNA	601496774F1 NIH_MGC_70 Homo sepiens cDNA clane IMAGE:3898989 51	801496774F1 NIH_MGC_70 Homo sepiens cDNA clone IMAGE:3898699 5'	Homo sepiens chramosome 21 segment HS21C010	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE EI EMENT	first Entire Control of the Specific CONA Breat Home control CONA close CONA	finite to regional genomic DNA specific collection by home seciens above critical finite (6 Regional genomic DNA specific above the part Home seciens above classical specific above the part Home seciens above classical specific above the part of the part home seciens above the part of the part	IL 2-ST0162-131099-006-d12 ST0162 Homo seplens cDNA
Top Hit Databese Source	. T N	EST HUMAN	EST HUMAN	EST HUMAN	Į.	Į,	LN LN	N F	EST_HUMAN	TOTAL TOTAL	EST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	F	۲	EST_HUMAN	EST_HUMAN	E	NAM H TOT	EST HIMAN	EST HUMAN	EST_HUMAN
Top Hit Acession No.	3.0E-35 AF223391.1	3.0E-35 AW 003063.1	2.0E-35 N88965.1	2.0E-35 T11909.1	2.0E-35 AB018413.1	0912459 NT	6912459 NT	2.0E-35 AB020702.1	2.0E-35 BE247575.1	0E047E7E 4	2.0E-35 H49239 1	2.0E-35 BF332417.1	2.0E-35 BE832636.1	2.0E-35 BE832636.1	2.0E-35 AV723718.1	2.0E-35 AV723718.1		2.0E-35 BF332417.1	6912459 NT	6912459 NT	2.0E-35 BE904978.1	2.0E-35 BE904978.1	2.0E-35 AL163210.2	188065.1	-		
Most Similar (Top) Hit BLAST E Value	3.0E-35	3.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	20 20 2	20F-35	2.0E-35	2.0E-35	2.0E-35	20E-35	2.0E-35	2.0E-35 X59417.1	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2.0E-35	2 0F-35 N88965 1	1 0F-35/	1.0E-35/	1.0E-35/
Expression Signal	1.42	1.12	1.88	1.55	5.73	1.12	1.12	96.0	0.78	82.0	257	27	0.95	0.95	0.45	0.45	2.24	1.28	1.72	1.72	1.38	1.36	5.96	88	6.81	6.84	19.5
ORF SEQ ID NO:		36839	25567	26582	27683	28714	28715		29279	20280	7787	31192	32749	32750	33563	33594	36626	31192	28714	28715	31120	31121		26567	25498	25497	26165
Exem SEQ ID NO:	22050	22.22	15535	13019	14943			16300	16640	10040	17356	18294	19696	19696	20471	20471	23388	18204	16066	16066	24577	24577	24900	15535	12874	12874	13509
Probe SEQ ID NO:	8388	10074	106	1165	2215	9088	3306	3545	0668	JOBE	4621	5495	7007	7004	9///	7775	10697	11817	11889	11889	12062	12062	12572	12689	15	45	735

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Single Exon Plobes Expressed in Drain	Top Hit Descriptor	IL 2-ST0162-131099-006-412 ST0162 Homo sepiens cDNA	yd83a01.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:115752 5' similar to SP:A44252 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;	Homo sapiens hypothetical protein (LOC51233), mRNA	ht09g01.x1 NCI_CGAP_Kid13 Homo sepiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3 MER29 repetitive element ;	ht09g01.x1 NCI_CGAP_Kid13 Hamo septens cDNA clone IMAGE:3146256 3' similar to contains MErX2.03 MER29 repetitive element :	Homo sapiens transcription elongation factor B (Sill), polypeptide 1-like (TCEB1L) mRNA	AV650422 GLC Homo sepiens cDNA clane GLCCEF08 3"	AV650422 GLC Homo sepiens cDNA clone GLCCEF08 3'	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA	Homo sepiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mKNA	Homo sepiens mRNA for KIAA1279 protein, partial cds	Homo sepiens KIAA0645 gene product (KIAA0645), mRINA	AU158595 PLACE3 Homo septems oDNA done PLACE3000382 3	AU158595 PLACE3 Homo sepiens cDNA done PLACE3000382 3'	nae06d08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA done IMAGE:3254051 3' similar to 1R:031341 031341 BETA-GALACTOSIDASE;	naa06d06.x1 NCI_CGAP_Prz8 Homo sapiens cDNA done IMAGE:3254051 3' similar to TR:O31341	031341 BETA-GALACTOSIDASE;	Homo sapiens mRNA for KIAA1057 protein, partial cds	Homo saplens mRNA for KIAA1057 protein, partial cds	promma-7.001.r bytumor Homo sapiens cDNA 5'	Homo sapiens fibulin 1 (FBLN1), mRNA	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'	EST54838 Hippocempus II Homo sepiens cDNA 5' end simifar to simifar to endogenous retrovirus 9, 5' LTR	CM1-CT0315-091299-063-d07 CT0315 Hamo saplens aDNA	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA	Human carcinoembryonio antigen gene family member 12 (CGM12) gene, exons L and L/N	Human carcinoembrychic antigen gene family member 12 (CCIM12) gene, exons L and LIN
IO EXON PIOD	Top Hit Database Source	EST_HUMAN	T HUMAN		EST_HUMAN	HUMAN		HUMAN	EST_HUMAN						EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	L		EST_HUMAN	LN		EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT.	LN L
Sing	Top Hit Acession No.	1.0E-35 AW389473.1		7705994 NT	1.0E-35 BE350127.1	1.0E-35 BE350127.1 EST_	0000000	1.0E-35 AV650422.1	1.0E-35 AV650422.1	7856905 NT	7858905 NT	6236	1.0E-35 AB033105.1	11418002 NT	1.0E-35 AU158595.1	1.0E-35 AU158595.1	1.0E-35 BF589594.1		1.0E-35 BF589594.1	1.0E-35 AB028980.1		1.0E-35 AI525119.1	11418274 NT	11418110 NT	1.0E-35 BE792832.1	8.0E-36 AA348480.1	7.0E-36 AW857579.1	4557498 NT	J06672.1	106872.1
	Most Similar (Top) Hit BLAST E Value	1.0E-35 A	1.0E-35 T87947.1	1.0E-35	1.0E-35	1.0E-35 E	1.0E-35	1.0E-35 /	1.0E-35	1.0E-35	1.0E-35	1.0E-35	1.0E-35 /	1.0E-35	1.0E-35	1.0E-35 /	1.0E-35		1.0E-35	1.0E-35/	1.0E-35/	1.0E-35/	1.0E-35	1.0E-35	1.0E-35	8.0E-36	7.0E-36	7.0E-38	7.0E-36 U06672.1	7.0E-36 U06872.1
	Expression Signal	19.5	1.3	1.68	1.09	1.00	1.81	3.3	3.3	3.93	3.83	1.41	0.86	1.18	2.16	2.16	0.7		0.7	1.46	1.48	1.91	1.37	1.63	2.13	0.58	1.1	3.84	5.92	283
	ORF SEQ ID NO:	26166		27996		28218	28549	28570	28571	_	29757	30934	33141	33311	35297	35298	36352		36353		37881					34983			33327	
	Exen SEQ ID NO:	13509			<u> </u>	15475		15924	15924	17125	17125	L	20063	20211	25125		23123	L	23123		24349	l_		1_	<u> </u>	21817	1	15881	20224	20224
	Probe SEQ ID NO:	735	889	2544	27.70	2770	3140	3161	3161	4388	4388	5423	7383	7541	9442	9442	10477		10477	11758	11758	11768	11917	12121	12471	9720	2831	3118	7554	7554

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens ninjurin 2 (NINJ2), mRNA	Homo sapiens TCLB gene, excn 12	UI-H-BW1-env-c-12-0-UI.s1 NCI_CGAP_Sub7 Homo sepiens cDNA clone IMAGE:3083542 3'	th93b08.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo septiens cDNA done IMAGE:2128195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);	hoo6h02.x1 NCI_CGAP_Co14 Homo sepiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN ALPHA-2 SUBUNIT;	Homo sapiens syncytin precursor, mRNA, complete cds	C16927 Clontech furman eorta polyA+ mRNA (#6572) Homo sapiens cONA clone GEN-535C11 5'	t95c09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA done IMAGE:2107024 3' similer to contains MER9.b2 MER9 repetitive element;	Homo sapiens Xq pseudoautosomal region; segment 1/2	601285587F1 NIH_MGC_44 Homo saplens cDNA clore IMAGE:3607289 5'	Homo sapiens chromosome 21 segment HS21C009	Homo saplens API5-like 1 (API51.1), mRNA	Homo sapiens APIS-like 1 (APISL1), mRNA	Homo sapiens N-effrykmaleimide-sensitive factor (NSF), mRNA	Homo sapiens Xq pseudoautosomal region; segment 1/2	Homo saptens calcinisurin binding protein 1 (KIAA0330), mRNA	PM3-BN0176-100400-001-g04 BN0176 Homo septens cDNA	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONING EASEI	601298574F1 NIH MGC 19 Homo septens cDNA clone IMAGE:3628386 5	2820020.5prime NIH_MGC_7 Homo sepiens cDNA clone IMAGE.2820020 5	601282266F1 NIH_MGC_44 Homo septems cDNA clone IMAGE:3604168 5	601282266F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3604168 5	y19f05.r1 Soares placenta Nb2HP Homo sepiens cDNA clone IMAGE:139713 6'	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), trancript variant 3, mRNA	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29	Homo sapiens DNA for emyloid precursor protein, complete cds	Homo sepiens DNA for amyloid precursor protein, complete cds	zu69c10.r1 Soares_testis_NHT Homo sepiens cDNA done IMAGE:743250 5	Homo sepiens nuclear factor of activated T-cells, cytopiasmic 2 (NFATC2), mRNA	AV753629 TP Homo sapiens cDNA ctone TPGABH01 5'
le Exon Probe	Top Hit Database Source		TN	EST_HUMAN (EST_HUMAN Q	HUMAN		EST_HUMAN (EST_HUMAN	L	EST_HUMAN							EST_HUMAN F	FOGGGGIA	Т	T	EST_HUMAN		EST_HUMAN		LN TN	NT		T_HUMAN		HOMAN
Sing	Top Hit Acessian No.	7708622 NT				6.0E-36 AW780143.1			6.0E-36 Al380499.1	6.0E-36 AJ271735.1		5.0E-36 AL163209.2	5729729 NT	5729729 NT	11079227 NT	AJ271735.1	11417862 NT	4.0E-36 BE010038.1		74.1			4.0E-36 BE389299.1		11497041 NT				4.0E-36 AA400370.1	20516	4.0E-36 AV753629.1
	Most Similar (Top) Hit BLAST E Value	6.0E-36	6.0E-36/	6.0E-36	6.0E-36	6.0E-36/	6.0E-36	6.0E-36 C16927.1	6.0E-36	5.0E-36/	5.0E-36	5.0E-36	5.0E-36	5.0E-36	5.0E-36	5.0E-36	5.0E-38	4.0E-36	040000	4.0E-36	4.0E-36/	4.0E-36	4.0E-36	4.0E-36 R64023.1	4.0E-36	4.0E-36 M33320.1	4.0E-36 D87675.1	4.0E-36 D87875.1	4.0E-36/	4.0E-36	4.0E-36/
	Expression Signal	2	5.58	0.71	3.54	3.57	2.33	0.51	3.11	10.74	5.75	1.45	2.15	2.15	19:0	3.63	3.45	8.	5	3 6	2.13	0.82	0.82	0.84	233	1.63	1.62	1.62	2.84	2.09	7.3
	ORF SEQ ID NO:	27456		29023	30682	32756	34385		37443	25592	28202	28991	30104	30105	33464	25592	31103	26619	7000	27074		28763	28764		31707	33326	34285	34286	36835		
	Exon SEQ ID NO:	14734	15139	16383	18054	19701	21242	22773	24138	12949	15460	16352	17468	17468	20350	12949	24650	13955	2,7,3	14388	14947	16108	16108	18426	18746	20223	21145	21145	23589	24655	25199
	Probe SEQ ID NO:	1998	2418	3630	5248	2009	8550	10125	11536	73	2756	3500	4736	4738	7686	11887	12168	1203	4433	1640	2219	3349	3340	6829	5904	7553	8453	8453	10909	12183	12227

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	Top Hit Descriptor	Homo sapiens mRNA for KIAA0027 protein, partial cds	Homo saplens neuradn III-alpha gene, partial cds	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial ods	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial ods	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Mus musculus Junctophilin 1 (Jp1-pending), mRNA	601458531F1 NIH_MGC_66 Hamo sapiens aDNA clane IMAGE:3862086 5'	601106343F1 NIH_MGC_16 Hamo sapiens aDNA clane IMAGE:3342706 5'	QV0-OT0030-240300-174-h04 OT0030 Homo seplens cDNA	Mus musculus p47-phox gene, complete cds	EST06648 Infant Brain, Bento Soares Homo septens cDNA clone HIBBJ28 5' end	yc44a07.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'	UI-H-BW1-amu-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo sapiens ubiquitin specific protesse 13 (isopeptidase T-3) (USP13) mRNA	801300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'	RC1-HT0217-131198-021-h07 HT0217 Homo sepiens cDNA	RC1-HT0217-131199-021-h07 HT0217 Homo sepiens cDNA	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5	Home sapiens human endogenous retrovins W proC6-19 protesse (pro) gene, partial cds	Homo saplens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA	w637c12x1 NCI_CGAP_GC6 Homo sapiens cDNA done IMAGE:2307862 3' similar to contains Alu repositive element;	1938910.11 Soares Infant brain 1NIB Homo sapiens CDNA clone IMAGE:34529 5' similar to septembrilly and passage of a property of a party of a pa	Under 1 States infant brain ANIR Home contains a CNA clane IMACE: 24520 5' cimilar to	SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN;	DKFZp761A229_r1 761 (synonym: harmy2) Hamo sapiens cDNA clone DKFZp761A229 5'	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA	Homo septens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA	zo51a12.r1 Stratagene endotheltal cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
21 1100	Top Hit Database Source	NT	NT	NT	TN.	Į.	N-	EST HUMAN	EST_HUMAN	EST_HUMAN	INT	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN:	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Į.	NT	EST HUMAN	EOT CLIMAN	NOW TO LEG	EST_HUMAN	EST_HUMAN	M	N	EST_HUMAN	EST HUMAN
5	Top Hit Acession No.	4.0E-36 D25217.2	3.0E-36 AF099810.1	3.0E-36 AF110239.1	3.0E-36 AF110239.1	7862401 NT	10181130 NT	3.0E-36 BF035327.1	2.0E-36 BE259267.1	2.0E-36 AW 880378.1	2.0E-36 AF267747.1	T08756.1	2.0E-36 T69629.1	2.0E-36 BF512794.1	4507848 NT	4507848 NT	1.0E-36 BE409310.1	1.0E-36 BE146523.1	1.0E-36 BE146523.1	1.0E-36 BF673761.1	1.0E-36 AF156962.1	4827084 NT	1.0E-36 AI867714.1	4 OF 30 D2504.2 4	20012.1	1.0E-36 R25012.1	1.0E-36 AL120542.1	11426108 NT	11426108 NT	1.0E-36 AA148034.1	1.0E-36 AA148034.1
	Most Similar (Top) Hit BLAST E Value	4.0E-36	3.0E-36	3.0E-36	3.0E-36	3.0E-36	3.0E-36	3.0E-36	2.0E-36	2.0E-36	2.0E-38	2.0E-36 T08756.1	2.0E-36	2.0E-36	2.0E-36	2.0E-36	1.0E-36	1.0E-36	1.0E-36	1.0E-38	1.0E-36	1.0E-36	1.0E-36	90 30	1.05-20	1.0E-36	1.0E-36/	1.0E-38	1.0E-36	1.0E-36	1.0E-36
	Expression Signal	1.44	2.58	1.32	1.32	121	5.88	1.59	2.38	5.45	3.1	3.95	12.22	1.07	67.0	67.0	1.81	1	-	1.36	1.16	1.29	4.19	3	7	1.21	6.73	0.85	0.85	5.13	5.13
	ORF SEQ ID NO:		26100	28917	26818	27757	2882	36991	28579	30248	30892	31471	32248	35126	35172	35173	26304	27603	27604	27664		31527		0000	350025	32053	32359	33087	33088		33680
	Exen SEQ ID NO:	25047	13455	14231	14231	15022	17203	23720	15930	17631	18198	18550	19248	21955	21900	21989	13634	14871	14871	14928	16099	18599	18868	0000	200	19069	18345	5000	20005	20555	20555
	Probe SEQ ID NO:	12798	080	1484	1484	2297	4467	11050	3167	4904	2398	89/9	6481	8878	9440	8449	3865	2141	2141	2199	3330	5810	0609	805	2000	9539	6582	7326	7326	7860	7860

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	nc60e08.r1 NCI_CGAP_Pr1 Homo septens cDNA clone IMAGE:745670	nc60e08.r1 NCI_CGAP_Pr1 Hamo septens cDNA clane IMAGE:745670	AU141688 THYRO1 Homo seplens cDNA clone THYRO1001033 6	AU141688 THYRO1 Homo sepiens cDNA clone THYRO1001033 5'	xe82b07.x1 NCI_CGAP_Bm35 Homo septens cDNA clone IMAGE.2614357 3'	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA	RC3-CT0279-040500-017-a10 GT0279 Homo saplens cDNA	RC3-CT0279-040500-017-410 CT0279 Homo saplens cDNA	CM3-NN0081-140400-147-h12 NN0061 Hamo sepiens aDNA	UI-HF-BNO-ale-c-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5	RC-BT091-210199-110 BT091 Homo saplens cDNA	RC-BT081-210199-110 BT091 Homo sepiens cDNA	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens chromosome 21 segment HS21C013	Homo sapiens Sad1 uno-84 domain protein 2 (SUN2) mRNA, partial cds	ws80b07.x1 NCL_CGAP_Co3 Hamo sapiens cDNA clane IMAGE:25042453'	ws80b07x1 NCI_CGAP_Co3 Hamo saplens cDNA clane IMAGE;2504245 3'	7304 Human retina cDNA Tsp5001-cleaved sublibrary Homo sapiens cDNA not directional	Homo sapiens chimerin (chimaerin) 2 (CHNZ) mRNA	CM0-UT0003-050800-503-d09 UT0003 Homo saplens cDNA	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA done IMAGE:3146256.3' similar to contains MER29.b3 MER29 repetitive element;	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to contains MER29.b3	VEN LA INDIAN GRAINS	RC1-CN0008-210100-012-e09_1 CN0008 Homo sapiens cDNA	H.sepiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14	DKFZp434E0422_r1 434 (synonym: htes3) Homo sepiens cDNA clone DKFZp434E0422 5	Homo sapiens Jun dimertzation protein gene, perdal ods; cros gene, complete ods; and unknown gene	Homo sapiens jun dimerization protein gene, partial ods; cfoe gene, complete cds; and unknown gene	wk25b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA done IMAGE.2413341 3' similar to contains PTR5.t2 PTR5 repetitive element;	
jie Exon Prob	Top Hit Detabase Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	IN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST HUMAN		ESI HOMAN	EST_HUMAN	5	T HUMAN		Į.	EST_HUMAN	
SIN	Top Hit Acession No.	VA420467.1	VA420467.1	1.0E-36 AU141688.1	1.0E-36 AU141688.1	1.0E-36 AW103658.1	1.0E-36 BF364169.1	1.0E-36 AW855868.1	1.0E-36 AW855868.1	1.0E-36 AW897636.1	1.0E-36 AW 504143.1	1.0E-36 Al905536.1	\B05536.1	1.0E-36 11418177 NT	.2	.1	W009277.1	W 009277.1		4757979 NT	7.1	3E350127.1			8.0E-37 AW840840.1		7.		24		
	Most Similar (Top) Hit BLAST E Value	1.0E-36 AA420467	1.0E-36 AA420467	1.0E-36/	1.0E-36	1.0E-36/	1.0E-36	1.0E-38	1.0E-36/	1.0E-36/	1.0E-36/	1.0E-36/	1.0E-36/	1.0E-36	1.0E-36 AL163213	1.0E-36 AF202723	9.0E-37	9.0E-37 AW00927	9.0E-37 W22818.	8.0E-37	8.0E-37 BE69807	8.0E-37 BE35012		8.0E-37 BE33012	8.0E-37 /	9 OE:37 XB7344 4	7.0E-37	7.0E-37 AF111167	7.0E-37 AF111167	7.0E-37 AI817700.	
	Expression Signal	1.34	1.34	0.61	0.61	2.71	3.88	0.56	0.56	3.3	4.17	1.45	1.45	3.81	3.03	3.23	2.12	2.12	1.35	0.99	1.58	3.75		3.73	8.24	8	3.03	78.0	76:0	8.69	
	ORF SEQ ID NO:	33770	33771	33902	33903	34762	35878	38086	36087	36795	37347	37302	37303				33042	33043		28765		31451			31507	1		27179	27180	36585	
	Exen SEQ ID NO:	20647	20647	20773	20773	21618	22662	22874	22874	23547	24044	23999	23889	24675	24855	25011	19965	19965	24733	16100	17971	18530		2000	18578	20470	14011	14480	14480	23348	
İ	Probe SEQ ID NO:	7952	7952	8079	8079	8927	10014	10228	10226	10867	11354	11393	11393	12060	12501	12747	7281	7281	12309	3350	5168	5738		8	5787	7872	1262	1738	1738	10657	

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Table 4
Single Exon Probes Exonesid in

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					•	25.	חומים בעלון וספס בעלון פססס וון מווון
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vælue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3192	15955		1.08	1.0E-37	1.0E-37 AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
3943	16693			1.0E-37	1.0E-37 AF189011.1	LN	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4888	17615	30234	235	1.0E-37	1.0E-37 BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
5914				1.0E-37	LN 0963067	F	Mus musculus otogelin (Otog), mRNA
8113	20807	33940		1.0E-37	1.0E-37 BE546032.1	EST_HUMAN	601072419F1 NIH_MGC_12 Hano saplens cDNA clane IMAGE:3458308 5
							zp21b02.r1 Stratagene neuroepitheium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to
8834	\perp			1.0E-37		EST_HUMAN	contains L1.12 L1 repetitive element;
10597		36529	2.96	1.0E-37	1.0E-37 M22878.1	니	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12363	24766		2.81	1.0E-37	1.0E-37 BE771814.1	EST_HUMAN	CM3-FT0096-140700-243-407 FT0096 Homo sapiens cDNA
9880		31402		9.0E-38	10048482 NT	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
1200	13952	26616	2.02		11436955 NT	¥	Homo sapiens Grb2-essociated binder 2 (KIAA0571), mRNA
2502	15219	27962	1.8	8.0E-38	8.0E-38 BF346221.1	EST_HUMAN	602018401F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153992 5'
12420	13952	26616	1.6	8.0E-38	11436955 NT	Ę	Homo sepiens Grb2-associated binder 2 (KIAA0571), mRNA
4197	16938		£1.0	7.0E-38	7.0E-38 H19092.1	EST_HUMAN	yn51f07.1 Soares aduit brain N2b5HB557 Homo sapiens cDNA clone IMAGE:171973 5
5039			1.31	7.0E-38	7.0E-38 AF287283.1	L	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
3037	15803	28450	1.2	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo septens cDNA clone IMAGE:3859348 6'
5502		31189	1.8	8.0E-38		TN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5502			1.6	8.0E-38	11425114 NT	L	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7228		32986		8.0E-38	8923130 NT	L	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
11918	24480		2.57	8.0E-38	11435947 NT	LN	Homo sepiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12395		31038	12.79	6.0E-38	6.0E-38 AB002059.1	TN	Homo sapiens DNA for Human P2XM, complete cds
12767		30900	1.7	8.0E-38	11418164 NT	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
710	13484	26133	1.38	5.0E-38	5.0E-38 AW971819.1	EST_HUMAN	EST383908 MAGE resequences, MAGL Homo sapiens cDNA
2455		27912	0.99	5.0E-38	5.0E-38 AJ237740.1	NT	Homo sapiens RIBIIR gene (partial), exon 8
3840	16446	29086	0.85	5.0E-38	7549804 NT	L	Homo saplens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
							yd40h07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to
3917	16667	29307	0.92	5.0E-38	5.0E-38 T83107.1	EST_HUMAN	SP:OLF3_MOUSE P23275 OLFACTORY RECEPTOR;
				1			yd40h07.rf Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:110749 5' similar to
3917		20308	0.92	5.0E-38		EST HUMAN	SP:OLF3_MOUSE P23275 OLFACTORY.RECEPTOR;
6930		32712		5.0E-38	0.1	EST_HUMAN	601450148F1 NIH_MGC_65 Hamo septens cDNA clone IMAGE:3854074 5'
118	\Box	25575		4.0E-38		NT	B.taurus mitochondrial aspartate eminotransferase mRNA, complete CDS
116		25576		4.0E-38		NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2083	_ }		5.25	3.0E-38	3.0E-38 AF003530.1	L	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3684	16437		2.19	3.0E-38	7549807 NT	LN	Homo sepiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA

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Single Exon Probes Expressed in Brain	Most Similar A Database O: Signal BLASTE No. Signal ORF SEQ Expression (Top) Hit Acession Database O: Value Surce Source			7309 1.47 3.0E-38 BE278301.1 EST_HUMAN 601157633F1 NIH_MGC_21 Homo sapiens aDNA clane IMAGE:3504272 5	3.0E.38 AL163300.2 NT Homo septems chromosome 21 segment HS21C100	32900 0.56 3.0E-38 AW 302481.1 EST_HUMAN	33252 8.26 3.0E-38 BF373684.1 EST_HUMAN	34383 2.1 3.0E-38 H85494.1 EST_HUMAN	1240 34384 2.1 3.0E-38 H85494.1 EST_HUMAN yv88b04.11 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775.5	2522 2.24 3.0E-38 AL 163248.2 NT Homo septens chromosome 21 segment HS21C048	30488 1.65	2878 25504 1.4 2.0E-38 AL163248.2 NT Homo sapiens chromosome 21 segment HS21C048	1106 26781 2.99 2.0E-38 5902097 Homo sepiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA	2.0E-38 AA437353.1 EST_HUMAN SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE;	NVMI IT ITSELF FOR SOLVE STORY	1010 102 1000 1000 100 100 100 100 100 1	2/865) 1.45 2.0E-38 W /65/1.1 ESI_HUMAN	31339 0.69 2.0E-38 226634.2 NT	31340 0.69 2.0E-38 226634.2 NT	33395 1.46 2.0E-38 AV72/103.1 EST_HUMAN	1075 4.38 2.0E-38 BE165980.1 EST_HUMAIN MR3-HT0487-150200-113-g01 HT0487 Homo sepiens cDNA	1485 34631 0.56 2.0E-38 F06450.1 EST_HUMAN HSC18F031 normalized infant brain oDNA Homo saplens cDNA clone c-18f03	34700 2.04 2.0E-38 AF069755.1 NT Homo saplens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds	hudgg02x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3166130 3' similer to TR:002710 002710	36212 1.71 2.0E-38 D63479.2	37151 1.37 2.0E-38 AA595480.1 EST_HUMAN	1.37 2.0E-38 AA595480.1 EST HUMAN E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE.:	37382 5.79 2.0E-38 BE712790.1 EST_HUMAN	1235 37557 3.52 2.0E-38 AF190501.1 NT Homo septens feucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
				6		L				5											2			-					
	SEQ ID NO:	3 16587	3 16587	17309	5 25097	19831		3 21240	3 21240	22522	17896	12878	14106	14387	44287	1			_1		2 21075		1 21555	21809	3 22993	23865	23865	24073	24235
	Probe SEQ ID NO:	3836	3836	4574	9655	7144	7488	8548	8548	9872	12630	49	1358	1641	1844		2408	5632	5632	7619	8382	8783	8864	9121	10346	11200	11200	11472	11638

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Hamo saplens feucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, pertial cds	AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5	Homo sapiens gene for kinesin-like protein, complete cds	CHR220580 Chromosame 22 exam Hama septens cDNA clane C22_788 57	E1 beta=pyruvate dehydrogenese beta (promoter) [human, placenta, Genomic, 1280 nt]	Homo sapiens sulforransferase-related protein (SULTX3), mRNA	zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element ;	Homo sapiens guenine nucleotide binding protein-like 1 (GNL1), mRNA	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA	Homo sapiens cyclin K (CCNK) gene, exon 7	Homo sapiens chromosome 21 segment HS21C003	Homo saplens chromosome 21 segment HS21C003	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA	Mus musculus otogelin (Otog), mRNA	Mus musculus otogelin (Otog), mRNA	Homo sapiens mRNA for KIAA0612 protein, partial cds	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA	ht09g01.x1 NCI_CGAP_Kid13 Homo saplens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;	yf96b08.r1 Soares Infant brain 1NIB Homo sepiens cDNA clone IMAGE:30488 5	Homo sepiens KIAA0426 gene product (KIAA0426), mRNA	Homo sapiens chromosome 21 segment HS21 0084	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA	Homo sepiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA	wh53f10.x1 NCL_CQAP_Kld11 Homo sepiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P97890 POL PROTEIN ;	Homo seplens chromosome 21 segment HS210027	QV1-BT0631-040900-357-f02 BT0631 Homo sepiens aDNA	7e34c03.x1 NCI_CGAP_Lu24 Homo septiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6	CE00828;	Homo sepiens X-linked enhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	
Ie Exon Prope	Top Hit Database Source	- ±	EST_HUMAN 4	NT TN	EST_HUMAN C	NT		EST HUMAN N			LN	노	IN TN						HUMAN	EST HUMAN					HUMAN	T	EST HUMAN	Τ	EST HUMAN	Ä	
Sing	Top Hit Acession No.	2.0E-38 AF190501.1	2.0E-38 AV726988.1	2.0E-38 AB012723.1			11418248 NT	1.0E-38 AA401570.1	4885288 NT	7661969 NT	1.0E-38 AF270831.1			8922543 NT	7305360 NT	7305360 NT	1.0E-38 AB014512.1 NT	11422250	1.0E-38 BE350127.1		7662109 NT	1163284.2	4502312	8.0E-39 4758229 NT	8.0E-39 A1823404.1				6.0E-39 BE670394.1	5.0E-39 AF003528.1	
	Most Similar (Top) Hit BLAST E Value	2.0E-38	2.0E-38	2.0E-38	2.0E-38 H55641.1	2.0E-38 S74906.1	2.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38 /	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38 R18512.1	1.0E-38	1.0E-38	8.0E-39	8.0E-39	8.05-39	7.0E-39	6.0E-39		6.0E-39	5.0E-39/	
	Expression Signal	3.52	3.05	2.06	6.45	1.43	3.78	2.55	2.53	1.11	2.34	1.23	1.23	7	4.71	4.71	3.15	0.71	5.13	0.58	1.28	22	15.3	1.45	127	5.79	2.24		1.06	1.57	
	ORF SEQ ID NO:	37558			31081				27450	27475	27960	29655	29656	28921	31677	31678	33063	34898	35150	36163	37503		25510	26796		27550	36639			26412	
	Exan SEQ ID NO:	24236	24517	24518	24705	24742	25031	13829	14728	14747	15216	17029	17029	17283	18719	18719	19987	21740	21977	22948	24187	25140	12882	14121	14560	14819	23400		24979	13750	
	Probe SEQ ID NO:	11638	11971	11973	12280	12323	12777	1071	1992	2012	2489	4290	4290	4558	5937	5937	7304	9051	9310	10301	11588	12118	ន	1373	1821	2087	10711		12696	987	

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r	 ,		_				_	_	_	_	_	_	_			_	_	_	_			т		_	_	_		 ,	_
	Top Hit Descriptor	at36b04.x1 Barstead colon HPLRB7 Homo sepiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.t1 LTR7 repetitive element ;	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA	Chlorocebus sethicos mRNA for ribosomal protein S4X, complete cds	Homo sapiens chromosome 21 segment HS21C010	ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA done IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element;	Homo sapiens DNA for prostacyclin synthese, exon 2	Homo sapiens DNA for prostacyclin synthase, exon 2	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	QV0-FN0063-260600-278-c06 FN0063 Homo sapiens cDNA	finifc16 Regional genomic DNA specific cDNA library Homo sepiens cDNA clone CR12-1	first 16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1	finfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1	cactions 1 Sceres IntriMPu_S1 Homo septens cDNA clone IMAGE:1660996 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;	ox63a10.s1 Soarss_NhHMPu_S1 Homo sapiens cDNA dons IMAGE:1680x986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE :	yp51c06.s1 Soares retina N2b4HR Homo septens cDNA clone IMAGE:190954 3'	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'	promme-7.D01.r bytumor Homo sapiens cDNA 5'	Homo sapiens homogenitisate 1,2-dloxygenase gene, complete cds	PM0-BT0340-211299-003-402 BT0340 Homo sapiens cDNA	rw21g02.s1 NC _CGAP_GCB0 Homo saplens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element;	Homo sapiens chromosome 21 segment HS21C048	RC4-FN0037-290700-011-e10 FN0037 Homo sapiens cDNA	ng86f03.s1 NCI_CGAP_Pr6 Homo septens cDNA clone IMAGE:941693	znoet02.r1 Stratagene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:546651 5	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens chromosome 21 segment HS21C002	Rattus norvegicus putative four repeat ion channel mRNA, completa cois	am88c11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'
שני וויאים טונ	Top Hit Database Source	EST_HUMAN	NT	NT	TN	EST_HUMAN	N	NT	. IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	IN	EST_HUMAN	EST HUMAN	IN	EST HUMAN	EST_HUMAN	EST HUMAN	NT	NT	П	EST_HUMAN
5	Top Hit Acession No.	5.0E-39 AI750154.1	11420289 NT	4.0E-39 AB015610.1	4.0E-39 AL163210.2	4.0E-30 AA682949.1	4.0E-39 D84116.1	384116.1	11418177 NT	4.0E-39 BE836452.1	3.0E-39 AA631949.1	3.0E-39 AA631949.1	3.0E-39 AA631949.1	3.0E-39 A1084557.1	3.0E-39 Al084557.1	137903.1	2.0E-39 BE409203.1	2.0E-39 AI525119.1	2.0E-39 AF000573.1	2.0E-39 AW372318.1	2.0E-39 AA720574.1	2.0E-39 AL163248.2	2.0E-39 BF370207.1	2.0E-39 AA508880.11	2.0E-39 AA080867.1	2.0E-39 AL163202.2	2.0E-39 AL163202.2	2.0E-39 AF078779.1	VA984531.1
-	Most Similar (Top) Hit BLAST E Value	5.0E-39	5.0E-39	4.0E-39	4.0E-39	4.05-30	4.0E-39	4.0E-39 D84116.1	4.0E-39	4.0E-39	3.0E-39	3.0E-39	3.0E-39	3.05-39	3.05-39/	3.0E-39 H37903.1	2.0E-30	2.0E-39/	2.0E-39/	2.0E-39	2.0E-39	2.0E-39	2.0E-39	2.0E-39 /	2.0E-39	2.0E-39/	2.0E-39	2.0E-39	2.0E-39
	Expression Signal	8.62	2.04	6.78	0.97	1.27	0.58	0.58	4.47	2.71	14.86	14.88	14.86	4.35	4.35	5.82	6.8	14.08	4.2	11.91	3.28	1.84	1.48	421	2.38	0.72	0.72	79'0	0.55
	ORF SEQ ID NO:	28397		25954	18882	33791	35078	35079			25498	25499		37257	37258					-	27419	28089	29743	30907	33029	33195		34038	
	Exan SEQ ID NO:	15750	24793	13320	16314	20669	21907	21907	24802	24878	12875	12875	12875	24511	24511	24541	13846	13661	13769	14287	14702	16348	17108	18203	19963	20108	20108	20903	22056
	Probe SEQ ID NO:	2984	12410	537	3559	7974	8228	8228	12427	12534	84	46	8	11983	11983	12006	44.8	8832	1009	1520	1986	2834	4370	5403	7289	7431	7431	8209	9394

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Table 4
Single Exon Probes Expressed in Brain

- 1			_			~	_	_	-	_	_	_			_	_	_	_	-	_	_		_	_				
Single Excit Flobes Exploseed III blaiii	Top Hit Descriptor	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds	Homo sepiens chromosome 21 segment HS210046	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family	EST70527 T-oell lymphoma Homo saplens cDNA 5' end similar to similar to zinc finger protein family	hz40g01x1 NCI_CGAP_GC8 Homo septens dDNA clone IMAGE:3210480 3'	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA	Homo seplens fatty acid desaturase 1 (FADS1), mRNA	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'	AV653028 GLC Homo sepiens cDNA clone GLCDGF04 3'	#91b01x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2248873 3' similar to TR:073505 073505	POL PROTEIN.;	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	Homo seplens KIAA0433 protein (KIAA0433), mRNA	AU127831 NT2RP2 Homo sepiens cDNA clone NT2RP2002172 5	nv34e10.r1 NCI_CGAP_Br4 Hamo sepiens cDNA clane IMAGE:1222122	PMO-BN0167-070500-002-h12 BN0167 Homo septens cDNA	PMO-BN0167-070500-002-h12 BN0167 Homo sepiens cDNA	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA	wh12f07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'	Homo sepiers seme domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semephorin) 54 (SEMA5A), mRNA	Homo sapiens HBV associated factor (XAP4) mRNA	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	Rattus norvegicus putative four repeat ion channel mRNA, complete cds	Homo saplens serine threonthe protein kinase (NDR), mRNA	xd9dh02.x1 Soeres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE;2805491 3' similer to TR:Q15804 Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS	qg52h08.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1838847.3'
פום באסנו רוס	Top Hit Database Source	뉟	Ę	EST_HUMAN	EST HUMAN	EST HUMAN	¥	LN.	Z	EST_HUMAN	EST_HUMAN		EST_HUMAN	뒫	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	N.	F	LN LN	NT	Į.	EST HUMAN	EST HUMAN
	Top Hit Acession No.	7.0E-40 U60325.1	7.0E-40 AL163246.2	6.0E-40 AA361275.1	8.0E-40 AA361275.1	_	TN 681999 NT	11439783 NT	11439783 NT	6.0E-40 AV653028.1	6.0E-40 AV653028.1		4.0E-40 AI686005.1	4.0E-40 AF003528.1	82117	4.0E-40 AU127831.1	AA742809.1	4.0E-40 BE009416.1	4.0E-40 BE009416.1	4.0E-40 AW841585.1	3.0E-40 Al925949.1	11417342 NT	5454167 NT		3.0E-40 AF078779.1	6005813 NT	3.0E-40 AW118799.1	П
	Most Similar (Top) Hit BLAST E Value	7.0E-40	7.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40	6.0E-40		4.0E-40	4.0E-40	4.0E-40	4.0E-40	4.0E-40	4.0E-40	4.0E-40	4.0E-40	3.0E-40	3.0E-40	3.0E-40	3.0E-40	3.0E-40	3.0E-40	3.0E-40	2.0E-40
	Expression Signal	2.03	2.27	8.41	8.41	2.24	1.11	3.56	3,56	10.25	10.25		1.78	227	90.6	0.5	6.22	6.17	5.17	3.03	1.02	7.02	3.62	1.25	1.42	8.36	2.23	8.53
	ORF SEQ ID NO:	33391	36732	28174	28175			32522	32523	35722	35723		27318		29729	33606	33714	34793	34794	36548	29481	32313	34115	34704	34963	37182	37473	
	Exan SEQ ID NO:	20282	23498	15437	15437	18636	18835	19498	19498	22527	22527		14607	14832	17094	20481	20585	21844	21644	23309	16854	10308	20974	21559	21799	23805	24162	13120
	Probe SEQ ID NO:	7616	10813	2730	2730	5849	6055	6836	6836	28877	7288	į	1869	2101	4356	7786	7890	8953	8953	10616	4111	6543	8280	8888	9111	11232	11583	317

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Top Hit Acession Database Top Hit Descriptor No. Source	xr24e10.x1 NC _CGAP_Ut4 Homo saplens cDNA clone MAGE:2761098 3' similar to SW:RS5_MOUSE BST_HUMAN P97461 40S RIBOSOMAL PROTEIN S6. :	1.1 EST_HUMAN AV731601 HTF Hamo sepiens cDNA clone HTFAZE05 6'	Homo saplens proteasome (prosome, macropain) subunit, aipha type, 7 (PSMA7) mRNA, and translated products	Homo sapiens protessome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products	w80e11.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514715 3' similar to TR:Q81929 Q91929 EST HUMAN ZINC FINGER PROTEIN.;		EST_HUMAN	53592 NT	TN	ΤΝ	EST_HUMAN nc09e09.s1 NCI_CGAP_Pr1 Homo sepiens cDNA done IMAGE:1007608	EST_HUMAN 601460375F1 NIH_MGC_66 Homo sepiens aDNA done IMAGE:3863803 5	bb79810.y1 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 EST_HUMAN SYNTAXIN 17.;	EST_HUMAN 602068604F1 NIH_MGC_58 Homo sepiens cDNA clone IMAGE:4067736 5'	T_HUMAN		4508012 NT Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products	EST_HUMAN zh79f11.s1 Soeres_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:418317.3"		EST_HUMAN	I EST HUMAN		I EST_HUMAN	EST HUMAN	TAN IL	EST HIMAN	NT
	DE-40 AW30386	DE-40 AV73160			DE-40 AI968562.		DE-40 BE275932		DE-40 AL163280.	DE-40 AL.163280.2	E-40 AA225989.1	E-40 BF036881.1)E-40 BE018348.1	E-40 BF541030.1	BF54103		E-40 45(E-40 W92708.1	E-40 W92708.1	E-40 AA573201.	E-40 AA57320	E-40 P26808	E-40 AU149345	E-40 AA614255	E-40 AAR440E	E-40 BF33411	E-41 AL16320
Most Similar Expression (Top) Hit Top Hit Signal BLAST E Value	1.61 2.0E-40 AW303868.	0.92 2.0E-40 AV731601.	1.58 2.0E-40	1.58 2.0E-40	1.21 2.0E-40 AI968562.1	2.48 2.0E-40	BE27593	2.0E-40		1.68 2.0E-40 AL163280.2	1.78 1.0E-40 AA225989.1	0.93 1.0E-40 BF036881.1	1.34 1.0E-40 BE018348.1		1.0E-40 BF54103	1.0E-40	1.0E-40					0.69 1.0E-40 P26808	8.34 1.0E-40 AU149345.	1.89 1.0E-40 AA614235.1	1 80 1 DE 40 AAB14055 4		
Most Signal BLAST E Signal Value	1.61	0.92	27375 1.58 2.0E-40	27376 1.58 2.0E-40	27522 1.21	27630 2.48 2.0E-40	1.44 2.0E-40 BE27593	28529 4.28 2.0E-40	30197 1.68	30198 1.68	1.78	28083 0.93	1.34	28185 1.18	28186 1.18 1.0E-40 BF54103	1.27 1.0E-40	29934 4.52 1.0E-40	31907 0.75	31908 0.75	32727 1.77	32728 1.77	32886 0.69	36768 8.34	37612 1.89	37613 1 80	10.09	33643 1.62
Most Similar Expression (Top) Hit Signal BLAST E Value			1.58 2.0E-40	1.58 2.0E-40	1.21	14895 27630 2.48 2.0E-40	15404 1.44 2.0E-40 BE27593	15888 28529 4.28 2.0E-40	17573 30197 1.68	17573 30198 1.68	13632 1.78	0.93	15401	15447 28185 1.18	15447 28186 1.18 1.0E-40 BF54103	16053 1.27 1.0E-40	17306 29934 4.52 1.0E-40	18938 31907 0.75	18938 31908 0.75	19680 32727 1.77	19680 32728 1.77	19820 32886 0.69	8.34	1.89	8,1	25274 10.09	20517 33643 1.62

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	wp04h04.x1 NCI_CGAP_Ktd11 Homo sapiens cDNA clone IMAGE:2463895 3'	wp04h04.x1 NCI_CGAP_Kld11 Hamo septens cDNA clone IMAGE:2463895 3'	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'	601282077F1 NIH_MGC_44 Homo sepiens cDNA clone IMAGE:3803955 5	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA	Human platelet activating factor acetyfrydrolese, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4	Homo saplens guanine nucleotide binding protein 10 (GNG10) mRNA	Homo saplens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens DSCR5b mRNA, complete cds	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	601340485F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3682677 51	UI-H-BW1-amp-b-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'	yc03e10.s1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:79626 3'	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA	QV0-HT0367-150200-114-g09 HT0367 Homo saplens cDNA	AU119344 HEMBA1 Homo sapiens cDNA done HEMBA1005583 5	ow45e06.s1 Soeres_peraftyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE.;contains LTR5.b1 LTR5 repetitive element;	ow45e06.s1 Sogres_paraffyrdd_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1849794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element;	Homo sapiens gene for activin receptor type IIB, complete cds	tm89c04.xt NCI_CGAP_Bm25 Hamo septens cDNA clone IMAGE;2165958 3' similar to contains OFR.b1 OFR repetitive element;	Homo sapiens 959 to config between AML1 and CBR1 on chromosome 21q22; segment 1/3	Homo sapiens 959 kb cartig between AML1 and CBR1 an chromosome 21q22; segment 1/3	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
e Exon Probes	Top Hit Database Source	EST_HUMAN WPO	EST_HUMAN wpo	EST_HUMAN 601	EST_HUMAN 601				NT		Homo Homo NT Spliced		Hon		EST_HUMAN 601:	EST_HUMAN UI+	EST_HUMAN you		EST_HUMAN PM4	EST_HUMAN QVO	EST_HUMAN AU1	OW4 EST_HUMAN TR:	OW4 EST_HUMAN_TR:	NT	TIMEST HUMAN OFF	Hon	NT Hon	NT H.sa
Sing	Top Hit Acession No.		7.0E-41 AI934364.1	7.0E-41 BE389592.1 E	7.0E-41 BE389592.1	11545770 NT	11419208 NT	11433010 NT	7.0E-41 U72335.1	4758445 NT	7.0E-41 AF223391.1	11417972 NT	6.0E-41 AB037163.1	7657042 NT	6.0E-41 BE567816.1	6.0E-41 BF513783.1 E	5.0E-41 T62828.1	4885636 NT		4.0E-41 BE156318.1	4.0E-41 AU118344.1	4.0E-41 Al027117.1 E	4.0E-41 AI027117.1 E	4.0E-41 AB008681.1	4.0E-41 AI500408.1 E	4.0E-41 AJ229041.1	1.1	4.0E-41 X92885.1
	Most Similar (Top) Hit BLAST E Value	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	7.0E-41	6.0E-41	6.0E-41	6.0E-41	6.0E-41	5.0E-41	5.0E-41	5.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41
	Expression Signal	1.24	1.24	0.92	0.92	1.2	3.49	0.81	0.68	2.23	1.73	4.35	1.19	2.04	0.91	1.44	1.11	1.07	2.29	2.42	1.26	15.51	16.51	1.88	6.08	3.55	3.55	224
	ORF SEQ ID NO:	26246	26247	29976	29977	30507	31656	32009	30528	37366	37552		25724	27569	29797	33692	27244				26492	26810	26811	26830	27065	28302	28303	29493
	Exen SEQ ID NO:	15553	15553	17344	17344	17961	18703	19034	17971	24060	24228	25271	13081	14835	17169	20566	14535	16830	19220	13169	13834	14135	14135	14150	14378	15658	15658	16866
	Probe SEQ ID NO:	808	808	4609	4609	6183	5918	6260	\$689	11411	11631	12782	274	2104	4433	1871	1795	4087	6452	382	1076	1388	1388	1403	1632	2891	2891	4124

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	Top Hit Descriptor	AV758295 BM Homo septiens cDNA clone BMFBHC06 5'	601888096F1 NIH_MGC_17 Hamo sapiens cDNA clane IMAGE:4122119 5'	AV710480 Cu Homo sapiens cDNA clone CuAACC07 5'	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, Commission eds)	H.seplens mRNA for putative p64 CLCP protein	Homo saplens mRNA for KIAA1387 protein, partial cds	EST64683 Jurkat T-cells VI Homo septens cDNA 5' end	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	af17f10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'	601762940F1 NIH_MGC_20 Hamo saplens cONA clane IMAGE:4026081 5'	Human ribosomal protein L23a mRNA, complete cds	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end	Human mRNA for KIAA0207 gene, complete cds	G.gorilla DNA for ZNF80 gene homolog	Human ribosomal protein L23a mRNA, complete cds	zkille Soares_total_fetus_Nb2HF8_9w Homo sepiens cDNA clone IMAGE:785839 5	Homo sapiens chromosome 21 segment HS21C067	Homo sapiens chromosome 21 segment HS21C087	xm47706.x1 NCI_CGAP_GC6 Homo saplens oDNA done IMAGE:2087363 3' similar to TR:070343 070343 PPAR GAMMA COACTIVATOR 1.	Homo sapiens Integrin, beta 8 (ITGBs) mRNA	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete ods	Human B-cell specific transcription factor (BSAP) mRNA, complete cds	Human B-cell specific transcription factor (BSAP) mRNA, complete cds	EST31723 Embryo, 12 week I Homo sepiens cDNA 5' end	ZINC FINGER PROTEIN 135	Homo sepiens KIAA0433 protein (KIAA0433), mRNA	Homo sapiens KIAA0433 protein (KIAA0433), mRNA	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end	801445647F1 NIH_MGC_85 Homo sapiens cDNA done IMAGE:3849803 5'
201 11100-016	Top Hit Detabase Source	EST_HUMAN A	EST_HUMAN 6	EST_HUMAN A	EST_HUMAN A	EST_HUMAN 8		1 C			EST HUMAN E		EST_HUMAN &	EST_HUMAN 6	Z	EST_HUMAN E	TN FN	NT	H IN	EST_HUMAN z	H	IN IN	X X HUMAN P	ř		I	E	EST_HUMAN E	SWISSPROT Z			EST_HUMAN E	\neg
3	Top Hit Acessian No.	4.0E-41 AV758295.1	4.0E-41 BF304683.1	4.0E-41 AV710480.1	4.0E-41 AV708431.1	4.0E-41 BE887118.1	-	3 0F 41 AB028808 4		3.1	-					2.0E-41 AA331940.1				1.		2.0E-41 AL163267.2	2 0F-41 AW236547 1	4778	2.0E-41 AF038404.1			2.0E-41 AA328285.1		11417118 NT	17118		
	Most Similar (Top) Hit BLAST E Value	4.0E-41	4.0E-41	4.0E-41	4.0E-41	4.0E-41	3.0E-41	3 OF 41	3.0E-41 X87889.1	3.0E-41	3.0E-41	3.0E-41	3.0E-41	3.0E-41	2.0E-41 U43701.1	2.0E-41	2.0E-41 D86962.1	2.0E-41 X89631.1	2.0E-41 U43701.1	2.0E-41	2.0E-41	2.0E-41	2 05-44	2.0E-41	2.0E-41	2.0E-41 M96944.1	2.0E-41 M96944.1	2.0E-41	2.0E-41 P52742	2.0E-41	2.0E-41	2.0E-41	1.0E-41
	Expression Signal	1.41	7.24	11.07	1.63	1.69	2.68	2,45	7.78	1.50	0.71	1.26	1.52	1.48	5.17	1.84	1.64	3.34	4.65	1.41	1.17	1.17	ő	0.76	8.08	1.45	1.45	1.12	1.61	0.52	0.52	2.78	1.05
}	ORF SEQ ID NO:		35430			30971	26358	20000	30908	32043	32916	37647			26987	27300	27684	27730	26987	28731	28942	29943	30475	32300	33346	33786	33787	33818	34710	35155	35156	37379	28616
	Exan SEQ ID NO:	19184	22246	24286	25184	24898	13894	17040	18204	19061	19846	24323	24485	24825	14209	14686	14944	14990	14290	16081	17314	17314	17850	19296	20241	20062	20862	20890	21585	21984	21984	24071	15984
	Probe SEQ ID NO:	6416	8693	11671	12546	12727	927	4304	5404	6288	7159	11730	11924	12456	1817	1051	2216	2264	2831	3321	4579	4579	1715	8530	7572	1981	1961	9062	8874	8317	8317	11468	3201

PC1/US01/00667

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 			_		_		_								_	_			_		_		_	_						
Top Hit Descriptor	801445847F1 NIH_MGC_85 Hamo septens cDNA clane IMAGE:3849803 5'	Mus musculus tubulin alpha 6 (Tuba6), mRNA	yc18b03.s1 Soeres melencoys 2NbHM Homo septens cDNA done IMAGE:262061 3'	qr75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755868 3/	IL3-CT0213-190200-040-F08 CT0213 Homo sapiens cDNA	Homo septens hypothetical protein FLJ20454 (FLJ20454), mRNA	RCO-HT0613-210300-032-g01 HT0613 Homo saplens cDNA	Homo saplens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sepiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	Home saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete eds)	nh07c02 s1 NCI_CGAP_Thy Homo sapiens cDNA clone IMAGE:943586 shriller to TR:G434304 G434304 3678P EXPRESSED SEQUENCE TAG MRNA.	xx97a04.x1 NG_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.t2	Urin reporting element; Henry septeme characterise 21 septembril HS24 CA85	France seprents were the september of th	HOUGHTAN OCAN DE LINE AND THE CONTRACT TO ALLO S	micogo, at INC, CGAP Pri Home sectors conset MAGE 914652	Homo explens phosphetidylinosital 4-kinase 230 (pl4K230) mRNA, complete cds	Hamo septens phosphetidylinosital 4-kinase 230 (pl4K230) mRNA, complete cds	xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741789 3' similar to contains L1.t1 L1	repounte element	Figure septens misus to KLA-110V probin, partial cds	Home sapiens mixiva for NIAA1007 protein, partiell cds	Hamo saplens. Xq pseudosutosamai regian; segment 1/2	hv31e11.x1 NCI_CGAP_Lu24 Hamo expiens cDNA clone IMAGE:3175052 3'	Hamo septens SET domain and martner transposase fusion gene (SETIMAR) mRNA	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	Homo septens ublquittin protein ligase E3A (furnan papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	Homo septens ubliquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA	
Top Hit Detrabese Source	EST HUMAN	LN 1	EST_HUMAN	EST HUMAN	EST_HUMAN	1	EST_HUMAN	N	N	N	뒫	EST HUMAN		EST HUMAN	ECT LINIAN		EST HUMAN		N		EST HUMAN	- N	Z	LN L	EST HUMAN	TN	TN	Į.	Ę	
Top Hit Acession No.	1.0E-41 BE869735.1	6678468 NT	1.0E-41 H99079.1	1.0E-41 AI217868.1	1.0E-41 AW847812.1	11526291 NT	9.0E-42 BE179191.1	11560161 NT	11580151 NT	8.0E-42 AF003530.1	8.0E-42 AB026898.1	B.0E-42 AA493898.1		8.0E-42/AW086062.1	7 OF 42 A1204358 4	7.0E-42 ALEOROD 4	7.0E-42 AA569592.1	6.0E-42 AF012872.1	6.0E-42 AF012872.1		6.0E-42/AWZ38656.1	C.UE-42 ABUZBBBU.1	6.0E-42 AB02880.1	5.0E-42 AJ271735.1	5.0E-42 BE217913.1	5730038 NT	5730038 NT	11433063 NT	11433063 NT	
Most Similar (Top) Hit BLAST E Velue	1.0E-41	1.0E-41	1.0E-41	1.0E-41	1.0E-41	1.0E-41	9.0E-42	9.0E-42	9.0E-42	8.0E-42	8.0E-42	8.0E-42	0, 10, 0	8.0E-42	7 05 42	7.05-42	7.0E-42	6.0E-42	6.0E-42		6.0E-42	O.UE-4Z	6.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	5.0E-42	
Expression Signal	1.05	14.08	0.66	1.69	1.66	2.81	1.14	3.49	3.49	7.71	0.92	4.4		1.36	124	1.07	5. 6.	324	3.21		3.83	3.5	- 1	7.53	1.41	2.67	2.74	1.04	1.04	
ORF SEQ ID NO:	28617	29897	30582	35157	37056			34922	34923	22875	77567			-	35030	L					72000	300/1	L/ags		25859			32363	32364	
Exon SEQ ID NO:	15984	17264	17918	21985	23781	24571	21111	21761	21761	13236	14833	25277	3	43678	24874	22205	23785	14588	14586	,	7000	10101	18181	12047	13214	13260	13261	18350	19350	
Probe SEQ ID NO:	3201	4529	6749	9318	11111	12054	8418	9072	9072	450	2102	12093	3	117	84.8	45.5	11128	1848	1848		787	8	8	132	428	474	476	6687	6587	

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Single Excit Flores Expressed in Drain	Top Hit Descriptor	Homo sapiens myctubularin related protein 3 (MTMR3), mRNA	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete	cds	Homo sapiens reelin (RELN) mRNA	Homo sapiens mRNA for KIAA1294 protein, pertial cds	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA	Homo sapiens MHC class 1 region	Homo sapiens MHC class 1 region	Homo sapiens ribonuciesse III (RN3) mRNA, complete cds	H.saplens PROS-27 mRNA	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA	Homo sepiens zino finger protein 177 (ZNF177) mRNA	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA	RC1-ST0278-040400-018-h11 ST0278 Hamo saplens cDNA	801458631F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5	RCO-TN0079-110900-024-507 TN0079 Homo sepiens cDNA	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA	2819283.3prime NIH_MGC_7 Homo septems cDNA clone IMAGE:2819283 3'	EST367438 MAGE resequences, MAGC Homo sepiens oDNA	EST367438 MAGE resequences, MAGC Hamo septens aDNA	ow83d05.x1 Sourse_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417.3'	801061284F1 NIH_MGC_10 Hama septens aDNA alone IMAGE:3447620 5	RIBONUCLEASE K3 (RNASE K3)	RIBONUCLEASE K3 (RNASE K3)	Homo sapiens chromosome 21 segment HS210048	Human endogenous retrovirus pHE.1 (ERV9)	UI-H-Bi1-afth-e-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:27218713'	Homo saplens partial C9 gene for complement component C9, exon 1	Homo sapiens partial C9 gene for complement component C9, exon 1	Homo sepiens NADH-ubiquinone addoreductass AGGG subunit precursor homolog mRNA, nuclear gene	encoding mitochandrial protein, complete cds	Homo sapiens NADH-ublquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds	
פול בצמנו בומ	Top Hit Detabase Source	TN		TN	TN	N	TN	Į,	TN	NT	뉟	NT	N F	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	L	LN	EST_HUMAN	TN	NT		NT	IN	
	Top Hit Acession No.	11417957 NT		5.0E-42 AF071569.1	4826977 NT	6.0E-42 AB037715.1	8923162 NT	4.0E-42 AF055066.1	4.0E-42 AF055068.1	4.0E-42 AF189011.1		4.0E-42 AF246219.1	4506496 NT	4508008 NT	4.0E-42 AW818830.1		4.0E-42 BF035327.1		_	2.0E-42 AW 250059.1	2.0E-42 AW955368.1	2.0E-42 AW955368.1	2.0E-42 A1052586.1	2.0E-42 BE538919.1			2.0E-42 AL163246.2		1.0E-42 AW 295809.1	1.0E-42 AJ251818.1	1.0E-42 AJ251818.1		1.0E-42 AF067156.1	1.0E-42 AF067188.1	
	Most Similar (Top) Hit BLAST E Value	5.0E-42		5.0E-42	5.0E-42	6.0E-42	5.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42 X59417.1	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0E-42 P81649	2.0E-42 P81649	2.0E-42	1.0E-42 X57147.1	1.0E-42	1.0E-42	1.0E-42/		1.0E-42	1.0E-42	
	Expression Signal	3.12		1.39	75.0	3.65	2.44	5.09	5.09	3.46	1.22	1.07	4.15	15.12	1.56	1.58	1.5	2.81	2.92	222	7.8	7.8	1.48	1.32	0.68	99.0	1.37	1.21	1.1	1.18	1.18		16.49	16.49	
	ORF SEQ ID NO:	32662		32854	33489	34515	36849	26167	26168	26462	29541	29670	29589	29909	36475	36476	37297	26902		27879	31379	31380	32429	35596	35807	35808	37660	28143	26441	28495	26496		28841	26642	
	Exen SEQ ID NO:	19619		19789	20375	21369	23600	13510	13510	13803	16911	16943	16964	17278	23241	23241	23995	14213	15134	15146	18465	18465	19416	22392	22603	22603	24334	13490	13779	13837	13837		15563	15563	
	Probe SEQ (D NO:	6704		7101	7711	7298	10920	736	736	104	4171	4202	4223	4543	10545	10545	11389	1488	2413	2425	9299	5870	9854	144	9955	9955	11742	717	1019	1079	1079		1220	1220	

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Single Exoli Flobes Expressed III Didiri	Most Similar Top Hit Acession Cap Hit Acession BLAST E No. Source Source	.13 1.0E-42 11423219 NT Homo sepiens rec (LOC51201), mRNA	1.0E-42 5174458 NT Homo sapiens major histocompetibility complex, cless II, DM alpha (HLA-DWA) mRNA	Homo sapiens origin recognition complex, subtrnit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products	2.6 1.0E-42 7662027 NT Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	1.0E-42 AL.163267.2 NT	1.0E-42 AL163280.2 NT	1.0E-42 AW8136	1.0E-42		1.0E-42 4506758 NT	.08 1.0E-42 4501912 NT Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA	1.0E-42 4501912 NT	1.03 9.0E-43 4757969 NT Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA	8.0E-43 AV736824.1 EST_HUMAN	8.0E-43 AV736824.1 EST_HUMAN	8.0E-43 8923276 NT	8.0E-43 8923276 NT	8.0E-43 8923276 NT	8.0E-43 H13952	7.0E-43 AW246442.1 EST_HUMAN 2822251.5prtme NIH_MGC_7 Homo saplens dDNA clone IMAGE:2822251 5	wp69b01.x1 NO_CGAP_Bn25 Home sapiens cDNA clone IMAGE:2466985 3' strailer to TR:015475 7.0E-43 Al936748.1 EST_HUMAN 015475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element;	6.0E-43 AA491890.1 EST HUMAN	6.0E-43 AV708201.1 EST_HUMAN	Homo saplers ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA MRP3B, mRNA	NYMIN LOD 1/100097/NV 07 D0 9	6.0E-43 AW 468897.1 EST HUMAN	235e08.r1 Soares_NhHMPu_S1 Homo sepiens cDNA clone iMAGE:065410 5' shriler to TR:G529641 EST_HUMAN G529841 DB1, COMPLETE CDS. ;contains element PTR7 repetitive element;	5.0E-43 AL119159.1 EST_HUMAN DKFZp761L1712_r1 781 (synonym: hamy2) Homo saplens cDNA done DKFZp761L1712 6	5.0E-43 AL163213.2 NT
	Expression (Top) Signal BLAS	1.13	1.63	10.26		1.17 1.0	1.92	0.75 1.0	1.88 1.0		6.02	1.08 1.0	1.08	4.03	19.69 8.0				8.03	0.76 8.0	6.42 7.0	4.09		2.25 6.0	2.24 6.0	•	Z.09	2.16 6.0	2.55 6.0	2.64 5.0
	Exan ORF SEQ Exp SEQ ID NO:	14439 27137	15261 27998	15730 28380	16449 29088	16655 29298	16962 29587	17289 29918	17431 30062	17431 30063	17460 30097	17763 30378	17763 30379	22634 35844	13416 26052	13416 26053	13459 26104	13459 26105	13459 26106	18408 31321	18385 29025	21359	14070	15314	18983 31969		19409 32492	22402 35607	23714	12963
	Probe Ex SEQ ID SEC NO: NO	. 1696 14	2548 15	2964 15	3695 16	3905 16	4221 16	4554 17	4697 17	4697 17		5044 17		9886 22			684 13		684 13	5612 18	3632 18	8667 21		2600 15	6219 18		9090	9751 22	11044 23	138 12

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Single Exon Probes Expressed in Drain	Most Similar Top Hit Acession ID NO: Signal BLASTE No. Squree Source Source	25909 4.55 5.0E-43 AA382780.1 EST_HUMAN	28264 1.52 5.0E-43 AV732578.1 EST_HUMAN	1.17 5.0E-43 AI613509.1 EST_HUMAN tw22e07.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3	163 32484 0.72 5.0E-43 Ai013509.1 EST_HUMAN fw22e07.x1 NCI_CGAP_Bm62 Home sapiens cDNA clone IMAGE:2280452 3'	170 0.48 5.0E-43 H74277.1 EST_HUMAN yu49g12.r1 Soares fetal liver spleen INFLS Homo saplens cDNA clone IMAGE:228510 6'	25098 0.47 5.0E-43 AA04450.1 EST_HUMAN gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);	35099 0.47 5.0E-43 AA044450.1 EST_HUMAN	35186 4.44 5.0E-43 AA465288.1 EST_HUMAN	231 6 DE 43 A1733244 1 EST HUMAN PV/14 GENE ::	36201 1.21 5.0E-43 AL049110.1 EST HUMAN	36593 5.29 5.0E-43 AW863007.1	36822 1.84 5.0E-43 W 29011.1 EST_HUMAN 5584 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA	Homo sapiens X-linked amhidrottic ectodermal dyspissia protein gene (EDA), excn 2 and flanking repeat regions 5.9 4.0E-43 AF003528.1 NT regions	30502	32026 0.7 4.0E-43 6996009 NT	722 4.0E-43 11416793 NT Homo sapiens protocedherin beta 6 (PCDHB6), mRNA	33900 5.21 4.0E-43 A1244341.1 EST_HUMAN	4778402.x1 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3	36074 1.23 4.0E-43 6005967 NT	37228 1.68 4.0E-43 T77380.1 EST HUMAN	3.05 4.0E-43 R20950.1	Homo eaplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and pertial cds. alternatively spliced	27130 2.07 3.0E-43/X97889.1 INT	28950 1.31 3.0E-43 S99002.1 NT	29629 1.04 3.0E-43 AA548154.1 EST HUMAN	
																				ot					<u></u>		***************************************
	SEQ ID NO:	13275	15618	3 19463	19463	3 21470	3 21927	1	1_	22044		L	L	15519	١	J	19722	7 20771	20771		L	J	13943			16999	
	Probe SEQ ID NO:	490	2850	6213	6802	8778	9248	9248	9264	10297	10335	10863	10891	952	6178	6276	7030	8077	77.08	10213	11275	12030	1191	1690	3558	4258	

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Top Hit Descriptor	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1	Mus musculus otogelin (Otog), mRNA	Mine review this chosen (Obo), mRNA	History Statement BNA instrument hinding fraction (UBTF) gene, partial cds	Constitution of the state of th	THR.2 THR repetitive element;	Homo sapiens hypothetical protein (HSA011916), mRNA	Homo sepiens similar to curithine carbamoyltransferase (H. sapiens) (LOC63648), mRNA	qd61c09.x1 Scares_testis_NHT. Homo septens cDNA clone IMAGE:1733968 3' similiar to contains PTR7.t3	PTR7 PTR7 repetitive element;	hussaea.x1 NCI_CGAP_Bm41 Homo sapiens curva done invace3 (3) 30 3 similia to curionic societa. MFR40 recettive element:	Herang v1 NCI CCAP Brn41 Homo sabiens cDNA clone IMAGE:3173750 3' similar to contains element	MER40 repetitive element;	UI-H-BI1-aff-a-09-0-UI.s1 NCI_CGAP_Sub3 Homo septens cDNA clone IMAGE:2/21712.3	Human ribosoma protein L238 mrtVA, complete cas	31Gb Feda Drain, Strangare Truits expenses secretarions among the and	Home sapiens Kas-like G i P-binding protein (IAND2/A) years, extra 15 and 2	OTHO SECTION TO THE CLIFT-CANDING PROCEST (CANDEN) BOTTO, WOLLD TO THE CLIFT OF THE	Homo sapients chromosome 21 asgiment float Loud.	60/20/22/313F1 NCI CGAP BINO/ Inditio septents curion citato introductivo con control	Homo sapiens pyruvara denyknogenese na meso, redenjansko vijera ovijera omo sapiens operaniscription levico (or 4) minum	Homo sepiens ope transcriptor i actual (of 14) in actor. Homo sepiens ope transcriptor in actual (of 14) in actor.	yg40e01.r1 Soares infatt brain 1NIB Homo sapiens curva ciono invasti	Homo saplens vacuolar sorting protein 35 (VPS35) mRNA, complete cds	Homo sepiens 8q22.1 region and MTG8 (CBFAZT1) gene, partial cds	EST375749 MAGE resequences, MAGH Homo septens cDNA	EST365289 MAGE resequences, MAGB Homo sepiens cDNA	wr87h01.x1 NCI_CGAP_Kd11 Homo sepiens cDNA clone IMAGE:2494705 3	Homo eaplens calctum channel, voltage-dependent, appra TE suburnt (CACMATE), mixtura	DKFZp761D1015_r1 761 (synonym: hamy2) Homo eagless curk clorie DAY-2p761D1015 5	W69504XT NC_CGAP_T/26 hand separate contractive contra	
Top Hit Databese Source	H				12	EST HUMAN T				EST_HUMAN P	E NAME I FOR	1	EST_HUMAN N	EST HUMAN	╗	HOMAN			П	T_HUMAN				EST_HUMAN 8	I IN	Ę	EST_HUMAN	EST HUMAN	T_HUMAN		_ [EST HUMAN
Top Hit Acession		7205260	2002001	303300		3 0F-43 AA458824.1	861721	11420217INT		2.0E-43 AI190784.1	1000011	Z.UE-43 DEZZZ110.1	2.0E-43 BE222778.1	.1			-	_	2	1.0E-43 BF348283.1	4885544 NT	4507168 NT	4507168 NT	1.0E-43 R19751.1	1.0E-43 AF175285.1	1.0E-43 AF198490.1	1.0E-43 AW963676.1	1.0E-43 AW953229.1		1.0E-43 11424378 NT	1.0E-43 AL137964.1	1.0E-43 A1675416.1
Most Similar (Top) Hit BLAST E	3 0F-43 D34613.1	700	3.05	3.0€-43	3.0E-43 U65487.1	3 OF 43	3 OF 43	3.0F	2	2.0E-43	100	Z.UE-43	2.0E-43	2.0E-43	2.0E-43	2.0E-43	1.0E-43	1.0E-43					1.0E-43		L			L				
Expression Signal	07.0		77.7	2.24	4.29	e e	1 87	10.	200	79.7	,	1.13	1.13	1.32	5.50	4.94	2.94	2.94	1.57		0.74	8.45	8.45	1.36								1.89
ORF SEQ ID NO:	24548				32404		24554	34554		_		32151	32152				27080	27081			30788	32280	32281	30542			34574					31079
	Te	31		38	8	1	70/20	27411	2410	12991		19152	10452	19862	20901	23823	14391	14391	14443	15434	18128	19279	19279	17947	20528	20660	21428	27837	23564	24028	24520	24699
Exen SEQ ID NO:	40500	2	19038	19038	19390		₹ ĕ	5 S	1	- 5	<u> </u>	8383	A383			L		L	<u></u>	Ĺ	L	L		<u> </u>	1_	L	8778			_		1

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Single Exon Probes Expressed in Brain	Coession Top Hit Descriptor Source Source	1418322 NT Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	.1 EST_HUMAN qh23g01.x1 Soares_NR_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'	EST_HUMAN	NT		1423497 NT Homo saplens small proline-rich protein 2C (SPRR2C), mRNA	NT Homo saplens mRNA for thymidine kinase, partial	NT Home sepiens myosin mRNA, pertial cds			1418099 NT Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA	EST_HUMAN	5031896 NT Homo septens LIM domein-containing preferred translocation partner in lipoma (LPP) mRNA	9.1 NT Homo sapiens minisatellite ms32 repeat region	NT Homo sapiens minisatelitie ms32 repeat region	1.2 NT Homo septions chromosome 21 segment HS21C084	9.1 NT Hans sepiens chramosame 21 unknown mRNA	INT	4505646 NT Homo saplens proprotein convertase subtilisin/kadn type 2 (PCSK2) mRNA	EST_HUMAN	EST_HUMAN	1 EST HUMAN		1.1 NT Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	•	EST HUMAN	EST_HUMAN	INT	EST_HUMAN	NT Human fibrillin (FBN1) locus polymorphism	3.1 EST_HUMAN RC3-HT0585-010400-023-d08 HT0585 Homo saplens cDNA	TN	1.1. EST_HUMAN zp18b05.r1 Stratagene fetal retina 937202 Homo septens cDNA clone IMAGE:609777 5'
	Top Hit Acession No.	11418322 NT	8.0E-44 AI222985.1 ES	8.0E-44 AI222985.1 ES	(94354.1 NT	11423497 NT	11423497 NT			11527389 NT	11418086 NT	11418099 NT		5031886 NT	7.0E-44 AF048729.1 NT	7.0E-44 AF048729.1 NT	7.0E-44 AL163284.2 NT	7.0E-44 AF231919.1 NT	7.0E-44 AF231919.1 NI	4505846 NT	7.0E-44 AU159839.1 ES		1	5.0E-44 AJ289880.1 NT	5.0E-44 AJ289880.1 NT					4.0E-44 BE883178.1 ES		4.0E-44 BE176618.1 ES		3.0E-44 AA169851.1 ES
	Most Similar (Top) Hit BLAST E Value	9.0E-44	8.0E-44	8.0E-44	8.0E-44 X94354.1	8.0E-44	8.0E-44	8.0E-44 Y10498.2	8.0E-44 L29139.1	8.0E-44	8.0E-44	8.0E-44	7.0E-44 R06035.1	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	7.0E-44	8.0E-44 Z20948.1	6.0E-44	5.0E-44	5.0E-44		5.0E-44	5.0E-44	4.0E-44	4.0E-44	4.0E-44 L21948.1	4.0E-44	4.0E-44 U90878.1	3.0E-44
	Expression Signal	3.41	6.23	6.23	2.67	0.47	0.47	3.78	1.36	4.09	1.38	2.55	0.69	1.05	2.58	2.58	2.54	1.12	1.12	1.01	2.28	0.94	1.78	3.3	2.72		4.96	2.34	3.75	0.68	0.78	0.51	5.38	2.77
	ORF SEQ ID NO:	31032	26309	26310	34286	36097	36098	37064	37606	31073	30976	30808		27696	28381	28382	29231	29581	29582	30476	33808	31756	37702				33607		28816	33131	33995		37153	28500
	Econ SEQ ID NO:	24835	13639	13639	21129	22884	22884	23787	24283	24673	25009	25186	13423	14956	15732	15732	16594	16958	16958	17860	20779	18793	24372	13102	13124		20483	22038	16167	20050	20863	21469	23866	16850
	SEQ ID NO:	12469	870	870	8437	10236	10238	11117	11688	12207	12248	12589	944	2228	2966	2998	3843	4217	4217	5142	8085	6012	11781	296	323		7788	9284	3409	7370	8169	8777	11202	3094

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	Top Hit Descriptor	z/88g/11.r1 Sceres_testis_NHT Homo sepiens cDNA clone IMAGE:729476 5'	Homo sapiens transcription factor (SHM enterrors 3, JMT I protein, JMM protein, Am gynaptophysin genes, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,	complete cds; and L-type calcium channel a>	601009.81 Sogress Nithming of Thomas spinors controlled the spinors have	Homo sapiens aprile DIVA, MT Homomer Mos	HOTIO SEPTIONS SIGNED CHAN, WILL HAMPING SPACE CONA	EVISTALATIVA OF TAXABLE MACE Home seniors CONA	ESIS/819/ MAGE resolutations, which includes the second of	Homo septens critical and the septens of the IMAGE 2009028 3'	possgu/ XT No. Judah Good Hallis Sapara Com Com Com Com Com Com Com Com Com Com	AV /1400b DUB registration sequence of the control	Homo septents Sustri Court reposal, curtaining (broad-br)	RCI-CIOTBR-15086COTT-COS CTOTOS LAmo sarlans CDNA	RCI-CIOISGE-011-COO CIOISGE INTRA CELECTOR MENA	Homo septer is hypothesical product to 100 (F. 110379). mRNA	THURD September In South Care Kill A A A DOOR Franklin norting cols	Hamp separate introduction of the control of the co	HOTIO September 11 Contractor Water (17 Contractor of the Contract	Homo septens I RN-tused gene (NO IL. Horrow and China	CMU-NINCOUR CONTROL Dama seniers CONA 5' end	EST SUCES Syndring and Coling Livers environ Colone IMAGE:2313802 3' similar to contains L1.tf L1	Wheedback included in the common of the comm	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2/82509 3 Birnian to SW 1213A HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;	Homo eapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA	Homo sepiens chromosome 21 segment HS21C003	CMA-CN0044-180200-515-f01 CN0044 Hamo sapiens cDNA	tagatio7.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE	P09084 PAIRED BOX PROTEIN PAX-1:	立22d03.s1 Soeres_tests_NHT Homo sapiens CDNA clone IMA(生:/2/8// 3 Smiller to contents evention. TAR1 receitive element:	Homo sabiens MCP-1 gene and enhancer region	
2001 1110000	Top Hit Detabase Source	EST HUMAN			T HUMAN		Т	Т	HOMAN	Т	HOMAN	T HUMAN		Т	HUMAN		Z	₩.	Z	Į.	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Į.	Į.	EST HUMAN		EST_HUMAN	NAME IN FOL	ESI TOMOR	2
- A	Top Hit Acession No.	1.0E-44 AA398099.1						1				1.0E-44 AV714608.1	2864	٦	1.0E-44 AW846967.1	8922391 NT		AB023212.1	5174718 NT	5174718 NT	8.0E-45 AW892763.1	8.0E-45 AA377985.1	6.0E-45 A1675425.1	B OF 45 AW157570 1	11418213 NT		5.0E 45 RE333877 1		5.0E-45 AI523766.1	١,		5.0E-45 718933.1
	Most Similar (Top) Hit BLAST E Value	1.0E-44 A		1.0E-44	1.0E-44 A	1.0E-44	1.0E-44 A	1.0E-44 A	1.0E-44 A	1.0E-44 A	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44 /	9.0E-45	9.0E-45		8.0E-45	8.0E-45	8.0E-45	8.0E-45	8.0E-45	90 00	A OF 45	5.0E 45	2.0E 45	70.0	5.0E-45		١	5,05-45
	Expression Signal	0.96		44.1	3.73	1.04	1.04	96.0	86.0	96.0	0.69	4.04	3.92	3.17	3.17	1.38	1.38	1.31	3.12	6.41	0.68	0.91	- 5		4.03	3	20.1	20.0	1.79			1.31
	ORF SEQ ID NO:	27746		28211	-	30385	30386	33988	33989	34380			37427		37497	29906	29907	32323	27982	30355	32181	33830				+		7/400	2002			31669
	Exen SEQ ID NO:	15590		15468	18465	17787	17767	20857	20857	21238	21615	I _	1_	1_	L	17274	17274	19317	15243	L	19182	20701	10077	1	16/09	_		14/31	45057	1_	- 1	18713
	Probe SEQ ID NO:	2280		2763	3712	5048	5048	8163	8163	8544	8924	10938	11518	11683	11583	4539	4639	6552	2527	5023	414	8008	7,546	200	3000	12000	872	<u>8</u>	3304	1	6425	5929

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Γ			7						П		П													Γ								01	
	Top Hit Descriptor	801284360F1 NIH_MGC_44 Homo sapiens dDNA clone IMAGE:3608183 6'	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete ods	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA	Homo sapiens mRNA for KIAA1591 protein, pertial cds	601289118F1 NIH_MGC_8 Homo saplens dDNA clone IMAGE:3619803 57	yr05b02.r1 Sogres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5	Homo sapiens percetsomal biogenesis factor 14 (PEX14), mRNA	Homo sapiens perodsomal biogenesis factor 14 (PEX14), mRNA	Homo sapiens DNA for amyloid precursor protein, complete cds	801511228F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3912535 51	Human mRNA for KIAA0299 gene, partial ods	Homo saplens alpha-caterin-like protein (VR22), mRNA	Homo saplens protein kinase C, alpha binding protein (PRKCABP), mRNA	Homo sapiens hypothetical protein FLJ20454 (FLJ20464), mRNA	Homo saplens Ran GTPase activating protein 1 (RANGAP1), mRNA	Homo sapiens calcium channel, voltage-dependent, alpha 11 suburit (CACNA1), mRNA	Mus musculus keretin complex 2, gene 6g (Krt2-6g), mRNA	Homo sapiens chromosome 21 segment HS21C009	2822449.5prime NIH_MGC_7 Homo septens cONA clone IMAGE:2822449 5	t32708.x1 NCI_CGAP_Gas4 Homo sepiens cDNA done IMAGE:2132199 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAM (HUMAN):	#3208.x1 NCI_CGAP_Gas4 Homo septens cDNA done IMAGE:2132199 3' similar to gb:J00314_ma2	TUBULIN BETA-1 CHAIN (HUMAN);	RC5-HT0508-280200-012-C12 HT0508 Homo saplens cDNA	Rattus norvegicus espin mRNA, complete cds	801277292F1 NIH_MGC_20 Homo saplens cDNA done IMAGE:3618119 5	RC4-BT0310-110300-015-110 BT0310 Homo sepiens cDNA	Homo saplens hypothetical protein FLJ10847 (FLJ10847), mRNA	801822835F1 NIH_MGC_77 Homo sepiens cDNA clone IMAGE:4042736 5	wm31f08x/1 NCj_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similer to contains MER19.12 MER19 repetitive element ;	
	Top Hit Detrebesse Source	EST_HUMAN	FA.	N.	TN	N	NT	EST_HUMAN	EST_HUMAN	N-	Z.	Į	EST_HUMAN	L	Z	5	NT	Z	Į.	N	LN LN	EST_HUMAN	FST HIMAN		EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	LN L	EST_HUMAN	EST HUMAN	4
, 	Top Hit Acession No.	BE389855.1	4506412 NT	TN 0627290		8650558 NT	1.0E-45 AB046811.1	1.0E-45 BE396633.1		11422236 NT	11422236 NT		1.0E-45 BE887843.1	1.0E-45 AB002297.1	TN 9570 NT	11419099 NT	11526291 NT	11418177 NT	11418157 NT	9910293 NT	9.0E-46 AL163209.2	9.0E-46 AW246964.1	8 DF 46 A1433281 1		8.0E-46 AI433261.1	8.0E-46 BE167244.1		7.0E-46 BE386165.1	7.0E-46 BE064386.1	8022708 NT	7.0E-46 BF105845.1	6.0E-46 AI884381.1	
	Most Similar (Top) Hit BLAST E Value	1.0E-45	1.0E-45	1.0E-45	1.0E-45 U32169.1	1.0E-45	1.0E-45	1.0E-45	1.0E-45 H57443.1	1.0E-45	1.0E-45	1.0E-45 D87675.1	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	1.0E-45	9.0E-46	9.0E-46	9.0E-46	8 OF 48		8.0E-46	8.0E-46	7.0E-46 U48007.1	7.0E-46	7.0E-46	7.0E-46	7.0E-46	6.0E-46	
	Expression Signal	2.17	1.38	1.79	7.42	1.38	1.19	5.01	1.04	0.77	0.77	96.0	5.08	122	1.33	6.83	11.18	5.28	2.6	1.7	5.86	11.23	13.63		13.53	5.60	1.03	3.38	1.33	4.01	1.14	3.90	
	ORF SEQ ID NO:		25887		28507	28897	28962	20804		33752	33753	34341	34861		37851	31125			30991	33958		36239	27800		27900		27700			31692	32170		
	Exan SEQ ID NO:	13185	13245	13906	15866	16240	16315	17178	17411	20625	20625	21197	21709	22100	24327	24592	24708	24711	24909	20821	21224	23024	15/67		15162	20648	14980	17278	17487	18733	19171	15464	
	Probe SEQ ID NO:	\$	8	1151	3101	3483	3560	4442	4677	7830	7230	8505	8019	2250	11734	12087	12263	12269	12680	8127	8532	10378	2443		2443	7053	2232	155	4755	5951	9402	2759	

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	ains MER19.t2	0363 060363	S DNAJ					3202				ma1	Tage.	Taa'										65	
Top Hit Descriptor	wm31f08xf NCI_CGAP_Ut4 Homo sepiens cDNA done IMAGE:24375753' similar to contains MER19.t2 MER19 repetitive element;	te58h10.x1 NCI_CGAP_Kid8 Homo sepiens cDNA clone IMAGE:2232835 3' similar to TR: 060363 060363 SA GENE.	xx42x04.x1 NCL_CGAP_LITH Homo septens CDNA clone IMAGE:2706654 3' stmiler to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HLIMAN):	601478409F1 NIH MGC 68 Home septens oDNA clone IMAGE:3880895 F	Homo sablens chromoegne 21 segment HS21C010	7481g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408.31	7481g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 31	nas38f07x1 NCI_CGAP_Kid11 Home saplens cDNA clane IMAGE:3258757 3' similar to TR:075202 075202 HOMOLOG OF RAT KIDNEY-SPECIFIC	602021164F1 NCI CGAP Bm67 Homo seniens cDNA clone IMAGE:4159370 5	QV4-ST0212-120100-075-f09 ST0212 Homo seniors CDNA	262c08.s1 Soares tests NHT Hamp sapiens cDNA clane IMAGE 726926.31	no54e09.s1 NCI_CGAP_SS1 Homo sepiens oDNA clone IMAGE:1104520 3' similar to gb:X53741 FIBULIN-1, ISOFORM A PRECURSOR (HIJMAN)	H86c03.x1 NCI_CGAP_Lu24 Homo saptens cDNA clone INAGE:3008836 3' similar to gb:X14008_ma1 1 YS/37YAMF C PRECI IPS/OR /HI IMAN 1) contains demonstrated to the contains of the	N86-03.xf NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3008836 3' similær to gb:X14008_marl YSOZYAFE C PRECY IRSOR (HI IMAN): contract along a MED 27	Human endocenous retroving RTVI H2	Homo sapiens mRNA for KIAA0822 protein pertial cds	Homo sapiens mRNA for KIAA0622 protein partial cds	Human ig germline gamma-3 heavy-chain gene V region, partial cals	Human Ig germline gamma-3 heav-chain gene V racion partial cds	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens solute carrier family 35 (CMP-stalic acid transmorter) member 1 (SI C3584) mBN	Homo sapiens VAMP-essociated 33 kDs protein mRNA complete of	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA	H.sapiens ig iembde light chain variable region gene (7c.11.2) germilne; ig-Light-Lambda; VLæmbda	
Top Hit Database Source	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	FST HUMAN	L	N	Z	NT	N	Ę	N-	Z L	۲۲	۲	
Top Hit Acession No.	Al884381.1	Al635448.1			AL163210.2	BE677194.1	BE677194.1	BF590442.1	BF347229.1	AW 582253.1	AA398381.1	AA601143.1				-	_				5453620		4506376		
Most Similar (Top) Hit BLAST E Value	6.0E-46	6.0E-48	6.0E-46	6.0E-46	5.0E-46	5.0E-46	5.0E-48	5.0E-48	5.0E-46	5.0E-46	5.0E-48	4.0E-46	4.0E-48	4.05.48	4.0E-48	4.0E-48	4.0E-46	4.0E-46	4.0E-46	4.0E-46	3.0E-46	3.0E-46	3.0E-48	3.0E-46	
Expression Signal	3.99	10.94	0.72	2.04	8.9	1.07	1.07	1.86	4.29	0.62	0.47	1.4	ත න	88.8	2.62	1.04	1.04	2.43	2.43	2.71	6.0	96.0	0.79	1.2	
ORF SEQ ID NO:	28208	31779	32868				28930	32413	32570	32736	35350		27140	27141	28188	29763	29754	30834	30835	31014	27618	27884	29735	30094	
Exan SEQ ID NO:	15464	18818	19804				16275	19398	19542	19687	22168	13405	14442	14442	15449	17121	17121	18153	18163	24863	14885	15150	17100	17456	
Probe SEQ ID NO:	2759	9038	7116	11364	199	3519	3519	9839	6842	6005	9515	929	1089	1699	2743	4384	4384	5350	6350	12513	2155	2429	4382	4724	
	Exam ORF SEQ Expression ID NO: Crop Alt Acrossion Signal Crop Hit Acrossion ID NO: Top Hit Acrossion ID NO: Top Hit Acrossion ID NO: Acrossion ID NO: Acrossion ID NO: Database	Exam SEQ ID NO: ORF SEQ Signal NO: Expression Signal Value (Top) Hit BLASTE Value Top Hit No. Top Hit Database Source 15464 28208 3.99 6.0E-46 AI884381.1 EST_HUMAN	Exam SEQ ID NO: ORF SEQ Signal ID NO: Expression Signal Value (Top) Hit BLASTE Na. Top Hit Na. Top Hit Database Source 15464 28208 3.99 6.0E-46 AI884381.1 EST_HUMAN 18818 31779 10.94 6.0E-46 AI835448.1 EST_HUMAN	Exam SEQ ID NO: ORF SEQ Signal ID NO: Expression Signal Value (Top) Hit BLASTE Value Top Hit No. Top Hit Source 15464 28208 3.99 6.0E-46 Al884381.1 EST_HUMAN 19804 32898 0.72 6.0E-46 AW513244.1 EST_HUMAN	Exam SEQ ID NO: ORF SEQ Signal ID NO: Expression Signal S	Exam SEQ ID ID NO: ORF SEQ Signal Signal ID NO: Expression Signal Signal Value (Top) Hit ID NO: Top Hit ID HO: Top Hit Source 15464 28208 3.99 6.0E-46 AI884381.1 EST_HUMAN 18818 31779 10.94 6.0E-46 AR635448.1 EST_HUMAN 23175 2.04 6.0E-46 AW613244.1 EST_HUMAN 23175 2.04 6.0E-46 BE784971.1 EST_HUMAN 23175 6.0E-46 BE784971.1 EST_HUMAN 23175 6.0E-46 BE784971.1 EST_HUMAN 8:9 5.0E-46 AL163210.2 NT	Examt SEQ ID ID NO: CRF SEQ ID ID NO: Expression Signal S	Examt SEQ ID ID NO: CRF SEQ ID ID NO: Expression Signel (Top) Hit Top Hit Acession No. Top Hit Top Hit Top Hit Top Hit Acession No. Top Hit Top Hit Top Hit Top Hit Acession No. 15464 28208 3.99 6.0E-46 Al884381.1 EST_HUMAN 18818 31779 0.72 6.0E-46 Al885448.1 EST_HUMAN 19804 32898 0.72 6.0E-46 Al88544.1 EST_HUMAN 13012 8.9 5.0E-46 BE74971.1 EST_HUMAN 16275 28930 1.07 6.0E-46 BE677194.1 EST_HUMAN 16275 28930 1.07 6.0E-46 BE677194.1 EST_HUMAN	Expn SEQ ID ID NO: ORF SEQ Signal Signa	Expn SEQ ID ID NO: ORF SEQ Signal Signa	Expn NO: CRF SEQ ID NO: Expression Signal Signal NO: (Top) Hit PLASTE Value Top Hit Acession No. Top Hit Acession Source Source Top Hit Acession Source Top Hit Acession Source 15464 28208 3.99 6.0E-46 AIB84381.1 EST_HUMAN 18904 32868 0.72 6.0E-46 AM635448.1 EST_HUMAN 13012 2.04 6.0E-46 BE784971.1 EST_HUMAN 16275 28929 1.07 6.0E-46 BE677194.1 EST_HUMAN 16275 28930 1.07 6.0E-46 BE677194.1 EST_HUMAN 18386 32413 1.08 6.0E-46 BE677194.1 EST_HUMAN 18386 32570 4.28 6.0E-46 BE677194.1 EST_HUMAN 18642 32570 4.28 6.0E-46 BE677194.1 EST_HUMAN 19687 32736 6.0E-46 BE677194.1 EST_HUMAN 19687 5.0E-46 BE677194.1 EST_HUMAN 18642 5.0E-46 BE677194.1 EST_HUMAN	Expn NO: CRF SEQ ID NO: Expression Signal S	Expn NO: ORF SEQ ID NO: Expression Signal PLASTE (Top) Hit No. Top Hit Acession Place Nalue Top Hit Acession Place Nalue Top Hit Acession Place Source Top Hit Acession Place Source Top Hit Acession Source Top Hit Acession Place Source Top Hit Acession Source Top Hit Acession So	Exant SEQ ID NO: CRF SEQ Signal Signal Signal No: Most Similar No: Top Hit Acession No: Top H	Exam ORF SEQ Expression (Top) Hit Top Hit Acession No. Top Hit Acession Signal Top Hit Top Hit Acession Source No. Top Hit Top Hit Acession Signal Top Hit Top Hit Acession Source No. Top Hit Top Hit Acession Source Source National Signal Top Hit Top Hit Top Hit Acession Source National Signal Top Hit Top Hit Top Hit Top Hit Acession Source National Signal Top Hit Top Hi	Exam Signal Most Similar (Top) Hit Acession Top Hit Acession Signal (Top) Hit Acession Top Hit Acession Signal (Top) Hit Acession Top Hit Acession Signal (Top) Hit Acession Top Hit Acession Signal (Top) Hit Acession Top Hit Acession Signal (Top) Hit Acession Top Hit Acession Scalars Top Hit	Expr Moet Similar Signal Moet Similar No. Top Hit Acession Signal No. Moet Similar No. Top Hit Acession Signal Signal No. Top Hit Acession Signal No. Top Hit Acession Source No. Top Hit Acession Source No. Top Hit Acession Source No. Top Hit Acession Source No. Top Hit Acession Source No. Top Hit Acession Source No. Top Hit Acession Source No. Detablese Source No. Top Hit Acession Source No. Detablese Source No. Top Hit Acession Source No. Detablese No. Detablese Source No. Detablese	Exon NO: ORF SEQ Signal Expression Signal Most Similar (Top) Hit Asbed Top Hit Acession No. Top Hit Source Source Source Top Hit Source 15464 28208 3.99 6.0E-46 AR835446.1 EST_HUMAN 19804 32988 0.72 6.0E-46 BR63240.1 EST_HUMAN 23175 2.04 6.0E-46 BE784971.1 EST_HUMAN 13012 8.9 5.0E-46 BE77194.1 EST_HUMAN 16275 28829 1.07 5.0E-46 BE77194.1 EST_HUMAN 16376 32736 0.62 5.0E-46 BF50442.1 EST_HUMAN 19542 2.0540 6.0E-46 BF50442.1 EST_HUMAN 19542 32736 0.62 5.0E-46 BF50442.1 EST_HUMAN 19638 32736 0.62 5.0E-46 BF50442.1 EST_HUMAN 14442 27140 6.86 4.0E-46 Ax308381.1 EST_HUMAN 14442 27140 6.86 4.0E-46 Ax308381.1 EST_HUMAN	Expn NO: ORF SEQ ID NO: Expression Signal (Top) Hit ILASTE Nale Top Hit No. Top Hit Acession Patchese Top Hit Source 15464 28208 3.09 6.0E-46 ANB35448.1 EST_HUMAN 19804 32868 0.72 6.0E-46 ANB13244.1 EST_HUMAN 19305 32875 0.72 6.0E-46 BE784971.1 EST_HUMAN 16275 288229 1.07 6.0E-46 BE784971.1 EST_HUMAN 16275 288229 1.07 6.0E-46 BE784971.1 EST_HUMAN 16376 32570 4.29 5.0E-46 BE677194.1 EST_HUMAN 19589 32570 4.29 5.0E-46 BE677194.1 EST_HUMAN 19580 32736 0.47 5.0E-46 BF500442.1 EST_HUMAN 19581 35360 0.47 5.0E-46 BF500442.1 EST_HUMAN 13442 3743 1.4 4.0E-46 ANB3831.1 EST_HUMAN 14442 27141 6.86 4.0E-46 ANB770	Expn NO: ORF SEQ ID NO: Expression Signal (Top) Hit ID NO: Top Hit Signal Top Hit ID NO: Top Hit Signal Top Hit ID NO: Top Hit	Expn NO: ORF SEQ Signal Expression (Top) Hit Value Moet Similar No. Top Hit Acession Value Top Hit Acession Source To	Expn NO: ORF SEQ Signal Expression (Top) Hit Value Moet Similar (Top) Hit Value Top Hit Acession (Top) Hit Asian Top Hit Acession (Top) Hit Asian (Top) Hit Asian Top Hit Acession (Top) Hit Asian (Top) Hit Asian (T	Expn NO: ORF SEQ Signel Expression (Top) Hit Pales Moest Similer Value Top Hit LAST E Top Hit Dispession Top Hit Dispession Top Hit Dispession Top Hit Dispession Top Hit Source 16464 28208 3.90 6.0E-46 Al884381.1 EST_HUMAN 18804 32888 0.72 6.0E-46 Al884381.1 EST_HUMAN 19804 32888 0.72 6.0E-46 Al884381.1 EST_HUMAN 19804 32888 0.72 6.0E-46 Al884381.1 EST_HUMAN 19675 28820 1.07 5.0E-46 BE7077194.1 EST_HUMAN 16275 28830 1.07 5.0E-46 BE7077194.1 EST_HUMAN 19687 32736 0.62 5.0E-46 BE707429.1 EST_HUMAN 19687 32736 0.47 5.0E-46 BE70742.1 EST_HUMAN 13405 1.4442 27140 6.86 4.0E-46 ANT7054.1 EST_HUMAN 17121 29764 1.04 4.0E-46 ANT7054.1 EST_HUMAN<	Expn NO: 15 (10) ORF SEQ ID NO: 10 NO: 15 (10) Expression (Top) Hit 10 NO: 10	Exon NO: ORF SEQ Signed Signed Expression Signed Public Most Similar Public Top Hit Acession Value Top Hit Acession Source Top Hit Acession Source Top Hit Acession Source 15464 28208 3.50 6.0E-46 AR884381.1 EST_HUMAN 18818 31779 10.34 6.0E-46 AR884381.1 EST_HUMAN 19804 32808 0.72 6.0E-46 BE784971.1 EST_HUMAN 13012 28829 1.07 6.0E-46 BE77194.1 EST_HUMAN 16275 28829 1.07 6.0E-46 BE77194.1 EST_HUMAN 16376 32570 0.0F-46 BE77194.1 EST_HUMAN 16340 32570 0.07 6.0E-46 BE75042.2 EST_HUMAN 19642 32570 0.07 6.0E-46 BE75042.1 EST_HUMAN 19642 32570 0.07 6.0E-46 BE75042.1 EST_HUMAN 113405 32730 0.07 6.0E-46 BE75042.1 EST_HUMAN 11442 27140 6.86

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Single Extended Expressed III Diam	Top Hit Descriptor Top Hit Descriptor Source	NT H.sapiens ig lambda light chain variable region gene (7c.11.2) germilne, ig-Light-Lambda; VLambda	wj49c04.x1 NCI_CGAP_Lu19 Hamo septens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 EST_HUMAN THR repetitive element;	П	ne08e09.s1 NCI_CGAP_Co3 Homo sepiens cDNA done IMAGE:880408 3' similar to contains THR.b2 THR EST_HUMAN repetitive element;	EST_HUMAN 727/811.81 Sogres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactocidase A (GLA), L44-like ribosomal protein NT (L44L) and FTP3 (FTP3) genes, complete ods	Z59e02.r1 Sceres_testis_NHT Homo septens cDNA clone IMAGE:726650 5' similer to SW:RSP1_MOUSE EST_HUMAN Q01730 RSP-1 PROTEIN.;	Г	EST_HUMAN 001445137F1 NIH_MGC_65 Home sepiens cDNA clone IMAGE:3849297 5'	EST_HUMAN yr32d01.r1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:206977 5"	T_HUMAN	4 NT Homo sapiens cell division cycle 10 (namologous to CDC10 of S. cereviside) (CDC10) mRNA		T HUMAN	EST_HUMAN EST48b095 WATM1 Hamo sapiens aDNA done 48b095	Inp78602.st NCI_CGAP_Pr2 Homo septems cDNA clone IMAGE:1132395 similar to gb:X76717 H.saplems EST_HUMAN MT-11 mRNA (HUMAN);	NT Homo septens mRNA for KIAA0980 protein, peritial cds	EST_HUMAN 7092b01.xf NCI_CGAP_Ov18 Homo septens cDNA clone IMAGE:3643705 3'				EST_HUMAN df50e03.y1 Marton Fetal Cochlea Hamo sepiens aDNA clane IMAGE:2486861 5		EST_HUMAN 602072264F1 NCI_CGAP_Bm67 Hamo septens cDNA clane IMAGE:4215398 5'	EST_HUMAN 602072264F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'	T HUMAN	NT Homo sapiens Xq pseudoautosomel region; segment 1/2
Ō	Most Similar (Top) Hit Top Hit Acession BLAST E No. Value	2 3.0E-46 273660.1	3.0E-46 AI831462.1	9 3.0E-46 D31765.1			3 2.0E-46 U78027.1	2 2.0E-46 AA399286.1	2.0E-46 991		5 2.0E-46 H48391.1	2.0E-46 AW2772	1.0E-48	3 1.0E-46 7862177 NT	1.0E-46 AW9785	6 1.0E-46 H97330.1	5 1.0E-46 AA631912.1	7 1.0E-46 AB023197.1	8 1.0E-46 BF194707.1	4 1.0E-46 8923762 NT	4 1.0E-46 8923762[NT	7 1.0E-46 BF194707.1	3 1.0E-46 AW023178.1	3 1.0E-46 AW023178.1	8 1.0E-46 BF631102.1	8 1.0E-46 BF331102.1		8 9.0E-47 AJZ71735.1
ם		1.2	7.59	2.19	7.64	1.56	3.43	121	7.67 2.0E-46 991	1.46	1.5 2.0E-46 H48391.1	3.38 2.0E-46 AW2772	7.67 1.0E-48	1.22 1.05-40	3.44 1.0E-46 AW9785	3.06	33.4	3.17	6.88	8.14 1.0E-46	6.14 1.0E-46	5.27	1.53	1.53	2.28	2.28		6.18 9.0E-47 AJ271735.1
Ō	ORF SEQ Expression (Top) Hit ID NO: Signal Value	30092	34483 7.59	37474 2.19	26255 7.64	1.56	27070 3.43	30258	33142 7.67 2.0E-46 991	1.46	1.5	30902 3.38 2.0E-46 AW2772	26628 7.67 1.0E-48	27000 1.23 1.0E-46	27745 3.44 1.0E-48 AW9785	27857 3.06	28654 4.55	3.17	31322 6.88	31617 6.14 1.0E-46	31618 6.14 1.05-46	31322 5.27	37865 1.53	37866 1.53	31115 2.28	31116 2.28	237	6.18
Ō	Most Similar Expression (Top) Hit Signal BLAST E Value	1.2	21339 34483 7.59	37474 2.19	13588 26255 7.64	1.56	14383 27070 3.43	17645 30258 1.2	33142 7.67 2.0E-46 991	1.46		25170 30902 3.38 2.0E-46 AW2772	13961 28628 7.67 1.0E-48	1.22 1.05-40	15005 27745 3.44 1.0E-48 AW 9785	3.06	33.4	17549 3.17	6.88	25080 31617 8.14 1.0E-46	6.14 1.0E-46	5.27	1.53	1.53	2.28	24564 31116 2.28	237	

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					iso		
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
4879	17606	30229	3.02	9.0E-47	9.0E-47 AW 770928.1	EST_HUMAN	h93e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA done IMAGE:3009534.3' similar to TR:075703 075703 HYPOTHETICAL 12.4 KD PROTEIN.;
6284	19057	32037	0.0	9.0E-47	11425439 NT	NT	Homo saplens zinc finger protein ZNF286 (ZNF286), mRNA
12631	25270	30725	2	9.0E-47	11417966 NT	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1801	14541	27252	6.88			NT	Homo sapiens HLA-C gene, exon 5, Individual 18323
1801	14541	27253	6.88	8.0E-47	8.0E-47 Y18536.1	NT	Homo sapiens HLA-C gene, excn 5, individual 19323
27.22	15429	28167	1.04	8.0E-47	6463956 NT	¥	Homo sepiens protein phosphetase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3024	15790	28438	1.89	8.0E-47	8.0E-47 AJ229043.1	IN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3613	16366	29000	0.68	8.0E-47		NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3613	16366	29010	0.68	8.0E-47	8.0E-47 AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12004	25169		1.38	7.0E-47	7.0E-47 AV683284.1	EST HUMAN	AV683284 GKC Homo sapiens cDNA clane GKCASH11 5'
2550	15285	28000	1.68	6.0E-47	1.2	NT	Homo saplens chromosome 21 segment HS21 0048
8592	21284	34423	0.49	6.0E-47	6.0E-47 U77054.1	EST_HUMAN	HSU77054 Human Homo saplens cDNA clone N7
9176	21846	35012	6.78	6.0E-47	6.0E-47 AI695189.1	EST HUMAN	t298h02.x1 NCI_CGAP_KId11 Homo sepiens cDNA done IMAGE:2296659 31
9612	22285		89.0	6.0E-47	6.0E-47 AB042824.1	NT	Homo sepiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9812	22285	35451	0.68	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
648 2	19249		6.67	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisies, homolog) (CDC37), mRNA
10696	23387		5.27	5.0E-47	5.0E-47 M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (catt/936208) Homo sepiens cDNA clone HFBCF07
1379	14128	26801	3.20	4.0E-47	TN 9527556 NT	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6733	19567	32599	1.8	4.0E-47	4.0E-47 BE938898.1	EST_HUMAN	MR4-TN0108-280800-201-d04 TN0108 Homo septiens cDNA
8379	21072	34210	2.42	4.0E-47	4.0E-47 BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Hamo septems aDNA dane IMAGE:3622437 5
8379	21072	34211	2.42	4.0E-47	4.0E-47 BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA done IMAGE:3622437 5
8516	21208	34351	0.61	4.0E-47	4.0E-47 AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-f05 BN0034 Homo septiens cDNA
							xx86b07.xd NCI_CGAP_Lym12 Homo sepiens cDNA done IMAGE:2848597 3' similar to SW:INT6_MOUSE
11635	-1		2.83		4.0E-47 AW 515509.1	EST_HUMAN	GOSZSZ VIKAL IN EGYK I LON SI I E PRO I EIN IN I -S. [1];
531	13315		2.05		3.0E-47 BE907634.1	EST_HUMAN	601497839F1 NIH_MGC_70 Homo septens cDNA clone IMAGE:3859721 5
531	13315	25951	2.05	3.0E-47	3.0E-47 BE907634.1	EST HUMAN	601497639F1 NIH_MGC_70 Homo septens cDNA done IMAGE::3890721 51
799	13571	28232	6.45	3.0E-47	3.0E-47 N57483.1	EST_HUMAN	yy64b04.s1 Sceres_multiple_sclerosts_ZNbHMSP Hamo septens cDNA done IMAGE:277327 3'
924	13691	26355	10.25	3.0E-47	3.0E-47 AL163284.2	M	Homo saplens chromosome 21 segment HS210084
3296	16058	78707	62.0	3.0E-47	4504116 NT	NT.	Homo sapiens glutamate receptor, lonotropic, kalnete 1 (GRIK1) mRNA
3948			5.77	3.0E-47		NT	Homo sapiens ruciear dual-specificity phosphatase (SBF1) mRNA, partial cds
4329	17068	29696	1.32		3.0E-47 M12959.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
5922	18707	31659	5.41	3.0E-47	3.0E-47 AW 408800.1	EST_HUMAN	UHHF-BM0-ack-d-07-0-UI.r1 NIH_MGC_38 Hamo sapiens cDNA clane IMAGE:3063205 5'

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Hamo sapiens cDNA clone IMAGE:3063205 5'	dri04e07.x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:1843716.3'	EST375869 MAGE resequences, MAGH Hamo sepiens cDNA	EST375869 MAGE resequences, MAGH Hamo sapiens oDNA	Homo septens myosih phosphatase, target subunit 2 (MYPT2), mRNA	Homo explens chromosome 21 segment HS21C009	Homo sapiens chromosome 21 segment HS21C009	W498b02x1 NCI_CGAP_GOS Home septens cDNA clone IMAGE:2479851 3'	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA	ng43h12.s1 NCI_CGAP_Co3 Homo septens cDNA clone IMACE:637607 3'	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA	nf23g07.s1 NCI_CGAP_Pr1 Hamo sepiens aDNA clane IMAGE;914652	nf23g07.s1 NCI_CGAP_Pr1 Homo septens cDNA dons IMAGE:814652	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA	EST377239 MAGE resequences, MAGI Homo saplens cDNA	Homo septens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds	801463932F1 NIH_MGC_67 Hamo septens aDNA clane IMAGE:3867487 5'	901463932F1 NIH_MGC_67 Homo sepiens.cDNA clone IMAGE:3867487 5	Homo saplens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion	Homo saplens DNA for amykold precursor protein, complete cds	Homo sapiens DNA for emykold precursor protein, complete cds	Homo septens SPH-binding factor mRNA, partial cds	Homo septens BTG family, member 3 (BTG3), mRNA	Human tyrosine khase receptor (ad) mRNA, complete cds	y92e08.s1 Soares infant brain 1NIB Homo sapiens cDNA done IMAGE:23966 3' similar to contains OFR	repetitive element;	qp99h03.x1 Soeres_fetal_king_NbHL19W Homo saptens cDNA ctone IMAGE:1931189 3:	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA	et19e00.x1 Bersteed aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995 RAS-RELATED PROTEIN RAP-1A (HUMAN);	h84a11.x1 Soures_NR_T_GBC_S1 Homo septens cDNA clone IMAGE:2978972 3' similar to gb:M28326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
gle Exon Pro	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	NT	EST_HUMAN	TN	EST_HUMAN	N	EST_HUMAN	EST_HUMAN	ſ '	EST_HUMAN	Z L	EST HUMAN	EST_HUMAN	TN	TN	TN	NT	TN	NT		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Ŋ
CIN .	Top Hit Acession Na	3.0E-47 AW408800.1	3.0E-47 AI222413.1	3.0E-47 AW963796.1	3.0E-47 AW963796.1	4505318 NT	2.0E-47 AL163209.2	2.0E-47 AL163209.2	2.0E-47 AI989279.1	. 7662109 NT	2.0E-47 AA524514.1	4504866 NT	2.0E-47 AA569592.1	1	74648	2.0E-47 AW985168.1	2.0E-47 AF073921.1	2.0E-47 BE778475.1	2.0E-47 BE778475.1				2.0E-47 AF071771.1	11526136 NT	2.0E-47 M78125.1			1.0E-47 AI333429.1	1.0E-47 AW813906.1	1.0E-47 Al880888.1	1.0E-47 AW 664648.1	
	Most Similar (Top) Hit BLAST E Value	3.0E-47	3.0E-47	3.0E-47	3.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47	2.0E-47 L09731.1	2.0E-47 D87675.1	2.0E-47 D87675.1	2.0E-47	2.0E-47	2.0E-47		2.0E-47 R42423.1	1.0E-47	1.0E-47 /	1.0E-47	1.0E-47	1.0E-47 L30115.1
	Expression Signal	5.41	1.76	0.71	0.71	1.61	2.69	2.69	96.0	1.75	3.41	2	1.5	1.5	1.06	1.3	1.12	1.23	1.23	1.43	1.92	1.92	1.67	0.77	1.27		1.75	7.35	1.98	6.79	0.56	2.28
	ORF SEQ ID NO:	31660		34569		25600	26377	26378		27022	27111	29677	28722	29723	29832	30121	31411	31615	31616		33685	33686	34452	35222	36451		30709	26804	30347	32441		38112
	Exan SEQ ID NO:	18707	19236			12958	13713	13713	14307	14334	14418	17052	17090	17090	17206	17463	18490	18673	18673	25116	20559	20669	21310	22051	23218		25312	14131	17738	19426	21459	22802
	Probe SEQ ID NO:	5922	8469	8732	8732	143	947	8	1560	1588	1673	4313	4351	4351	4471	4761	2008	2887	5887	7598	7864	7864	8618	988 83	11451		12077	1384	5017	6944	8767	10254

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		T	Т	7_	Т	T		Т	\neg	T		_	Т	_	Т	_	7	-	_	_	_		_	-		_	
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sapiens chromosome X open reading frame 6 (CXORES) mRNA	Hamo sablens chromosome X open reading frame 6 (CXORER) mBNA	h14b12x1 NCI_CGAP_GU1 Homo septens GNN done IMAGE:2972255 3' similar to SW:DCRB_HUMAN PERSES DOWN SYNDROME CRITICAL DECIDION DOCTEN IN	MR4BT0657-080400-201-4-10 RT0657 Home contains - Child	Human endogenous netrovirus HERV-P-T47D	Inv03/05.s1 NCI_CGAP_Pr22 Homo septens cDNA clone IMAGE:1219137 3' similer to contains PTR5.b1	UI-H-BW1-4-1-4-10-00-10-10-10-10-10-10-10-10-10-10-10-	first? Regional genomic DNA specific cDNA library Home seniors cDNA close CD17 28	ym55e10_rf Soares infant brain 1NIB Homo septens cDNA clone IMAGE:52182 5' similar to SP:M6B MOUSE P36803 MEMBRANF GI YCOPROTEIN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukernia Baylor-HGSC project=TCBA Homo	Inc/8801 81 NCI CRAP Phet Home seniore ADMA Alone MAACE AAAAAAAAA	Inotagot st NCI CGAP Phot Home services and Action IMAGE 11010723	Homo septens mRNA for KIAA1501 number nestical rice	Homo sapiens mRNA for KIAA1501 protein, partial cds	Homo sapiens v-rei avian reticuloendotheliosis virai oncogene homolog A (nuclear factor of kappa light bolypentide gene enhancer in Banalla a (next) (PELA) mbana	AV743451 CB Homo serviews cDNA clare CRCCGG10 &	2/80/003,r1 Soares overy fumor NHOT Home seniors (ANA Senior Franch MA) CE-84/0057 Fr	801305064F1 NIH MGC 39 Homo sapiens cDNA clane IMAGE:3639782 5	ym55e10.r1 Soares Infant brain 1NIB Homo sepiens cDNA clone IMAGE:52182 5' similar to SP:M6B MOUSE P36803 MEMBRANE CA YCODPOTEIN .	Homo saplens displatin resistance-associated overexmessed motein (1 OCS1747) mRNA	Home services (A4) that (A4) the (A4) t	Homo sepiens RNA binding moiff problem 8 (RRAAR) mRNA	Homo saplens chromosome 21 seement MC24003	Homo saplens chromosome 21 segment HS21Ch48	Human endogenous retroviral DNA (4-1), complete ratroviral segment	td17c01.x1 NCI_CGAP_Co16 Home sepiens cDNA clone IMAGE:2075904 3' similar to TR:014588 014588 SIMILARITY TO U73941;
gle Exon Pro	Top Hit Derkabase Source	NT.	₩ F	EST HUMAN	EST HUMAN	¥	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HIMAN	EST HUMAN	EST HUMAN	LN	F	 	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN		<u> </u>	15	Į.	Į.	N.	EST_HUMAN
Silo	Top Hit Acession No.	4885170	4885170 NT	3.0E-48 AW664531.1	-	-	3.0E-48 AA659930.1				2.0E-48 BE246065.1		_	2.0E-48 AB040934.1	Ţ	11496238 NT	2.0E-48 AV743451.1		_		706534	4502168 NT	5032032 NT	1.0E-48 AL163302.2	1.0E-48 AL 163248.2		1.0E-48 AI889077.1 E
	Most Similar (Top) Hit BLAST E Value	3.0E-48	3.0€-48	3.0E-48	3.0E-48	3.0E-48	3.0E-48	3.0E-48	2.0E-48	2.0E-48	· 2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48 H24278.1	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48 M10976.1	1.0E-48 A
	Expression Signal	15.26	15.28	0.75	2.47	0.84	3.41	9.52	1.71	5.15	1.42	0.61	0.61	4.77	4.77	3.35	1.33	4.27	1.86	1.34	2.3	17.13	3.77	30.36	96.0	1.8	1.17
	ORF SEQ ID NO:	27422	27423	29017	31519	32701		36708	25495		29861	31438	31437	33182	33183	33197	34084	30486	30820		25511	26293	26691	27359	28894	30398	31948
	Exon SEQ ID NO:	14705	14705	16375	18594	19855	20984	23467	12873	13949	17231	18516	18518	20096	20096	20109	20947	17888	25232	13949	12883	13623	14023	14648	16238	17780	18971
	Probe SEQ ID NO:	1969	1969	3622	5804	6019	8230	10784	44	1197	4495	5724	5724	7419	7419	7432	8253	12041	12367	12716	8	853	1273	1911	3481	5061	6195

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ed in Brain	Top Hit Descriptor	td17cd1.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:014588 014588 SIMILARITY TO U73941	NF2 gene	Homo saplens mRNA for KIAA1071 protein, partial cds	Homo saplens mRNA for KIAA1071 profein, partial cds	Homo seplens huntingtin (Huntington disease) (HD) mRNA	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13) mRNA	Homo sapiens mitogen-ectivated protein kinase kinase kinase 13 (MAP3K13) mRNA	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA	mRNA for KIAA1245 protein, pertial cds	601888098F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5	Homo sepiens B cell linker protein (SLP65), mRNA	Homo sapiens B cell linker protein (SLP65), mRNA	Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds	Mus musculus T-box 20 (Tbx20), mRNA	Mus musculus T-box 20 (Tbx20), mRNA	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds	Homo sapiens gene for activin receptor type IIB, complete cds	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	Homo saplens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA	Homo saplens proteasome (prosome, macropain) 26S subunit. ATPase, 4 (PSMC4) mRNA	Homo sapiens chromosome 21 segment HS21C084	wt25h04.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350063 3' similar to TR:O54923 O54923 RSEC15.	DKFZp762C033_s1 762 (synonym: hmel2) Hamo sapiens cDNA clone DKFZp762Cn33 31	wt25h04.xt Sceres NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2359963 3' similar to TR:O54923 O54923 RSEC15.	be55g05.x1 NIH_MGC_10 Homo septens cDNA done IMAGE.2800504 3' striitst to gb.X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE):	DKFZp781A138_s1 761 (synonym: harmy2) Horno sapiens cDNA clone DKFZp761A138 3'
es Expressed		td17co1.x1 NCI_CGAP_C SIMILARITY TO U73941	Homo sepiens NF2 gene	forno sapiens m	formo sapiens m	lamo sepiens hu	lomo sapiens m	lomo sapiens m	lomo sapiens C	fomo sapiens m	01888096F1 N	omo sapiens B	domo sapiens B	fus musculus M	fus musculus T	fus musculus T.	uman inositol 1,	omo sapiens ge	omo sapiens pri	omo saplens pri	omo sapiens pre	omo sapiens pro	omo sapiens pro	omo sapiens pro	omo sapiens ch	wf25h04.x1 Soares O54923 RSEC15	KFZp762C033	wf25h04.x1 Soeres 054923 RSEC15.	Pe55g06.x1 NIH_MC RIBOSOMAL PROT CATALON MANAGER	KFZp761A138
Single Exon Probes Expressed in Brain	Top Hit Database Source	EST_HUMAN S		I	I					H	T_HUMAN							IN							NT	EST HUMAN O	Г	EST_HUMAN O	be Ri Ri EST HUMAN 00	П
Sing	Top Hit Acession No.	_		-	-	4755137 NT	4758695 NT	4758695 NT	502838	-	1	11429808 NT	11429808 NT	B026497.1	10048417 NT	10048417 NT	23850.1 N		572990 NT	5729990 NT	6729990 NT	5729990 N	5728990 NT	5729990 NT					-	
	Most Similar (Top) Hit BLAST E Value	1.0E-48 AI889077.	1.0E-48 Y18000.1	1.0E-48 AB028994	1.0E-48 AB028994.	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48 AB033071	1.0E-48 BF304883.	1.0E-48	1.0E-48	8.0E-49 AB026497.1	8.0E-49	8.0E-49	8.0E-49 U23850.1	8.0E-49 AB008681.1	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49	7.0E-49 AL163284.2	7.0E-49 AI807191.1	7.0E-49 AL120937.1	7.0E-49 AI807191.1	6.0E-49 AW731740.	6.0E-49 AL162091.1
	Expression Signal	1.17	0.94	0.71	0.71	2.52	92.0	0.78	0.84	6.4	5.33	4.08	4.08	1.13	3.43	3.43	3.17	1.15	-	1	1.73	1.73	2.94	2.94	3.4	2.11	1.46	0.67	12.12	1.27
<u> </u>	ORF SEQ ID NO:	31947		32268	32267	32913	34566	34567	34968	35004	35314	38127	36128	27461	31704	31705	34026	35733	25814	25815	25814	25815	25814	26815	20015	30862	30873	30862	25846	29464
	SEQ ID NO:	}	19176	19265	19265	19844	21422	2422	21801	21838	22134	22917	22917	14737	18744	18744	20888	22539	13171	13171	13171	13171	13171	13171	13951	18173	18183	18173	13005	16837
	Probe SEQ ID NO:	6195	9407	9200	820	7157	8730	8730	9113	24	88	0000 10000	10289	2002	2862	2985	8194	8886	135	135	8	\$ 8	3	g	138	5373	5383	5716	182	4095

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Single Exon Proces Explessed in Drain	Top Hit Descriptor	AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'	hd44602x1 Soares_NFL_T_GBC_S1 Hamo sapiens aDNA clane IMAGE:2912378 3' similar to TR:095636 095638 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.;	Mus musculus keretin complex 2, gene 6g (Krt2-6g), mRNA	Mus musculus keratin complex 2, gene 6g (Krt2-8g), mRNA	UI-H-BI3-ato-e-05-0-UI s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'	EST77626 Pancreas tumor III Homo sapiens cDNA 5' end	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end	2/29c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo saplens cDNA clone IMAGE:451694 3'	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosame 21 segment HS21CO10	zp29c07.r1 Stratagene neurospithollum (#637231) Homo saptens cDNA clone IMAGE:610960 5' similar to TR:0233226 0233228 RTVL-H PROTEIN, ;contains LTR7.t3 LTR7 LTR7 repetitive element;	Homo sapiens putative fumor suppressor ST13 (ST13) mRNA, complete cds	Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1) (H. sapiens) (LOC83362), mRNA	x08b01.x1 NG_CGAP_Ut4 Homo septens cDNA clone IMAGE:2675583 3' similer to WP:B0350.2B CE06703;	Homo sepiens UDP-N-ecety-alpha-D-galactosamine:polypeptide N-ecety/galactosaminytransferase 8 (GalNAc-T8) (GALNT8), mRNA	Homo sapiens UDP-N-ecetyl-alpha-D-galactosamine:polypeptide N-ecety/galactosaminytransferase 8 (GalNAc-T8) (GALNT8), mRNA	Horno septens KIAA0823 gene product (KIAA0823), mRNA	Homo sapiens copine III (CPNE3), mRNA	Homo sapiens copine III (CPNE3), mRNA	z/80/05.r1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:882977 67	Homo septems glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) cenes. complete cds	H.seplens mRNA for acetyl-CoA carboxylase.	2831c05.r1 Soares retina N2b4HR Homo septens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1	repetitive element ;	Human type IV collegen (COL4A6) gene, excn 40	EST25e12 WATM1 Homo saplens cONA clone 25e12
ום בייטוו גווחס	Top Hit Database Source	EST HUMAN	EST_HUMAN			T_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		NT	EST_HUMAN	Г		EST_HUMAN						EST_HUMAN	5			EST_HUMAN	П	EST_HUMAN
3110	Top Hit Acession No.	6.0E-49 AU140742.1	8.0E-49 AW511225.1	9910293 NT	9910293 NT	6.0E-49 AW462218.1		6.0E-49 AA386556.1	6.0E-49 AA707567.1			5.0E-49 AA172121.1		11436355 NT	4.0E-49 AW189633.1	11525737 NT	TN 7575737	7662209 NT	11425374 NT	11425374 NT	4.0E-49 AA210798.1	4 DE 49 AF240786 1			.1		
	Most Similar (Top) Hit BLAST E Value	6.0E-49	6.0E-49	6.0E-49	6.0E-49	6.0E-49	6.0E-49	6.0E-49	6.0E-49 /	5.0E-49	5.0E-49	5.0E-49	5.0E-49 U17714.1	5.0E-49	4.0E-49	4.0E.49	4.05.49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.05.49	3.0E-49 X88968.1		3.0E-49 A	3.0E-49 U46999.1	3.0E-49 H39479.1
	Expression Signal	0.94	0.69	0.45	0.45	2.5	2.6	2.6	2.03	7	7	3.49	4.25	2.04	47.84	98.0	900	60	0.47	0.47	4.21	4	133		1.9	2.33	11.87
	ORF SEQ ID NO:	32109	33076	35478	35479	37202	37579	37580		26117	26118	27235	28201	28678	25927	32030	32031	33488	34604	34605			25961			30264	33081
	Exan SEQ ID NO:	19118	19997	22285	22285	23910	24257	24257	25151	13470	13470	14527	15459	16029	13296	19858	10858	20374	21465	21455	25368	24730	13330		15364	17651	20002
	Probe SEQ ID NO:	6349	7314	9633	5833	11248	11661	11681	12362	989	605	1786	2754	3267	512	7172	7472	7710	8763	8763	12221	12306	547		2654	4923	7319

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Table 4
Single Exon Probes Expressed in Brain

		T	Τ	T	Ω.	\top	T	T	T	Т	Т	T	Т	1	T	T	T	Т	T	Т	τ_	Т	Т	Т	Т	Т	T	Т	T	\Box
טווקום באסור דוטנסט באינו סופונו	Top Hit Descriptor	EST42572 Endometrial turnor Homo sapiens cDNA 6' end	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	yx23d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:282571 5'	oz88d02x1 Sceres_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1682403 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN);contains Alu repetitive element.contains element MER22 inspetitive element.	UH-BIA-ens-4-02-0-UI st NOI CGAP Subs Homo seniens cDNA clone MAACE-2089838 2	AV717938 DCB Homo saplens cDNA clone DCBALB01 55	EST02558 Fetal brain, Stratagene (cat#938208) Homo sapiens cDNA clone HFBCY50	Homo sapiens SNCA Isoform (SNCA) gene, complete ods, alternatively apliced	601458531F1 NIH_MGC_66 Hamo septens cDNA clone IMAGE:3862086 5	Homo sapiens keratin 18 (KRT18) mRNA	601115769F1 NIH_MGC 16 Homo sepiens cDNA done IMAGE:3356273 5	601820053F1 NIH_MGC_58 Hamp sepiens cDNA done IMAGE:4052052 5	yn48h04.r1 Soarse adult brain N2b5HB557 Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:CBG1 HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) CAMMA-1 SUBUNIT	EST376713 MAGE resequences, MAGH Homo sepiens cDNA	AV703000 ADB Homo sepiens cDNA clone ADBCVD11 5'	AV703000 ADB Hamo septens cDNA clane ADBCVD11 5'	601290330F1 NIH_MGC_8 Homo septens cDNA clone IMAGE:3620863 57	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'	yw78g12.s1 Source_placenta_8to9weets_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258406.3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);	yw78g12.s1 Soeres, placenta, 8tb9weels, 2NbHP8tb9W Homo sapiens cDNA clone IMAGE;258406.3' similar to gb;X85873 KINESIN HEAVY CHAIN (HUMAN);	Homo sepiens succinete-CoA ligase, GDP-forming, eighs subunit (SUCLG1), mRNA	Homo septens succhnete-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA	Homo septens RNA binding motif protein 7 (LOC51120), mRNA	601300892F1 NIH MGC_21 Hamo septems aDNA done IMAGE:3635398 5	DKFZp434D2423_11 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5	AV751477 NPD Homo sepiens dDNA clone NPDAWE04 5'	Homo seplens brefeldin A-inhibited guenine rucleotide-exchange protein 1 (BIG1), mRNA	Homo septens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	Homo sapiens glyche N-methyltransferase (GNMT) gene, complete cds
פום באסוו דוס	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HIMAN	EST HUMAN	EST HUMAN	Z	EST_HUMAN	1	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	E	N.	L'A	EST HUMAN	EST_HUMAN	EST_HUMAN	- LN	NT	LN
	Top Hit Acession No.	3.0E-49 AA337561.1	2.0E-49 BE165980.1	2.0E-49 N26446.1	2.0E-49 A(187357.1			2.0E-49 M86033.1	2.0E-49 AF163864.1		4557887 NT	_	_	1.0E-49 H18291.1	1.0E-49 AW964640.1	1.0E-49 AV703000.1	AV703000.1	1.0E-49 BE398110.1	1.0E-49 BE398110.1	1.0E-49 N25884.1	1.0E-49 N25884.1	1321580	11321580 NT	9994184 NT	1.0E-49 BE408340.1	1.0E-49 AL043129.2	1.0E-49 AV751477.1	11427366 NT	18322	9.0E-50 AF101475.1
	Most Similar (Top) Hit BLASTE Value	3.0E-49	2.0E-49	2.0E-49	2.05-49	2 OF 49	2.0E-49	2.0E-49	2.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	1.0E-49	9.0E-50/
	Expression Signal	1.98	2.94	1.64	89.0	0.74	1.17	1.74	207	5	1.11	4.82	6.82	0.88	5.55	0.62	0.62	3.55	3.55	221	221	0.69	0.69	99.0	1.29	1.58	1.43	3.32	2.46	4:
	ORF SEQ ID NO:	37226		28630	30110	30118	32414				26978	27243	30737	31731	31736	32869	32870	32878	32879	32960	32961	33795	33796		34721	35889	36907	37236		1
	Exen SEQ ID NO:	23933	13425	15979	17478		10300	20693	25250	13648	14292	14534	18080	18787	18773	19805	19805	19811	19811	19886	19886	20672	20872	21267	21582	22874	23654	23942	24677	17865
	Probe SEQ ID NO:	11272	846	3216	4746	4758	6637	7998	12316	879	1548	1794	5275	5986	2882	7117	7117	7123	7123	7200	7200	7787	7767	8575	8891	10026	10979	11281	12215	4937

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	Top Hit Descriptor	601176250F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3531588 5	Homo saplens chromosome 21 segment HS21C002	Homo sapiens mRNA for VIP receptor 2	Homo seplens mRNA for VIP receptor 2	Homo sapiens actinin, alpha 1 (ACTN1) mRNA	Homo saplens capping protein (actin filament) muscle Z-line, beta (CAPZR), mRNA	Homo saplens hepatocyte growth factor(HGF) gene, exon 18	Inp62d06.s1 NCL CGAP_B72 Homo sapiens cDNA clone IMAGE:1130891 3' similar to gb:J05459 GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN):	QV0-BT0703-280400-211-608 BT0703 Homo seniens CDNA	RC6-TN0073-150900-011-A12 TN0073 Homo saniens cDNA	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA	ng58e12.s1 NCI_CGAP_Cc9 Homo sepiens cDNA clone IMAGE:1148206 3' similer to gb:X68391 60S RIBOSOMAL PROTEIN L6 (HUMAN):	wm55g11.x1 NCI CGAP Ut2 Homo sablens cDNA clone IMAGE-2430g08.31	601589565F1 NIH MGC 7 Hamo saplens cDNA clane IMAGE:3943577 5	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511.3' similer to contains MER29.b3 MER29 repetitive element:	EST182775 Jurkat T-cells VI Homo saplens cDNA 5' end	EST182775 Jurket T-cells VI Homo sapiens cDNA 5' end	CM0-BT0792-300500-398-b05 BT0792 Homo saplens cDNA	CM0-BT0782-300500-398-b05 BT0792 Homo sablens cDNA	n/45h10.s1 NOL CGAP_Pt4 Homo saplens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5 repetitive element;	no54e09.s1 NCI_CGAP_SS1 Home septens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1 FIRITI IN-1 ISOEODM & DEECTIDGOD (UTIMAN).	Homo sapiens chromosome 21 segment HS21ChAs	Homo saplens cysteiny-fRNA synthetise (CARS) mRNA	QV1-BT0681-280300-127-ff2 BT0681 Homo sequence CINA	Human endodernous retrovirus RTV/ H2	ob03f06.s1 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1322627.3'	CMYA5 Human cardiac muscle expression library Homo sepiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
21 11000	Top Hit Database Source	EST HUMAN	LN	N F	Ł	۲	12	ĻΝ	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HIMAAN	LN		EST HUMAN	12	EST HUMAN	EST_HUMAN
	Top Hit Acession No.	9.0E-50 BE295758.1	22	8.0E-50 X95097.2	8.0E-50 X95097.2	4501890 NT	4828858 NT	8.0E-50 D90334.1	8.0E-50 AA633467.1	7.0E-50 BE089591.1	Γ		7.0E-50 AA627822.1	7.0E-50 AI872/137.1		6.0E-50 BE044078.1	T					4.0E-50 AA801143 1		5883			2.3	3.0E-50 AW755254.1 E
	Most Similar (Top) Hit BLAST E Value	9.0E-50	8.0E-50	8.0E-50	8.0E-50	8.0E-50	8.0E-50	8.0E-50	8.0E-50	7.0E-50	7.0E-50	7.0E-50	7.0E-50	7.0E-50	6.0E-50	6.0E-50	6.0E-50	6.0E-50	5.0E-50	5.0E-50	5.05-50	4.0E-50 /	4.0E-50/	4.0E-50	4.0E-50 E	3.0E-50 M18048.1	3.0E-50	3.0E-50
	Expression Signal	0.95	4.05	2.54	2.54	2.82	1.48	15.7	1.29	0.76	1.06	1.06	9.0	7.65	0.68	5.67	12.6	12.6	1.1	1.1	5.26	1.71	0.99	0.98	1.95	4.13	1.24	1.14
	ORF SEQ ID NO:		25619	20125	26126	27201	28147		37293	26015	32643	32644	32968	38584			36646	36647	27233	27234		!	28847	32018	32888		28703	29124
	Exan SEQ ID NO:	25421		13477	13477		15410	14691	23992	13383	19604	19604	19890	23347	17048	20806	23406	23406	14526	14528	21680	13665	16197	19041	19822	14667	16054	16487
	Probe SEQ ID NO:	6310	168	702	702	1758	2703	2833	11385	909	2899	6687	7205	10656	4309	8112	10717	10717	1785	1785	8990	897	3441	6288	7135	1931	3233	3734

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens similar to sema domain, immunoglobulin domain (ig), short basic domain, secreted, (semaphorin) 3A (H. sepiens) (LOC83232), mRNA	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds	Homo sapiens FWE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete ods	Homo sepiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA	Homo seplens mRNA for KIAA1698 protein, partial ods	Homo sepiens t-complex 10 (a murine top homolog) (TCP10), mRNA	Mus musculus mRNA for neurobeachin	Human mRNA for KIAA0299 gene, perties ode	Homo sepiens Grb2-essociated binder 2 (KIAA0571), mRNA	Homo saplens CT2 oene	Homo septems MHC class 1 rection	Homo sepiens midline 1 (Opitz/BBB synchome) (MID1) mRNA	Homo sepiens decorin D mRNA, complete cds, attendatively enliced	Т	Г	Homo seplens TFF gene cluster for trefoil factor, complete cds	Human HALPHA44 gene for alpha-tubulin, exons 1-3	Human HALPHA44 gene for alpha-tubulin, excess 1-3	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Macaca mulatta cyclophtin A mRNA, complete cds	Homo seplens chromosome 21 segment HS210009	Homo saplens Xq pseudosutbeomal region; segment 1/2	Homo septens RGH2 gene, retrovirus-like element	1095636 CAMP-REGILI ATED (2) IANNE NI KY ECTION EXCLANCE EXCEDS (1) Similar to TR: 095636	Injeth03.81 NCI CGAP GCB1 Hamp sepiens aDNA clone IMAGE-1283381 3	ab23g04.x5 Strategere lung (#637210) Homo sepiens cDNA clone IMAGE:841686 3' similar to SW:PSM HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN	2451c09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA olone IMAGE:488352 6"
gle Exon Pr	Top Hit Database Source	TN	. LN	Ę	IN	Z	- F	LN	Ę	F	LN L	¥	F	Z	EST HUMAN	¥	N N	F	Z	Z	Þ	N _T	M	ħ	E	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN
Sir	Top Hit Acession No.	11421514 NT	3.0E-50 AF233436.2	3.0E-50 AF233436.2	9801589 NT	3.0E-50 AB046818.1	11418514 NT	3.0E-50 Y18276.1	3.0E-50 AB002287.1	36955	3.0E-50 AJ245621.1	2.0E-50 AF055088.1	4557752 NT	2.0E-50 AF138303.1		2.0E-50 AB038162.1			2.0E-50 X06956.1	D010293 NT	D910293 NT			5.1	1.0E-50 D11078.1	9.0E-51 AW511225.1	9.0E-51 AA744837.1		9.0E-51 AA043738.1
	Most Similar (Top) Hit BLAST E Vatue	3.0E-50	3.0E-50	3.0E-50	3.0E-50	3.0E-50	3.0E-50	3.0E-50	3.0E-50	3.0E-50	3.0E-50	2.0E-50	2.0E-50	2.0E-50	2.0E-60	2.0E-50	2.0E-50	2.0E-60	2.0E-50	2.0E-50	2.0E-60	2.05-50	1.0E-50	1.0E-60	1.0E-50	9.0E-51	9.0E-51	9.0E-51	9.0E-51
	Expression Signal	1.52	4.85	4.85	0.71	1.21	0.99	0.47	1.03	1.61	5.35	5.38	5.57	2.25	0.59	1.02	1.02	10.04	10.04	1.51	1.61	1.8	1.92	9.48	1.57	1.21	0.71	0.65	1.23
	ORF SEQ ID NO:	32618	33314	33315	34318	35567	35580	35942	36280	35984	38439		26476	26857	32539	34044	34045	34186	34187	35641	35642		25874		35956	31624	31876	34403	35075
	Exan SEQ ID NO:	19584	20214		21173	22369	22378	22725	23061	23715	23208	13532	13815	14171	19513	- 1	20909	21048	21048	22435	22435	24258	13235	15087	22741	18678	18908	21284	21903
	Probe SEQ ID NO:	6867	7544	7544	8481	9718	9727	1007	10415	11045	11441	, 8	1057	1424	6769	8215	8215	8365	8355	9784	9784	1980	84	2385	- - - - - - - - - - - - - - - - - - -	5893	6130	8572	8224

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Table 4
Single Exon Probes Expressed in

Brain	Top Hit Descriptor	eb23g04.x5 Stratagene lung (#637210) Homo eaclens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04809 PROSTATE-SPECIFIC MEMBRANE ANTIGEN	ab23g04.x5 Stratagene lung (#637210) Homo septens CDNA clone INAGE:841686 3' similer to SW:PSM_HUMAN 004600 PROSTATE-SPECIFIC MAINEDANIE ANTICEN.	W24006.r1 Marton Fetal Coches Hamp semiens cDNA close INA OF 2522.0 F	W24g06.r1 Morton Fetal Cochlee Homo sepiers cDNA clone IMAGE 253210 5	my67h03.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE-1283381 3	Homo saplens glycho amdinotransferase (Leroninine anziginotransferase) (GATA) mDNA	Homo sapiens glycine amidinotransferase (L-argining divide amidinotransferase) (GATM) mRNA	mp8e00.s1 NCI_CGAP_Lu1 Homo sepiens cDNA done IMAGE:1142440 3' similer to gb:X12671_me1 HETEROGENEOUS NUCLEAR RIBONIUS FORROTEIN A1 /HILLARN	Homo saplens POZ-73 northain (POZ-73ANV-COZ-81, mp.N.)	AU138590 PLACE1 Home servers of NA Alma Place Place ACT 100897 F	Homo septens PDZ-73 protein (PDZ-73/NY-CO-38) mRNA	xn34803.x1 NCI_CGAP_Kid11 Homo sapiens cDNA cine IMAGE:2695564 3' similar to TR:Q92340 092340 ATYPICAL PKC SPECIFIC BINDING DEOTERN	OVA-NTRO28-200400-180-406 NTRO28-100-100-100-100-100-100-100-100-100-10	DKF20434B2229 rt 424 (sunmum thes?) Homo seniore chivis chos DKE2, 234B2220 rt	DKFZ048779 1 434 (smoother: Hees) Home seelens CUI'm due DKFZ-12-10-00-00-00-00-00-00-00-00-00-00-00-00-	UI-H-BWO-BD-D-05-0-UI-s1 NCI CGAP Sirks Home series contact characters in A CE-27-26-27	31 mRNA, pertial cds	Homo sepiens KIAA0929 protein Msv2 interacting rucieer target (MINT) homolog (KIAA0929). mRNA	Homo septens KIAA0929 protein Msx2 Interaction reinterent farmer (MINITY browned NVIAA0929)	aled (Har) neme arm 3	Homo seplens mitoden-ectivated profess kinese kinese 4 (AMK KA) cases arms 4	Homo sapiens mitoder-ectivated protein kinasa kinasa 1 (MKKA) pena anan 4	Hamo sapiens ribosomal protein S6 kinasa, 70kD, polywanikła 1 /RPCS/R41 mPkiA	Homo saplens non-timese Cdo42 effector profein SPEC2 (LOCSGOO) mRNA	Homo saplens cerebral cell adhesion molecule (LOC51148). mRNA	Homo sepiens hypothetical protein FLJ11042 (FLJ11042), mRNA	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA	In (B9), mRNA
sed in Brain	7 35	Stratagene lung (#037210) Homo ser UMAN Q04809 PROSTATE-SPECII	Stratagene lung (#637210) Homo sag	Vorton Fetal Cooples Homo seplens	Vorton Fetal Cochiee Homo sepiens	NCI CGAP GCB1 Homo saplens of	is glycine amidinotransferage (L-argir	is glycine amidinotransferase (L-ardir	NCI_CGAP_Lu1 Homo septeme cDN NEOUS NUCLEAR RIBONUCLEON	S POZ-73 profite (POZ-73/NY-CO-3	LACE1 Homo septems CONA close E	8 PDZ-73 protein (PDZ-73/NY-CO-3	xm34e03.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone 092340 ATYPICAL PKC SPECIFIC BINDING PECTEIN	1-200400-180-405 NT0028 Home 20	2229 rl 434 (synonym: htms3) Homo	228 7 434 (synonym: htms3) Homo	PP-05-UISTNC CGAP START	Homo sapiens HSPC331 mRNA, pertial cds	s KIAA0929 protein Msx2 interacting	s KIAA0929 protein Msx2 interacting	Human habtodobin related (Horr) gene even 3	s mitogen-ecffveted protein kinges kin	s mitoden ectivated protein kinasa kin	s ribosomal protein S6 kinase 70kD	s non-lunese Cdc42 effector protein 8	s cerebral cell adhesion molecule (LC	s hypothetical protein FLJ11042 (FL)	hypothetical protein FLJ11042 (FLJ	Homo sapiens B9 protein (B9), mRNA
Single Exon Probes Expressed in Brain	Top Hit Database Source	EST HUMAN SW:PSM H		Т	Т	Г	1	Homo sapler	EST HUMAN HETEROGE	Т	EST HUMAN AU138590 P	Т	xn34e03.x17	Т	Т	Т	Т	Τ	Homo sapien	Homo saplen	Human hapto	Homo seplen	Homo sapien	Hamo sapien	Homo saplen	Homo saplen	Homo sapien	Homo sepien	Homo sapien
Single E	Top Hit Acession De No. S	9.0E-51 Al791154.1 EST	9.0E-61 A/791154.1 EST			9.0E-51 AA744837.1 EST	4503832 NT	4503932 NT	8.0E-51 AA610842.1 EST	39587	AU138590.1 EST H	39587	_	-	Γ		-	Z	7657286 NT	7657268 NT	01788.1 NT	F070083.1 NT		36736	11416751 NT	11429865 NT	11428525 NT	11428525 NT	7661535 NT
}	Most Similar (Top) Hit BLAST E Value	9.0E-51 A	9.0E-61 A	9.0E-51 H89078.1	9.0E-51 H89078.1	9.0E-51 A	8.0E-51	8.0E-51	8.0E-51 A	8.0E-51			7.0E-51 AW274720.	7.0E-61 AW889219.	7.0E-51 AL079628.1	7.0E-51 AL079628.1	7.0E-61 AW295803.	7.0E-51 AF161449.1	6.0E-61	6.0E-51	6.0E-51 X01788.1	6.0E-51 AF070083.1	6.0E-51 AF070083.1	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51	6.0E-51
	Expression Signal	0.98	0.66	1.89	1.89	1.43	1.45	1.45	8.43	2.24	1.13	2.02	6.0	1.45	1.37	1.37	271	1.34	4.96	14.73	1.56	9.95	9.85	1.02	0.97	. 2.2	0.68	0.68	2.18
	ORF SEQ ID NO:	35231	36232	36456	36457	31876	29770	29771	29896	33325	-	33325	28430	28687	29519	29520	29681	37603	27426	28876	31634	31648	31649	32015	32564	30540	34878	34879	35419
	Exen SEQ ID NO:	23062	22062	23252		18908	17142	17142	17285	20222	21939	20222	15781	16037	16888	16888	17067	24281	14708	16222	18686	18696	18696	19580	19336	17945	21725	21725	22235
	Probe SEQ (D NO:	9400	9400	11455	11455	11823	4405	4405	4530	7552	2384	11812	3015	3276	4148	4146	4318	11886	1972	3466	5901	5912	5912	888	6792	8888	9035	935	9582

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		T	Т	T	T	Т	1	Т	Т	T	T	Т	Т	$\overline{}$	7	٦	4	7	Т		TE	7	1			_	
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Human ankyrin (ANK1) cene exco 2	Homo sablens interleukin 17 recentor (II 17R) mRNA	Homo sapiens protein phosphatase 2. regulatory subsmit B (RRR), sinha landon (DDD) DEANDNIA	Homo serviens protein niversharese 2 montains and manual to Open Action	Home satisfies chromosome 21 segment HO2/CM2	Homo sablens T-cell hymphome investors and meteorises (/TIAM4) DNA	Novel human dene metodra to chomosome X	Homo saplens 26S protessome essociated bond1 homolog (POH1) mPNA	Homo saplens mRNA for nucleoportn 155	Hunan Ku (070/080) subserff mRNA convolete Ade	Human Ku (o70/o80) subunit mRNA complete cde	Homo sapiens RNA binding motif protein 3 (RRMs) mRNA	#81c09.x1 NCI_CGAP_Pan1 Homo saplens GDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN TYPE I CYTOSKEI ETAI 48 ALIIIAAN.1	Nove furnan cene manning to choraceme 22		ye47c08.r1 Sogres infant brain 1NIB Homo sapiens cONA clone IMAGE:53233 6' similar to gb:M14123_cds4 RETROVIDI IS DELATED DOL DOL DOL DOL DOL DOL DOL DOL DOL DO	Human InnRNP C2 andein mRNA	a04d06.Vf Human Pancingtic Islans Pancings CONA F	Homo septens ubkquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndroms) (UBE3A) mRNA	#30a05.11 Strategene NT2 neuronal precursor 837230 Homo septens cDNA clone IMAGE:884880 5' similar to TR-0233278, 0233278, EDIA LI DEDITEIN	#27gQ3.xf NCI CGAP Kid11 Home sentens Anna Alexa NACE 2127273	UI-H-BIT-edi-d-02-0-UI-ST NCI CGAP Subst Home senions con A committee of the contraction	obs4f09.35 NCI_CGAP_KId5 Home septens cDNA cone IMAGE:1325609 3' striller to SW:NINE1_MOUSE P35436 GLUTAMATE INMDA RECEPTOR SLIRI INIT EDS!! ON 4 DDEC: INSO,D	obs4f00 x6 NCI_CGAP_Kid5 Home septens cDNA close IMAGE:135008 stantier to SW:NME1_MOUSE P35436 GI UTAMATE INMA RECEPTOR SI DI NITTED SI	601470446F1 NIH MGC 67 Home series and a class that the constant of	Homo saplens diacyglycerol kinase jota (DGKI) gene, expn 23
JIG EXOLI PIO	Top Hit Detabase Source	LN	LN	Į.	5	LN.	7	FA	7	N	LN LN	I'V	5	EST HUMAN	Z		EST HIMAN	Т	T HUMAN		EST HIMAN	Τ	HUMAN			т	! L
3110	Top Hit Acession No.	6.0E-51 U50093.1	11526289 NT	5453949 NT	5453949 NT	AL163203.2	TN 002750	6.0E-61 AL133204.1	5031980 NT	5.0E-51 AJ007558.1			803136	3.0E-51 AI587348.1	3.0E-51 AL159142.1				3.0E-51 AW583777.1 E	7708	2.0E-51 AA233352.1		2.0E-51 AW137828.1 E				$\ \ $
	Most Similar (Top) Hit BLAST E Value	6.0E-51	6.0E-51	6.0E-51	6.0E-51	5.0E-51/	5.0E-51	5.0E-51	5.0E-51	5.0E-51	5.0E-61 M30938.1	5.0E-51 M30938.1	5.0E-51	3.0E-51 A	3.0E-51 A		3.0E-51 R15914.1	3.0E-51 M29063.1	3.0E-51 A	2.0E-51	2.0E-51.A	2.0E-51 A	2.0E-51 A	2.0E-51 AI732851.1	2.0E-51 Al732851.1	2.0E-51 BE782015.1	2.0E-51 AF219927.1
	Expression Signal	0.67	1.51	1.52	1.62	11.81	1.96	0.95	0.99	8.67	1.52	1.52	4.18	3.65	1.97		n	4.66	0.47	201	5.16	1.57	0.78	0.7	0.7	3.86	0.61
	ORF SEQ ID NO:		37169	37425	37428	28207	26219	28400	27038	28052	i		37203	28571	29659		33246			25796	27124	29107	29820	30837	30838	31663	
	Exan SEQ ID NO:		23884	24115	_	13546	13557	15557	14349	18315	- 1	- 1	23911	13908	17031	-	20152	21430	25430	13155	14427	16469	17194	18155	18155	18709	19894
	Probe SEQ ID NO:	9962	11221	11515	11515	77.4	785	970	1903	286	3925	3926	11249	1163	4292		7479	8738	8968	357	1683	3716	4458	5352	5352	5925	7209

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Single Extri modes Explessed in Blain	Top Hit Descriptor	Homo sapiens cell recognition molecule Caspr.2 (KIAA0888), mRNA	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'	801676787F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3959613 5/	Homo saplens disrupted in achizophrenia 1 (DISC1), mRNA	1674407.X1 NCI_CGAP_GC8 Home septens cDNA done IMAGE:2238980.3' similar to SW:TRKC_HUMAN Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR:	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA	Homo sepiens mRNA for KIAA0457 protein, partial cds	AV682474 GKB Hamo sapiens cDNA clone GKBAGF05 5	EST91298 Synovial sercome Homo sepiens cDNA 5' end	0034f09.x5 NCI_CGAP_KId5 Homo septens d'DNA done IMAGE:13256093' similer to SW:NME1_MOUSE P35436 GLUTAMATE INMDA! RECEPTOR SUBUNIT EPSILON 1 PRECURSOR:	0634f09.x5 NCI_CGAP_KId5 Homo sepiens cDNA clone IMAGE:13256093' striiter to SW:NME1_MOUSE P35436 GLUTAMATE INMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR:	Homo sapiens myeloid/lymphoid or mbred-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4	(****), III-LY-A	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA	AV742248 GB Homo sepiens cDNA clone CBFBCC12 5'	801464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5	b12056t Testis 1 Homo sapiens cDNA clone b12056	te39g02.xt Soeres_NhHMPu_S1 Homo saplens cDNA clone IMAGE.2089106.3	7066b02x1 NCI_CGAP_Ov18 Homo sepiens cDNA done IMAGE:3644091 3' similar to TR:P87892 P87892 PROTEASE;	AV760590 MDS Homo sapiens aDNA done MDSCBB02 5'	yd10h04.r1 Soares febal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:196567 5' similar to SP:YGAF ECOLI P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION:	1910h04.11 Soares fetal liver spleen 1NFLS Homo septens cDNA clone IMAGE:196567 5' similer to SP:YGAF_ECOLI P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION:	295e07.s1 Soeres, fetal liver spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.83 THR repetitive element;	rw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA done IMAGE:1241138 3' shriller to contains THR,t3 THR repetitive element;	H.sapiens mRNA for faminin-6, alpha3b chain
אום דייסון	Top Hit Database Source		EST_HUMAN 6	HUMAN		EST HUMAN C	Т			EST_HUMAN E							EST_HUMAN 8	EST HUMAN b	EST_HUMAN te	EST HUMAN P	Г	EST HUMAN S		EST_HUMAN &		H
	Top Hit Acesslan No.	7662349 NT	2.0E-61 BE901994.1		11037064 NT	2.0E-61 AI917078.1	2.0E-51 BE165980.1		2.0E-51 AV682474.1				2	8018141	33528		9.1		1.0E-51 AI572532.1	1.0E-51 BF434359.1	1.0E-51 AV780590.1			9.0E-52 AA777621.1	8.0E-52 AA720574.1	
	Most Similar (Top) Hit BLAST E Value	2.0E-51	2.0E-61	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	2.0E-51	100	Z-0E-01	1.0E-51	1.0E-61 /	1.0E-51	1.0E-51 T18862.1	1.0E-51	1.0E-51	1.0E-51	9.0E-52 R91638.1	9.0E-52 R91638.1	9.0E-52	8.0E-52/	8.0E-52 X84900.1
	Expression Signal	1.08	1.72	1.72	96.0	1.45	5.68	9.0	1.77	2.67	8.52	8.52	,		5.74	20.32	1.52	4.1	0.94	0.81	2	1.39	1.39	5.36	9.99	1.65
	ORF SEQ ID NO:	33116		34433	34766	35261	35336	35365	36199	36232	30837	30838	24047	1015	25571		30294	30769	33322	33619		36520	36521		25905	26915
	Exon SEQ ID NO:	20038				22090	22156	22172	22979	23016	18155	18155	7.48.70	200	12884	2 2 2 3 2 3	17684	18110	20219	20498	25434	23282	23282	24726	12963	14229
	Probe SEQ ID NO:	7357	8299	8599	8032	9412	503	8519	10332	10370	11298	11208	10503	12020	112	1479	4959	5305	7549	7803	11783	10587	10687	12301	148	1482

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Table 4
Single Exon Probes Expressed in Brain

					ES	gie Exon Pro	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1650	14396	27085	3.13	8.0E-52	11968028	ŢN	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1660	14396	27086	3.13	8.0E-62	11968028 NT	TN	Homo expiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3976	14396	27085	6.8	8.05-52	11968028 NT	LN	Homo septens hypothesical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3976	14396	27086	6.6	8.0E-52	TN 82088011	ΤΝ	Homo saplens hypothetical protein FL/13556 similar to N-mvc downstream reculared 3 (FL/13559) mRNA
7417	20094	33178	29.0	8.0E-52	TN 5859111	LN	Homo saplens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
7417	20094	33179	29.0	8.0E-52	11416585 NT	IN	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
8911	21602	34745	2.04		7.0E-52 W56471.1	EST HUMAN	2639406.11 Source_perathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element.
1164	13918		97.0	_	6.0E-52 BE072409.1	EST HUMAN	QV3-BT0537-271299-049-d07 BT0537 Homo sablens cDNA
1689	14433	27129	4.27	6.0E-52	6.0E-52 AF108907.1	Į.	Homo eaplens S164 gene, partial cds, PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5641	18436	31349	0.86		6.0E-52 AI208794.1	EST_HUMAN	9944f04.x1 Soares testis_NHT Homo sepiens cDNA clone IMAGE:1838947.3'
11170	23837	37119	1.84	6.0E-52	8.0E-52 BE048172.1	EST HUMAN	1248h04.71 NOI_COAP_Bm52 Homo septens cDNA done INAGE:2281671 5' similar to SW:PGBM_MOUSE Q05783 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR:
9292	21959	35132	9.0	6.0E-62	11437365 NT	N	Homo sepiens FSHD region gene 1 (FRG1), mRNA
1723	14468	27165	1.32	4.0E-52	4501922 NT	N TN	Homo septens adenyate cyclese activating polypeotide 1 (bituitany) recentor type ((ADCYAP1R1) mRNA
1780	14521	27.225	1.02	4.0E-52	4758843 NT	P.	Homo saplens nucleoporin 155kD (NUP155) mRNA
3906	16656	29297	66 '0	4.0E-52	4507500 NT	N.	Homo sapiens T-cell lymphoma invesion and metastasts 1 (TIAM1) mRNA
5204	18012	30633	1.33	4.0E-52	4506132 NT	N.	Homo septens phosphoribosyl pyrophosphete synthetase-associated protein 2 (PRPSAP2) mRNA
5204	18012	30634	1.33	4.0E-52	4506132 NT	FX	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
7938	20633	33760	1.74	4.0E-52	4.0E-52[BE622032.1	EST_HUMAN	901440887F1 NIH_MGC_72 Homo septens oDNA clone IMACE:3915836 6
8432	21125	34263	5.48	4.0E-52	11417035 NT	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12143	24631		5.11	4.0E-52	11418177 NT	N _T	Homo saplens Ran GTP ase activating protein 1 (RANGAP1), mRNA
12627	24930		5.23	4.0E-52	4.0E-52 AB002059.1	NT	Homo sepiens DNA for Human P2XM, complete cds
4071	10815		10.57	3.0E-52	11437042 NT		Homo sapiens hypothetical protein FLJ10675 (FLJ10875), mRNA
25 25 25	13332	25962	2.88	2.0E-52			Human endogenous retrovinal DNA (4-1), complete retrovinal segment
240	13332	25963	2.88	2.0E-52	2.0E-52 M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment

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Table 4
Single Exon Probes Exonessed in

	ſ	T-	1	Т	7	T	\top	Т	\top	Т	T	7	T -	Т	7			7	-	-	·	_	_	-	_	- -	_	
Single Exon Probes Expressed in Brain	Top Hit Descriptor	bb68b07.y1 NIH_MGC_9 Home septiens cDNA clone IMAGE:3030421 5' similer to gb:X16493 M.musculus mRNA for Zof-1 zinc finder protein (MOUSE):	602084710F1 NIH MGC 83 Homo septens CDNA cione IMAGE 4248891 5'	Novel human gene mapping to chromosome 20, similar to membrane transportans	qa56e05.s1 Soeres NiHMPu S1 Homo sepiens CDNA clone IMAGE: 1607264.31	qe58e05.s1 Soeres NHMPu S1 Homo septens CDNA clore IMAGE-1607784 31	IL3-CT0214-231299-053-E12 CT0214 Homo sepiens cDNA	Home sapiens interjeukin 21 receptor (IL21R), mRNA	Homo seplens mRNA for KIAA1081 protein, partial cds	0645412.y5 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1608311 6	Macaca mulatta beta-tubulin mRNA, complete cds	2/45g05.s1 Soares fetal liver splean 1NFLS S1 Homo sablens cDNA clone IMAGE 453272.3	Homo sepiens NADH dehydrogenase (ublquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA	Home sapers SET domain and mariner transmisses frishing care (SETMAD) DMA	Home spiers SET domain and mariner transposes frish news (SETALAD) mon A	W49cO4.x1 NC_CGAP_Lu19 Homo sepiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR receitive element:	W49c04.xt NG_CGAP_Lu19 Homo sepiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2	AV715377 DCB Home scales of DNA oftwa DCB & En	244912.r.1 Soares fetal heart NIDHH19W Homo septems CDNA close INARCE 344028 F	Homo saplens LIM domain kinase 2 (LIMK2), mRNA	xn72e07.x1 NCI_CGAP_CML1 Home sapiens cDNA clone IMAGE.2700036 3' similar to contains Alu repetitive element,contains element LTR2 repetitive element.	Wf67406.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859 0.46850 CARROXA EXTEDA SE	ZIZS112.61 Sources treatis NHT Home sentens CONA close MACE 742070 2	Homo sablens dutamate-ammonia ilgase (dutamine southese) (2 11) mONA	Homo saplens any suffatese D (ARSD), transcript variant 1, mRNA	polytewerse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 ntl	Human P-civcoyotein (MDR1) sene exm 4	Human PMS2 related (hPMSR2) gene, complete cds
gle Exon Pro	Top Hit Database Source	EST HUMAN	EST HUMAN	ii 💮	EST HUMAN	EST HUMAN	EST HUMAN	N	TN	EST HUMAN	FN	EST_HUMAN	¥	Ę	E	EST HUMAN	EST HIMAN	EST HUMAN		12 12	EST_HUMAN	EST HUMAN	EST HUMAN	4	T-Z	ΤΝ	L	N L
Sin	Top Hit Acession No.	2.0E-52 BE207575.1	20E-52 BF677892.1	20E-62 AL137188.3	2.0E-52 A1141802.1	2.0E-52 AI141802.1	20E-62 AW848041.1	11141868 NT			2.0E-52 AF147880.1	2.0E-52 AA778795.1	4758789 NT	5730038	F730038 NT	2.0E-52 AI831462.1		Ţ		417990	2.0E-52 AW 236297.1	2.0E-52 Al808985 1	Ţ	4028	4502238 NT			
	Most Similar (Top) Hit BLAST E Value	20E-52	20E-52	20E-62	2.0E-52	20E-62	20E-62	20E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-52	2.0E-62	20E-52	2.0E-62	2.0E-52	2 OF-52 /	20E-52/	2.0E-52 W70280.1	2.0E-62	2.0E-52	2.0E-52.A	1.0E-52 A	1.0E-52	1.0E-52	1.0E-52 \$61070.1	1.0E-52 M29426.1	1.0E-52 U38964.1
	Expression Signal	2.04	6.03	2.13	1.29	1.29	4.11	1.96	0.89	1.17	9.03	0.81	0.88	5.53	6.53	3.15	3,45	3.09	1.72	2.76	24.36	4.49	1.96	37.84	0.9	2.67	4.35	2.51
	ORF SEQ ID NO:	27983			30287	30288		32024	32390	32571		34672		35879	35880	37111	37112	37131			30801		25937	26773		28465	30684	32026
	Econ SEQ ID NO:	15220			17678	17678	18413	19047	19376	19643	21243	21528	21954	22063	22683	23832	23832	23845	24016	24215	25408	24756	13304	14098	15252	15821	18056	19073
	Probe SEQ ID NO:	2503	2740	4920	4952	4952	5817	6274	8613	8843	8551	8834	8379	10015	10015	11165	11165	11178	11325	11618	11961	12350	520	1350	2537	3055	5250	00059

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Single Exon Probes Expressed in Brain	Most Similar (Top) Hit Acession Database No. Source	1.0E-52 X07292.1 NT Human eldolase C gene for fructose-1.6-bisphosphate eldolase	1.0E-52 AL163227.2 NT Homo seplens chromosome 21 segment HS21C027	1.0E-52 AF078779.1 NT Rattus nonvegicus putetive four repeat ion channel mRNA, complete cds	1 EST_HUMAN	1.0E-52 AL163202.2 NT Homo sepiens chromosome 21 segment HS21C002	1.0E-52 U48296.1 NT Homo septems protein tyrosine phosphatese PTPCAAX1 (hPTPCAAX1) mRNA, complete cds	1.0E-52 11426321 NT Homo sepiens probesome (prosome, mecropain) subunit, beta type, 2 (PSMB2), mRNA	36064 NT	9.0E-53 AF001446.1 NT Homo sepiens core binding factor alpha1 subunit (CBFA1) gene, exon 3	7.0E-53 BF238465.1 EST_HUMAN 601904771F1 NIH_MGC_64 Homo sapiens cDNA done IMAGE:4132793 5	Haza	6.0E-53 BE295719.1 EST HUMAN 601175776F1 NIH MGC 17 Homo seciens cDNA clone IMAGE:3530946.5	38543 NT	AW813563.1 EST HUMAN	4.0E-53 AL163286.2 NT Homo sapiens chromosome 21 segment HS21C085	4.0E-53 AL163285.2 NT Homo sepiens chromosome 21 segment HS21C085	4.0E-63 7705414 NT Homo septens hook1 protein (HOOK1), mRNA	.1 EST_HUMAN	EST_HUMAN	EST_HUMAN	4.0E-53 BF128701.1 EST_HUMAN 601810969F1 NIH_MGC_48 Homo septions cDNA clone IMAGE:4053977 5'	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	FST HIMAN	N	26297 NT	BE160025.1 EST HUMAN	3.0E-53 Y10388.3 NT H.seplens graf gene	3.0E-53 Y10388.3 NT H.sepiers graf gene	\$72043	10835090 NT	5901953 NT	
		E-52 X07292.1	E-52 AL 163227 2	E-52 AF078779.1	E-52 AW020370.	E-52 AL 163202.2	E-52 U48296.1			E-53 AF001446.1	E-53 BF238465.1	E. E2 A1424762 4	E-53 BE 295719.1		AW8135	E-63 AL163285.2	E-53 AL 163285.2		E-53 AI613037.1	E-53 F13080.1	E-53 BF128701.1	E-53 BF128701.1	A A A A A A A A A A A A A A A A A A A	E-53 AW803563	E-53 AF001212.1		BE1600	E-53 Y10388.3	E-53 Y10388.3	\$72043			
	Expression (Top) Signal BLAS	5.31 1.0	1.2 1.0	0.75 1.0	1.03	1.39 1.0	1.61 1.0	2.09	1.05 9.0	1.96 9.0	3.18 7.0	4 63 7.0		228 5.0		2.78 4.0	2.78 4.0	1.03 4.0				2.78 4.0	14.7			0.82 3.0	0.85 3.0	1.04 3.0				١	2.79 3.0
	ORF SEQ EID NO:	33080		34940			36596		29161	29732			30422	29448		25502	25503	30125			37126	37127	28114	28014	30803	31243	31846	32740	32741	34034	34597		37746
	Exon SEQ ID NO:	20012	21057	91112	23122	23132	23356	23427	16523	17097	24660	25085	17805	16822	24688	12877	12877	17503	21983	22308	23842	23842	16376	17284	18142	18336	18879	19690	19690	20807	21450	21046	24410
ſ	Probe SEQ ID NO:	7330	8364	9087	10476	10486	10665	10740	3771	4359	12189	12800	208	4078	12236	84	8	4771	9316	9828	11175	11175	2885	45 45 45 45 45 45 45 45 45 45 45 45 45 4	5339	5538	9101	8669	8669	8203	8758	88	11828

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Table 4

Single Exon Probes Expressed in Brain	Most Similar Expression (Top) Hit Top Hit Acess Signal BLAST E No.	1.63 3.0E-54 11434806 NT Homo saplens color a inhamitive a (CO) CAE) DAIA	4.93 3.0E-54 BF345800.1 EST HUMAN	3 26 54 AA300900 1	O C C C C C C C C C C C C C C C C C C C		8.86 2.0E-54 En31900INT	0.96	1.37 2.0E-54 AA655008.1 EST HUMAN	1.22 2.0E-54 AW163175.1 EST HUMAN	1.65 2.0E-54 AL163210.2 NT	1.52 2.0E-54 AW057524.1 EST HUMAN	1.18 2.0E-54 AJZ78314.1 NT	3.2 2.0E-54 AA532925.1 EST HUMAN RIBOSOMAI PROTEIN I 22 HUMAN.	2842 NT	1.02 2.0E-54 7706446 NT	1.64 2.0E-54 4759089 NT	1.2 2.0E-64 BE047864.1 EST_HUMAN	5.04 2.0E-54 11428657 NT	13.89 2.0E-54 AB046811.1 NT	13.90 2.0E-54 AB046811.1 NT	0.68 2.0E-54 AF008915.1 NT	0.05 2.0E-54 AB023212.1 NT	0.65 2.0E-54 AB023212.1 NT	2 OF 64	4.11 2.0E-64/AB001025.1 NT	0.79 2.0E-64 11429127 NT	1.01 2.0E-54 11416762 NT	1.01 2.0E-54 11416762 NT
		1.63	4.93	386	0000	2.51	8.86	0.96	1.37																				
	ORF SEQ ID NO:	1/	36859	37336			28040		26972	27895	28062	28311	28721	-										32873	32772	35366			35886
	<u> </u>		23696	24031		\perp	13406	14092	14286	15255	15320		16071	16292				18314	18460	18562	18562	19324	19628	19628	19715	22182	22558	22689	22003
	Probe SEQ ID NO:	10949	11024	11341	12056	12097	627	1344	1530	2541	2608	2896	3311	3536	4181	4826	8388	5516	5875	27.1	9771	8220	6713	6	7023	9529	0066	10021	10021

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Single Exon Probes Expressed in Brain	Top Hit Descriptor Source	Homo sapiens EVI5 homotog mRNA, complete cds	Homo saplens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES4), mBNA	HUMAN 601899230F1 NIH MGC 19 Hamo sapiens CDNA clone IMAGE 4128535 51	Т	Г		Т	Т	Homo septems RFB30 cense for RING finane motion	1			Ţ	MAN AL138909 PLACE1 Home emises and a class of Artificial Places of Arti	T	Т	Т					Homo septens erylsulfatese E (chondrodysplasta punctata 1) (ARSE), mRNA	Homo septens any suffetase E (chondrodysplesea punctata 1) (ARSE), mRNA	Homo sapiens paracconase 2 (PON2) mRNA, and translated products	Homo saplens peracenese 2 (PON2) mRNA, and translated products	Homo septens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA	Homo sapiens speciale-type POZ protein (SPOP), mRNA	Homo sapiens BCL2-associated attenogene (BAG1). mRNA	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypentide (PTPRA) mRNA	HUMAN RC4-BT0310-110300-015-110 BT0310 Homo sepiens cDNA	П
ingle E		Σ	57454 NT	EST !	EST HUMAN	EST_HUMAN	EST HUMAN	EST		Ż	EST_HUMAN	EST HUMAN	FST HIMAN	EST HIMAN	FST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	뉟	EST HUMAN	EST_HUMAN	EST HUMAN	Ę	칟	Z NI	Z V	TN.	2 NT	LN	6302 NT	!∟ '	
ייסי	Top Hit Acession No.	2.0E-54 AF008915.1	78	1.0E-54 BF315418.1	1.0E-54 AA412409.1	1.0E-54 AA412409.1	1.0E-54 AU077341.1	9.0E-55 BE081469.1	8.0E-55 Y07829.2	8.0E-55 Y07829.2	8.0E-55 AW409714.1	7.0E-55 R09346.1	7.0E-55.AW103839.1	7 0E-55 AA889581 1	7.0E-55 AU139909.1	7.0E-55 AI581056.1	7.0E-65 AI561056.1	7.0E-55 H23396.1	6.0E-55 AB040934.1	5.0E-55 AA704971.1	5.0E-55 AA704971.1	5.0E-55 AW 206021.1	4502240 NT	4502240 NT	4505952 NT	4505952 NT	7382477 NT	11434422 NT	11528491 NT			5.0E-55 AB014511.1
	Most Similar (Top) Hit BLAST E Value	2.0E-54	2.0E-54	1.0E-54	1.0E-54	1.0E-54	1.0E-54	9.0E-55	8.0E-55	8.0E-55	8.0E-55	7.0E-55	7.0E-55	7.0E-65	7.0E-55	7.0E-55	7.0E-65	7.0E-55	6.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-55	5.0E-65	5.0E-55	5.0E-55
	Expression Signal	1.57	2.86	1.22	0.52	0.52	2.17	46.0	1.09	2.63	1.67	0.77	8.0	1.28	2,16	10.32	10.32	2.6	2.45	1.19	1.19	1.81	1.65	1.65	1.34	1.32	0.83	0.7	0.72	3.53	1.75	1.77
	ORF SEQ ID NO:	32331			36018	36019		36115				28470		34032	34968	37120	37121		37412	27205	27206	30086	17778	32212	32340	32341	32718	32955	33718	34777	1	35786
	SEQ ID	19324	24321	17168	22801	22801	24086	22905	14041	14044	23818	13817	21395	21769	21803	23838	23838	25303	24099	14505	14505	727	18214	19214	25094	23084	19872	19881	20588	21633	21898	22585
	Probe SEQ ID NO:	10947	11727	4432	10153	10153	12710	10257	1292	1295	11151	1059	8703	9080	9116	11171	11171	12682	11498	1783	1763	2/4	9,79	0	8288	8000	6937	7195	7893	8942	9218	8937

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Table 4
Single Exon Probes Expressed in Brain

Top Hit Descriptor	Homo sapiens mRNA for KIAA0611 protein, pertial cds	Homo sapiens nel (chirken) like 2 (NEL 12) mRNA	Homo saplens pescadillo (zebrafish) homolon 1 contraving RPCT domain (bccs)psi.	Homo sablens RNA binding motif protein V chromosome femily 4 manufacture A4 (508) 2444	Homo sepiens predicted osteoplast protein (GS378A) mRNA	Homo sablens predicted osteoblast protein (GS3786) mRNA	7/52b10x1 Sogree_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA done IMAGE:3390043 3' similer to contains £1.t3 L1 reputitive element	Homo sapiens protessome (procome mecronein) enhanti akke han 2/00/142) Dita	HOTO Sablers Drivescome (procure macronels) sub-us, spire, spire, 1 (2007) HILLY	Homo saciens discyclycerol kinese, camma (20147) (DCKG) mRNA	Omo septens discriptionerol kinase, narma (2017) (1000) mauni	Homo septens ublautiting continued anyone E2 variant 4 (1 DECA/4) DNA	Homo saciens Xa assudosubscanal nacion: seminant 1/2	Homo seciens chromosome 21 segment HS21CD10	43c5 Human ratina cDNA randomly adment Publishes. Home some CNA	801886575F2 NIH MGC 17 Homo servieus ciDNA close IMAGE-4120738 R	PM1-HT0603-090300-001-008 HT0603 Home sentens cDNA	Homo sapiens chromosome 21 securent HS21Ch84	Human endocencus retrovirus pHE 1 (FRVs)	Human endogencus retroviral DNA (4-1), combleta natroviral segment	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated provincts	CM1+HT0876-150800-357-g03 HT0876 Homo serviens cDNA	UHF-BNO-ake-f-08-0-ULT NIH MGC 50 Homo sapiens cDNA clone IMACE:3078275 5	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 31	hr78h08.x1 NCI_CGAP_Kid11 Homo eaplens oDNA clone IMAGE:3134463 31	am98h05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR to THR remarktus alement.	OVO-BINITAZI, 280400, 212, and BINISAZI Uses and in the state	AU119244 HEWBA1 Home semilars ADNA Alexandria and A	Homo sepiens mannose-6-phosphate recentry (cellan department) (14600)	Orcidiagus cuniculus New Zealand white alongshow factor 4 along to a contraction of the c	Homo sapiens mRNA for KIAA0903 protein, pertial cds
Top Hit Database Source	NT.	IN	F	ĬN.	MT	¥	EST HUMAN	L L	Į.	N F	Ę	¥	Z.	N.	T HUMAN	HUMAN	HUMAN	Т	Ę	토		T_HUMAN	Г	EST_HUMAN	EST_HUMAN	EST HUMAN	Т	T			
Top Hit Acession No.	AB014511.1	5453765 NT	11417972 NT	4826973 NT	7861713 NT	7861713 NT	4.0E-65 BF061411.1	8180	4505180 NT	4503314 NT	4503314 NT	TN 767794	4.0E-55 AJ271735.1			-	3.0E-55 BE178519.1	3.0E-55 AL163284.2			4507296 NT		1		2.0E-55 BF224452.1			Ī	0909		
Most Similar (Top) Hit BLAST E Value	5.0E-55	5.0E-55	6.0E-65	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55/	4.0E-55 /	4.0E-55 W28189.1	4.0E-55 E	3.0E-55 E	3.0E-55 A	2.0E-55 X57147.1	2.0E-55 M10978.1	2.0E-65	2.0E-55 B	2.0E-55 A	2.0E-66 B	2.0E-55 B	2.0E-55 Al002838.1	2.0E-55 B	2.0E-55.A	1.0E-55	1.0E-55 U09823.1	1.0E-55 AB020710.1
Expression Signal	1.77	2.48	2.73	65.4	1.78	1.78	1.7	76.0	76.0	6.47	6.47	2.29	1.21	8.37	2.3	3.05	1.5	1.85	1.98	1.13	13.79	2.91	0.76	0.52	0.52	6.23	0.72	1.95	3.01	8.22	3.53
ORF SEQ ID NO:		35984			26853	26854		27482	27483	27542	27543	27771			-				25807		26049	30090	33162	34804	34805		-	36798	25558	25636	26543
Exan SEQ ID NO:		22770	24626	13434	14169	14169	14250	14754	14754	14811	14811	15033	15310	20936	23859	24674	24536	24993	13164	13321	13413	17455	25113	21654	21654	21747	21828	23550	12921	12997	13883
Probe SEQ ID NO:	9837	10122	12137	657	1421	1421	1504	2019	2010	2079	2079	2308	2596	8242	11194	12057	11998	12721	368	238	834	4723	7403	8883	8063	9028	9140	10870	88	181	1127

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Table 4

					ris	igle Exon Pro	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1943	14678	27391	1.58	1.0E-55	1.0E-55 BE277861.1	EST HUMAN	601120116E1 NIH MGC 30 Home seations of NA state 1114 AP Secretary FI
1943	14678	27392	1.58	1.06-55	1.0E-55 BE277861.1	EST HUMAN	601120118E1 NIH MICC 20 Home services ONA ALCOHOLOGICA SI
2324	15049		248		5803174 NT	L	Homo servine SMA3 (SMA3) mDNA
2338		27799	1.17		AF000990.1	L	Hamo satisfies the file stands of the standard
2521		27978	9.05		1.0E-55 X13111.1	7	Human mRNA for HI A 411F a MHC class I molecule (molecule fundamental)
2550		28009	4.19		1.0E-55 AB007866.2	ĹΝ	Homo sanjans mRNA for KIAAAAA codes and code instructing instructing Complex)
2559		28010	4.19	1.0E-55	1.0E-55 AB007866.2	LN L	Homo seviens mRNA for KIAAAAA romain portion ods.
2017		28071	1.72	1.0E-55	Γ	LN	Homo seniens CI P MRNA bertial rela
3970		28353	4.28	1.0E-55	7.2	Į.	Homo satiens chromosoms 21 seconds HSA Cost
4262		29635	1.28	1.0E-55		L	Home sariens chromosome 21 segment II-23 Cost
4682	17416		1.02	1.0E-55		EST HUMAN	W44403 rt Sogeres Fariel lives solders a Milk Electric Colis 1
5410	18209	30917	0.97	1.0E-55	-	LN	How souline BDOAGES BANK
6178	18955	31929	6.82	1.0E-55	11433046	LN	Homo earliens had domain and DI D 2 (UED-CO). ENLA
6178	18955	31830	6.82	1.0E-55		FZ	Home analysis had demonstrated in the CHICACA, INC. A
7888	20583	33712	1.84	1.0E-55		LZ	Home earliest discussions (Cherces) many
7888	20583	33713	186	1 0F-55	11432004 NT		Home sections also also (Litrachania) normolog 2 (chapsyn-110) (DLG2), mRNA
7980	20875	33789	0.89	1.0E-55	1.0E-55 AF224492 1	LN	Homo earliers shown full for the south file of the south full for the south full full full full full full full ful
7980	20875	33800	0.80	1.0E-55	Π	TN	Transcription of production and all transcription of the complete cds
10829	23511	38751	1.75	1.0E-55		LN	Transcaption by Industrialized and Industrial Section 2018
10829	23511	36752	1.75	1.0E-55		L	Homo services chromosome 21 segment PSZICO10
11425		36423	2.53	1.0E-55		Z	Human infant brain unknown product mBNA complete cut
11444	23211	36442	1.5	1 05-55		T Liverage	seq1575 b4HB3MA Cot8-HAP-Ft Homo sepiens cDNA clone b4HB3MA-COT8-HAP-Ft61 6' similer to straiter
11569	24168	37482	235	1.0E-55	0587821		Hymn emisses DNA Linding Linding Account
7285	19949	33026	1.83	9.0E-56		T HUMAN	601237702F1 NIH MGC 44 Home canians a Pala Alama MA CE SOCIETO EI
2737	15444	28182	532	7.05-58	7 OF 58 H10034 1		yn62g03.r1 Soares adult brain N2b5HB56Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains
7540	20210	33309	1.67	7.0E-56	13.4	\top	I TI'N TEPEBUNG GEMENT
7540	20210	33310	1.67	7.0E-56/	T	T	RC1-CT0252-23109-013-007 CT0252 Home septents CJNA
1687	14431	27127	1.78	5.0E-56/		Т	RC3-RN0063-17020-041-604 BN0062 U
8050	21748	34908	0.86	5.0E-58		Т	UH-Blobeat-a-050-UI st NCI OSAP Sub Homo employs characteristics
10286	22934		1.01	5.0E-56		T	43c5 Human retine cDNA randomly primed eightfaven Homo conject only
12220	25359	30610	2	5.0E-58 H55090.1		T	CHR220038 Chromosome 22 each Homo services CONA Alone COS ER ET
8	12854	25469	8.58	4.0E-56	4.0E-56 AF141349.1	Г	Homo sapiens beta-tubulin mRNA, complete ods

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Table 4

						#	IUSPA	USPA																							T
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Horne consistent in the first the constant of	AND SAPERIS DEIZ-LIDIUM MYNA, complete cds	W 1902038FT NIF MICC & Hamo septens cDNA clane IMAGE:4081551 5	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA Homo sapiens tubulin, beta polypeptide (TUBB) mRNA	Homo sepiens X-linked arthidroffic ectodermal dysplasia protein gene (EDA), excn 2 and flanking repeat regions	WD09f08.x1 NCI_CGAP_GC6 Hamo septens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA PZ719 ORNITHINE DECARROXYA A SE	WD06f08.xf NCI_CGAP_GC8 Homo septens CDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA	HOWEN SERVICE OF CARBOXYLASE	Homo explicit the second bone marrow protein BM031 mRNA, complete cds	Homo seriens handoud.	Implication of the contraction o	misser 12 Min. Control Drings From septens control IMAGE: 2163046 3'	Homo services broothedical markets BOC4304 ADD CASA A	FST2888 Control in II Land and I	CST28880 Cerebaltum II Change Septemble CDINA 5 GPG	Hyproperations Multi Alexanders GUINA 6 GTG	Homo earlone Deur easte 1 region	Home earlies about syndrome certainages region 1 (DSCR1), mRNA	To an included the second of t	Homo serience energination in account activity & (5. cerevisiae homolog)—like (SKIV2L), mRNA	or of the desired of the second of the second (SPOCK) mRNA	Homo sepiens sparc/osteonectin, cwcv and kazal-like domains proteculum (hudiam) (CDOOM)	Homo sepiens lysosomel-espociated membrane numbin 2 (1 AMD)	Homo septens LIM binding domain 2 (I DR2) mBNA	Homo saciens LIM binding domain 2 (1 DB2) m DNA	Homo seciens from monthogonalis models (10 times - Chilis	Homo septems mRNA for KIAAA145 person 1 (DMFD), mrcNA	Homo sepiens KIAA0317 pene product (KIA 40247) - Daya	Homo septens mRNA, similar to ret myrmenalin complete od	Homo sepiens nuclear pare complex interacting protein (NPIP), mRNA
gle Exon Pro	Top Hit Database Source	FN	ECT LIBIAN	-1	L	F	EST HUMAN	EST HIMAN			Ę	FST HIMAN	Т		HIMAN	T	Т														
Sin	Top Hit Acession No.	4.0E-58 AF141340 1		867770	4507728 NT	4.0E-56 AF003528.1	4.0E-56 Al632488.1	4.0E-56 AR32488 1						24029			T	57042	3.0E-56 AL163268 2	2085	4759163 NT		4759163 NT	11421124 NT	4504970 NT	4504970 NT	11418704 NT		11434956 NT	B042556.1 NT	2013
	Most Similar (Top) Hit BLAST E Value	4.0E-58	4.0E-56	4.0E-58	4.0E-36	4.0E-56	4.0E-56	4.0E-56	4.0E-56	4.0E-56	4.0E-58/	4.0E-58/	4.0E-56/	3.0E-66	3.0E-56	3.0E-58/	3.0E-56/A	3.0E-56	3.0E-56/A	3.0E-56	3.0E-56		3.0E-56	3.0E-56	3.0E-56	3.0E-58	3.0E-56	3.0E-56 D83479.2	3.0E-56	3.0E-56 AB042556.1	3.0E-56
	Expression Signal	8.58	2.69	7.28	7.28	3.49	1.48	1.48	6.01	6.01	2.02	8.88	8.88	4.17	1.54	43.1	1.61	1.43	4.27	2.34	2.12	-	2.12	7.03	1.15	1.15	4.68	0.85	1.38	1.71	6.37
-	ORF SEQ ID NO:	25470		28157	28158	25929	28074	28075	31912	31913	36268	36784	36765	26742	28527	28528	-	29728	29759	20802	31302		31303	32547	32981	32082	34650	35562	36240	36571	37239
	Exam SEQ ID NO:	12854	14902	15419	15419	13297	15331	15331	18941	18941	23040	23523	23523	14068	15887	15887	16567	17093	17127	17260	18383	8	2000	19519	19908	19908	21407	22364	23025	23333	23945
	Probe SEQ ID NO:	82	2173	2712	2712	2815	2836	2836	6164	6164	10403	10841	10841	1319	3122	3122	3815	4355	4390	4534	5598	0011	0800	0/20	(223	(723	8715	9713	10379	10642	11284

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Table 4

								2063 °																				105875						
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo esplane minloss some community in the contract of the con	Homo septems NACR/ALLS CONTINUE CONTINUE CONTINUE (NPIP), mRNA	Homo earlane NAC D/elcho menicibility	Homo septems censoling (CAVA) and A	Home earling (ANS), middle	205008 of Statement of CAVO), Illinois	RC4-BT0310-110300-015-f10 BT0310 Home control CA-BT0310-11030-015-f10 BT0310 Home control CA-BT0310-110300-015-f10 BT0310-010-010-010-010-010-010-010-010-010	RC4 BT0310-110300-015-01-03-03-01-03-03-01-03-01-03-01-03-01-03-01-03-01-03-01-03-01-03-01-03-01-03-03-01-03-03-01-03-03-01-03-01-03-03-01-03-03-01-03-03-01-03-03-03-03-03-03-03-03-03-03-03-03-03-	Homo seniens mBNA for KIAA444 sector and all	AV703184 ADB Home series ADMA data ADDCEO18 1	Homo services SET downline and the contract of	Months Saprails SET UCHARIT and Internet transposase rusion gene (SETMAR) mRNA	Intercace resoluter is protein tyrosine phosphatase (PRL-1) mRNA, complete cds	hazaci i ki wa cana aco nano sepiens cuiva done IMAGE:29464523'	192351131 NG_CGAP_GGS Homo sapiens cDNA clone IMAGE:2946452 31	Mis misselve and the manufacture and the misselve and the	MR2 ST0003 480400 506 LOS ST5000 1	Home continue authors I uzus Hamo sepiens cDNA	Description agreement of the segment HS21C003	CCC-C10103-220889-001-E02 C10163 Homo sapiens cDNA	Home series Enhal (EDIAA) - DNA	Home seriers Epida (EDHAA) - DNA	Homo sapiens serine professe 17 (KTK4) cense commission	Homo sapiene serine protected 17 (KT K4) gene, consists	Homo sepiens mRNA for cardin 82 remolete calc	QV4-ST0234-181189-037-605 ST0234 Home emitter - Data	x05d10.x1 NCI_CGAP_Bm63 Home septems cDNA done INA GE:2759251 3' similar to gb:U05875	2/6/16/2 of Source feeds NHT Home section 2014	Home seriene EnhA4 (EDIAA) DNA	Homo sapiens EnhAZ (EDHAZ) - DAIA	Homo saniens of themselve the contraction of the Anna Anna Anna Anna Anna Anna Anna Ann	Homo saplens accultase 2, mitochondria (ACO2) mRNA	Homo saplens mRNA for KIAA0898 protein, partial cds
gle Exon Pr	Top Hit Detabase Source	TN	ΙΝ	LN	LZ	IN.	FST HIMAN	EST HUMAN	EST HUMAN	LN	EST HUMAN	L	NT.	EST HIMAN	EST HIMAN	EST HIMAN	L L	EST HIMAN		ECT LIBIANI	EST HIMAN		5	Z.	Ę	¥	EST HUMAN	EST HIMAN	EST HUMAN		E			F
Sin	Top Hit Acession No.	5902013 NT	3.0E-56 U46900.1	3.0E-56 U46900.1	11434876 NT	11434876INT	2.0E-56 AA199818.1	2.0E-56 BE064386.1	2.0E-56 BE064386.1	2.0E-56 AB037835.1	AV703184.1	2.0E-56 5730038 NT		Ţ	1.0E-56 AW 589833 1	T	81002	1.0E-56 AW609520 1	Γ	L		58279	4758279INT	9.0E-57 AF228497.1	Γ	9.0E-57 AB020981.1			T	8278	4758279 NT	4557830 NT	11418185 NT	
	Most Similar (Top) Hit BLAST E Value	3.0E-56	3.0E-56	3.0E-56	3.0E-56	3.0E-56	20E-56	2.0E-58	2.0E-56	2.0E-56	2.0E-56/	2.0E-56	1.0E-56/	1.0E-56/	1.0E-56/	1.0E-56/	1.0E-56	1.0E-56	1.0E-56	1 05-56 4	9.0E-57.A	9.0E-57	9.0E-57	9.0E-57 A	9.0E-57	9.0E-57 A	8.0E-57 A	8.0E-57 A	8.0E-57 A	8.0E-57	8.0E-57	8.0E-57	8.0E-57	8.0E-57 AB020705.1
	Expression Signal	6.37	1.74	1.74	1.52	1.52	1.7	1.05	1.05	1.18	1.64	1.47	1.84	215	2.15	0.00	0.97	0.57	0.50	1.71	2.52	1.14	1.14	2.17	2.17	1.48	3.01	6.36	1.51	96.0	96:0	1.3	3.29	1.85
	ORF SEQ ID NO:	37240	37590	37591	31083	31084		26141	20142	28390	28934	32731		29068	29057	30303	30453	32589		35800		29548	29549	37134	37135	37420	25738	26303	27264	28791	28792	30205	30728	32063
	Exen SEQ ID NO:	23945	24268		24597	24597	13205			15753	16279	19683	13724	16417	16417	17696	17836	19558	22505	22596	13389	16920	16920	23848	23848	24107	13086	13633	14549	16135	16135	17582	25278	19078
	Probe SEQ ID NO:	11284	11673	11673	12095	12095	511	718	716	2887	3523	0889	959	3664	3664	4972	5118	8724	9855	848	611	4180	4180	11183	1183	11506	8	408	1809	3376	3376	4852	5161	8308

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					;	101 1 100 01B	Single Labora Laplessed III Didiii
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
6372	19141	32137	12.87	8.0E-57	8.0E-57 AB023177.1	INT	Homo espiens mRNA for KIAA0960 protein, partial cds
6372	19141	32138	12.87	8.0E-57	8.0E-57 AB023177.1	TN	Homo sepiens mRNA for KIAA0960 protein, partial cds
7349	20030	33107	0.64	8.0E-67	7662263 NT	Z	Homo saplens KIAA0716 gene product (KIAA0716), mRNA
7648	20312	33423	1.7	8.0E-57	8.0E-57 AB020644.1	N	Homo eapiens mRNA for KIAA0837 protein, partial cds
7848	20312	33424	1.7	8.0E-57	8.0E-57 AB020644.1	L	Homo sepiens mRNA for KIAA0837 protein, partial cds
11460	17889	30487	3.29	8.0E-57	8923349 NT	Į.	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12459		31028	2.74	8.0E-57	11545732 NT	Z	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12473	24828	31028	1.69	8.0E-57	11545732 NT	Z Z	Homo sepiens SH3-domain binding protein 1 (SH3BP1), mRNA
12820	25060		2.07	8.0E-57	8.0E-57 AB037763.1	F	Homo saplens mRNA for KIAA1342 protein, partial cds
2639	15350	28093	1.71	7.0E-57	7667592 NT	FZ	Homo sephens sing GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2639	15350	28094	1.71	7.0E-57	7657592 NT	FZ	Homo saplens sing GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3244			6'0	7.0E-57	7242158	N F	Homo septens NME7 (NME7), mRNA
3244	16006	28656	6.0	7.0E-67	7242168 INT	Į.	Homo septens NME7 (NME7), mRNA
3265	16027	229677	1.08	7.0E-57	FN 6765009	LN	Homo saplens Kruppel-like factor 8 (KLFB), mRNA
3858	16608	29246	1.39	7.0E-57	7.0E-57 AF012872.1	N-	Homo saplens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
3858	16608	29247	1.39	7.0E-67	7.0E-67 AF012872.1	<u>F</u>	Homo sepiens phosphetidylinositol 4-kinase 230 (pl4K230) mRNA, complete cds
4398	17135		0.95	7.0E-57	7.0E-67 AF020503.1	F	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
,			į	ı			Homo sapiens large conductance calcium- and voltage-dependent potassium channel alpha subunit (MadK)
4/30		BBOOS	0.80	7.0E-0/		- 2	mknA, complete ods
12785	25310		2.63	5.0E-57	5.0E-57 AJ271735.1	L	Homo sapiens Xq peeudosuruscomal region; segment 1/2
3736	16489	29125	1.67	4.0E-57	4.0E-67 AB026898.1	ΗN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
786	13558	02292	0.78	3 0F-57	TN 8677784	Ę	Homo sapiens ublquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
	L						101307 st NCI CGAP Pri Homo septeme cDNA close INAGE-1008037 similar to SW-DC10 Lilinan
1308	14058		16.24	3.0E-57	3.0E-57 AA230279.1	EST_HUMAN	P48783 40S RIBOSOMAL PROTEIN S10.;
2390	15111	27848	2.99	3.0E-57	3.0E-57 AA348335.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
	,	į					7733b10.x1 NCI_CGAP_CLL1 Homo sepiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
2/0/	12/4	28151	0.95	3.0E-57	3.0E-57 BE676622.1	EST_HUMAN	OE 20283 ;
2707	15414	28152	0.05	3.0F-57	3.0E-57 BE678622.1	EST HUMAN	7733b10.x1 NCL_CGAP_CLL1 Hamo sepiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263 :
3550	16305	28955	1.74	3.0E-57	3.0E-57 AF232708.1	IN	Homo sapiens cell-line ta A201a chloride ion current inducer protein ((Cin) gene, complete cds
3685	16438		62.34	3.0E-57		EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Homa saplens cDNA

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Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (digomych sensitivity Homo sepiens coegulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA Homo saplens holocytochrone c synthase (cytochrome c heme-tysse) (HCCS) mRNA Homo saplens hypothetical protein FLJ10826 (FLJ10826), mRNA Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA 9910e02.r1 Soares Infant brain 1NIB Home saplens cDNA clone IMAGE:31693 5 HSC1TG081 normalized triant brain cDNA Homo saplens cDNA clone c-1tg08 AV712977 DCA Homo saplens cDNA clone DCAAZG04 5* Homo saplens 5-amindlevulinate synthase 2 (ALAS2) gene, complete cds Homo sepiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA Homo septens peptide YY (PYY) mRNA 602185789F1 NIH_MGC_45 Homo septens cDNA clone IMAGE:4308943 5' 602185789F1 NIH_MGC_45 Homo septens cDNA clone IMAGE:4308943 5' QV0-BT0702-170400-194-f09 BT0702 Homo septens cDNA Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA Homo sepiens Ran GTPese activeting protein 1 (RANGAP1), mRNA Homo sepiens E1B-66kOs essociated protein 5 (E1B-AP5), mRNA Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA Fop Hit Descriptor Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA Homo sapiens mRNA for KIAA1617 protein, pertial cds Homo sapiens mRNA for KIAA0611 protein, pertial cds Homo sapiens mRNA for KIAA0611 protein, pertial cds Homo sepiens chimerin (chimaerin) 1 (CHN1), mRNA Homo saplens chromosome 21 segment HS21C018 Homo sapiens chromosome 21 segment HS210085 Homo sapiens nibrin (NBS) mRNA, complete cds Homo sepiens nibrin (NBS) mRNA, complete ods Human beta prime adaptin (BAM22) gene, exan 3 conferring protein) (ATP50) mRNA Human mRNA, Xq terminal portion Single Exon Probes Expressed in Brain (F9) mRNA Top Hit Database Source EST HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN 11421330 NT 눌 4885400 NT 8922693 NT 눋 ż Ż 5231227 NT z Z L 11526293 NT 11426423 NT 11431079 NT 4502302|NT 11418177 NT 눋 4503648 NT 11424059 NT 4758981 NT 5031660 NI Top Hit Acession 4504634 5231227 11430647 5.0E-58 AB014511.1 5.0E-58 AL163285.2 5.0E-58 1142 5.0E-58 AP051334.1 5.0E-58 AF051334.1 AB046837.1 5.0E-58 AL163218.2 5.0E-58 AB014511.1 3.0E-58 BF569848.1 3.0E-58 AV712977.1 2.0E-58 AF068624.1 3.0E-58 BF569848.1 3.0E-68 BE089509.1 4.0E-58 D16470.1 3.0E-58 F07056.1 3.0E-58 R17879,1 U36251 5.0E-58 5.0E-58 5.0E-58 5.0E-58 5.0E-58 5.0E-58 5.0E-58 5.0E-58 Most Similar (Top) Hit BLAST E 4.0E-58 4.0E-58 3.0E-68 5.0E-58 4.0E-58 5.0E-58 4.0E-58 4.0E-58 4.0E-58 88.88 0.73 0.68 0.88 0.68 0.83 0.83 2.69 18 4.5 0.88 1.00 1.03 1.25 238 2.78 Expression 7.06 2.78 2 67 Signed ORF SEQ 32636 32752 33691 35089 35090 35614 38161 25804 20212 29113 35887 28729 37275 28585 28586 31915 32114 28883 ÖNO 28091 28791 32314 26350 19148 19597 SEQ ID 19074 19597 19698 20564 20945 21918 22408 21918 22671 22047 24405 25330 13162 16478 22947 25305 13340 23974 14116 13551 14180 16079 18944 25001 15837 15837 19122 19309 13686 ÿ 6301 6379 0880 9880 700G 7860 8251 9239 SEQ ID 9757 10023 10300 3319 10300 11819 1452 11315 12071 12512 12732 364 778 2837 326 1368 3174 3723 3174 6167 6362 4458 918

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Table 4
Single Exon Probes Expressed i

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	be08b07.y1 NIH_MGC_7 Homo sepiens cDNA done IMAGE:2823733 5' similar to gb:X60301 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE):	(2) 1499901F1 NIH MGC 70 Homo seelabs - DNA chara MACE-2004044 51	601499961F1 NIH MGC 70 Homo seniers and a doma IMACE sociations	UI-H-BW 1-ems-g-11-0-UI-s1 NCI CGAP Sub? Home septens cDNA close IMA CE: 3071090 3-	am57e02.x1 Johnston frontal cortex Homo sepiens cDNA clone IMAGE: 1539674.3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN	VIORING IT States fetal likes solders ANEL 9 House seed to 1814 1 1815 CT 1825 CT	Interview of the Court of the Server of the Server of the Server of the Interview of the In	Home sardens endocytic recently Educated Brush College Bru	Homo serdens endoxific receive Find-480 (END-480) minute, complete cas	801890812F1 NIH MGC 17 Homo sankers conversional Alexan MACE: 4134804 51	hm2508 x NG CGAP That Home seniors CDNA close IMAGE 201231 2	Human complement combonent C5 mRNA 31and	Homo sariers NADH dehutmoseses (usharakasa) 4 tata a tata (sariers and sariers	EST360252 MAGE resemblence MACAT Lown and the Succession of CZKU, 622) (NDUF89), mRNA	EST389252 MAGE resections: MAGD Home services CONA	Horro sapiens partial AF-4 gene, exces 2 to 7 and Altranear alements	Homo saplens stard regulatory element binding transcription factors of CEPEDESS - DAVA	Homo sapiens G protein-coupled receden 89A (GPR89A) mRNA	Homo sapiens chondroitin sulfate proteochoan 2 (versican) (CSPG2) mRNA	Homo saplens chondrollin suffate proteoghyean 2 (versicen) (CSPG2) mRNA	oz43h01.x1 Sorres NhHMPu S1 Home septems CDNA circle IMAGE 4678430.3	RC1-BT0254-280100-015-601 BT0254 Homo serolents C-NA	Homo sepiens hypothetical protein (LOC51280), mRNA	EST385637 MAGE recogneriose. MAGM Horro serviens china	Homo seplens momesh (M-crotein) 2 (18540) (MYOM) - PONA	AV751001 NPC Homo sabiens cDNA clone NPCACH09 5'	289705.⊓ Sogres tests NHT Home sachers cDNA clone IMA GE-720.407 F	zi99f05.r1 Soeres testis NHT Homo septems cDNA clone IMA CE-730.407 5	Homo sepiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
gle Exon Pro	Top Hit Detabase Source	EST HUMAN	EST HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N	L	EST HUMAN	EST HUMAN	LN	5	EST HUMAN	EST HUMAN	N-F	ラ	5	F	ラ	EST_HUMAN	Г		EST HUMAN		T_HUMAN	EST HUMAN	Г	
Sin	Top Hit Acession No.	2.0E-58 BE208532.1	2.0E-68 BE907186.1	BE907186.1	2.0E-58 BF513488.1	2.0E-58 A1124874.1	2.0E-58 R92567.1	-	Ŀ			2.0E-58 AW872641.1		0274549 NT		-		4750160 NT	6174444 NT	4758081 NT	4758081		1.0E-58 BE061860.1	2031	1.0E-58 AW973537.1	4505314 NT			1.0E-58 AA412397.1	2394
	Most Similar (Top) Hit BLAST E Value	2.0E-58	2.0E-68	2.0E-58	2.0E-58	2.0E-58	2.0E-58	2.0E-58	2.0E-58	2.0E-58	2.0E-58	2.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58	1.0E-58 /	1.0E-58 /	1.0E-58
	Expression Signal	10	3.4	3.4	1.12	1.88	0.8	1.12	2.83	2.83	21.77	2.43	0.86	241	1.61	1.61	1.13	237	1.6	0.88	0.88	4.75	1.31	0.8	0.5	0.88	0.91	99.0	99.0	13
	ORF SEQ ID NO:		80208	30734	31709	31771	31803	32511	32809	32810	38570	35813	26128	28464	26726	28727	26798	28251	27462	28838	28839	30256	31465	32533		34609	34714	34818	34819	32949
	Bæn SEQ ID NO:	14016	25065		18748	18811	18841	Ш			23332	23565	13480	13805	14053	14053	14124	15510	14738	16282	16282	17841	18543	19508	22 28 8 28	21480	21571	21669	21669	22734
	Probe SEQ ID NO:	1287	5273	5273	2966	6031	6062	6828	7056	7056	10841	10885	705	1046	1304	1304	1376	2802 2802	2834	3526	3520	4913	6751	9764	8013	8768	888	8070	8979	10080

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	Top Hit Descriptor	and light chain veriable region 14		ing brother (TBP) mRNA	1 Homo sapiens cDNA close IMA CE-2384474 9	Homo sapiens cDNA clone IMAGE:3862086 51	cn08h02.y1 Normal Human Trabecular Bone Cells Home saplems cDNA close NHTBC cn08h02 resultant	aug3h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone iMAGE;2783865 3' similar to TR:075786 075786 GANGLOSIDE-INDAGED DIFFERENTIATION ASSOCIATED BEOTERN A	au33h05.x1 Schneider fetal brain 00004 Homo sapiens CDNA clone INACE:2783865 3 similar to TR:075786 075786 GANG IOSIDE JND KOED DISEEDENTATION ASSOCIATED SOCIETY	W48c1 x1 Science NET CRC St Home section Charles and Control of Co	ed ERV9 long terminal repeat?	eu66c07.x1 Schneider fetal brein 00004 Homo sepiens cDNA clone IMAGE:2781228 3' similer to contains	A) III (DNA directed) (20kD) (DBC:20)Date	CONA Come MOSEICAS E	tein (LOCS7143) mRNA	ene partial cds	Homo saptiens caterin (cadherin-associated protein), detta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA	Homo sactions 12-bets hurtmacternid dehicitations IV (USDATED A)	the MACI Home september 2017 17 19 years, promoted region and extent	ordust (KIAA080) mRNA	fiveher fleets (DI ATe) mBNA	Weter Heave (PLATA) mRNA	1112 profein pertiel cris	1112 protein partial cds	Sencher profeso 1 (AKAP1) mRNA	anchor protein 1 (AKAP1) mRNA	(ycoprotein 2 (sperm receptor) (7P2) mRNA	sogment HS21C084	(K-related protein on Y (XKRY) mRNA
Single Exon Probes Expressed in Brain	Top Hit Descript	H.sapiens immunociobulin lenna light chain variable radion 14	Human MSH3 dene. econto	Homo sapiens TATA box binding protein (TRP) mRNA	wh50d06.x1 NCI CGAP Kid11 Home seniens cDNA close IMACE: 2384171 3	801458531F1 NIH_MGC 88 Homo sapiens cDNA clone IMAGE:3882086 5	2.y1 Normal Human Trabecular Bone Cells Homo sack	5.x1 Schneider fetal brain 00004 Homo sapiens cDNA 5786 075786 GANGLIOSIDELINIA CED DIFFERENT	5.X1 Schneider fetal brain 00004 Homo sepiens CDNA 5786 O76788 GANZI IOSIDEJANA ICED DIESEDENA	1 x1 Source NEI T GRC S1 Homo sentence ONIA 2	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat	au68c07.x1 Schneider fetal brein 00004 Homo septens cDNA	Homo sadens polymerase (RNA) III (DNA directed) (30/D) (BBC:30)	AV762869 MDS Homo serviene cONA clone MOSEIC12 5:	Homo sabiens hypothetical protein (LOC57143) mRNA	Human mRNA for KIAA0184 pene, pertial cds	Homo septiens catenin (cadherin-associated protein), detta 2 (n (CTNND2), mRNA	anjens 17-beischurtmustanie dehautmasses N/UCD	EST377582 MAGE resentances MAG! Homo esplane chunk	Homo sapiens KIAA0880 cene product (KIAA0890) mRNA	Homo saciens plasminoren activator flessa (Pl ATe) mPNA	Homo saplens plesminoden activator, flesse (PLATs) mRNA	Homo septens mRNA for KIAA1112 protein pertial cds	Homo seplens mRNA for KIAA1112 protein, pertial cds	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1) mBNA	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1) mRNA	Homo sapiens zona peliucida glycoprotein 2 (sperm receptor) (ZP2) mBNA	Homo sapiens chromosome 21 segment HS21C084	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA
-xon Probes E	Top Hit Detabase Source	H.sapi	Humar	Homo	EST HUMAN WHEOD	Т		EST HUMAN TR:07		T	Т	BST HIMAN seminar	┰	HUMAN AV762	Π	Human	Homo e	Homo	EST HUMAN EST37	Т	Homo	Homo	Homo	Homos	Homo	Homo s	Homo s	Homo s	Homo s
		ż	E	F	EST	EST	EST	EST	EST	FST	E	F.9.T	Į	11-	. 1	Ę	눌	늏	EST	ż	Ę	LN LN	F	Z	F	¥	Ę	Ę	둗
ਨੋ 	. Top Hit Acession No.	1.0E-58 X63392.1	1.0E-58 D61405.1	4507378 NT	8.0E-69 AI761963.1	6.0E-59 BF035327.1	6.0E-59 AI750970.1	5.0E-59 AW157281.1	6.0E-59 AW157281.1	5.0E-59 AI807484 1	5.0E-59 X83497.1	5.0E-59 AW 162304 1	11421778 NT	5.0E-59 AV762869.1	11434908 NT	4.0E-59 D80006.1	11034810 NT	4.0E-59 AF057720.1	3.0E-59 AW965524.1	7882247 NT		4605860 NT	3.0E-59 AB029035.1	3.0E-59 AB029035.1	4502014 NT	4502014 NT	4508044 NT	3.0E-59 AL163284.2	4759329 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-58	1.0E-58	8.0E-59	8.0E-59	6.0E-59	6.0E-59	5.0E-59	5.0E-59	5.0E-59	5.0E-59	5.0E-59	5.0E-59	5.0E-59	5.0E-59	4.0E-59	4.0E-59	4.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59	3.0E-59
	Expression Signal	2.11	1.57	29.49	2.49	1.74	0.61	1.32	1.32	6.98	6.55	7.5	1.04	1.62	3.78	1.58	1.03	1.91	6.13	4.58	8.2	8.2	5.59	5.59	3.77	3.77	1.45	86.0	0.92
	ORF SEQ ID NO:		37739		33904		33970	27189	27190		23978	30526	34544	35443	36745	26210	31138			25666	27147	27148	27585	27586	28534	28535	29189	30007	30107
	Exen SEQ ID NO:	24371	24404	14953	20774	15536	20838	14490	14490	15889	17345	17968	21397	22257	23506	13548	18249	25238	12836	13030	14448	14448	14856	14856	15891	15891	16557	17372	17470
	Probe SEQ ID NO:	11780	11818	2225	8080	173	8144	1748	1748	3124	4610	6892	8705	9604	10823	776	5450	12203	đ	219	1705	1705	2125	2125	3126	3128	3805	4638	4738

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Exam ORF SEQ Expression Most Similar Top Hit Acession Top				-			_	_													-												
Exam ORF SEQ Expression Most Similar Top Hit Acession Top	have + bes Expressed in Brain	Top Hit Descriptor	Homo sapiens protein tyrosine phosphatese resembs two T/DTDDT1DNIA	Human prohomone conventing enzyme (NEC2) game, exxm. 2	Hamo saciens hypothetical printein PRO1744 (DRO4744) DNA	Homo sablens nuclear recenter co-represent 4 (NCOB4) mBNA	Human mRNA for did proto-on-on-on-on-on-on-on-on-on-on-on-on-on	Human mRNA for dbi prote-processes	H. sapiens CKILalpha gene	H. saplens CKHabbe cene	Homo saplens camma-clutamytransferase like artikty ((CCT1 A1) mDNA	MR0-FT0144-250700-002-a10 FT0144 Homo cardene cDNA	EST180633 Jurkat T-cells V Homo samens cONA 5' and	RCO-NT0036-100700-032-907 NT0036 Homo entires CONIA	(h07h04x1 NIH MGC 17 Homo seniens chiva clava IMACE: 30648E4 F.	fh07h04x1 NIH MGC 17 Homo sapiens cDNA clane IMAGE-2861624 51	W49h09.r1 Soares fetal liver spleen 1NFLS Hamo sablens cDNA clone IMAGE 208672 51 similar to	SP-POL_FENV1 P31792 POL POLYPROTEIN;	We36c12.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone INAGE:2300182 3' similar to TR:Q86542	Homo sablens alpha-fithigh mRNA Associates Ale	801176757F1 NIH MGC 17 Homo seniens CDNA close IMAGE 3534927 51	ve25c09.r1 Stratagene lung (#937210) Homo saplens cDNA clone IMAGE:118768 5' similar to SP:S21348 S21348 HYPOTHETICAL IDDOTTENA	Homo saciens Xdha mRNA for vanithing dehir formance complete of	Homo sapiens Xdha mRNA for xanthine dehurtmoanasa complete cde	0656h11.s1 NG_CGAP_GCB1 Homo septens CDNA clone IMAGE: 3390229.3' similar to TR:Q13537 013537 MFR37 TRANSPOSARIE EI EMENT CONING THE CONSTRUCTION OF CONSTRUCT	Homo seciens mRNA for transcription factor	001111951F1 NIH MGC 16 Home sentions clove like GE 32 87802 81	801111951F1 NIH MGC 16 Home seniors chiva close two CE 2325282.3	Homo saciens zinc finger profein 275 (ZNE)275) mRNA	Homo saplens 3-hydraxyisobutyvy-Coenzyme A hydralese (HIRCH) mRNA	Homo sapiens 3-hydroxylsobutyry-Coenzyme A hydrolese (HIRCH) mRNA	Homo sepiens mRNA for transcription factor	EST389849 MAGE resequences, MAGO Homo sapiens cDNA
Exon NO: 17520 ORF SEQ ID NO: 1773 Expression Signal 1.67 (Top) Hit Yalue Nature 1.67 Top Hit Acess Nature 1.67 Top Hit Acess Nature 1.67 Most Similar Nature 1.67 Top Hit Acess Nature 1.67 Top Hit Acess Nature 1.67 No. 1.69 T427 0.1773 3.0143 1.57 3.0E-59 M95891.1 No. 1720 7.272 1.0E-69 P7427 1.0250 3.0220 1.94 3.0E-59 M95891.1 8624 6454 2.2592 3.5795 0.87 3.0E-59 K7256.1 1.417 2.2592 3.5795 0.87 3.0E-59 K7256.1 1.417 2.2592 3.5795 0.87 3.0E-59 K70251.1 1.417 2.2592 3.5795 0.87 3.0E-59 K70251.1 1.417 2.2420 3.5795 0.87 3.0E-59 KV410598.1 1.417 2.2421 3.6563 2.0 3.0E-59 KV410698.1 1.427 2.2421 3.6563 3.11 3.0E-59 KV410698.1 1.16E-59 BE256411.1	le Exon Pro	Top Hit Detabase Source	7	Ę	F	5	F	5	5	F	 	ST HUMAN	ST HUMAN	ST HUMAN	ST HUMAN	ST HUMAN		ST_HUMAN	ST HUMAN	1	ST HUMAN	ST HIMAN	_	L			П	HUMAN				П	EST HUMAN
Exon ORF SEQ Expression Total Sing	Top Hit Acession No.	7427522		8924074	6464137					7866										-				-	-	_	F	11419630 N	11428849 N			_	
Expn NO: ORF SEQ ID NO: Expression Signal 17520 30143 1.57 17520 30143 1.57 17713 31872 2.12 2 20527 33653 1.16 2 20527 33654 0.87 2 20527 33684 0.87 2 20357 36884 2.6 2 23070 37274 1.19 2 2582 35785 0.71 2 23071 6.32 2.6 2 2592 35784 2.6 2 2592 35785 0.71 2 2592 35784 2.6 2 2542 36884 2.6 2 25283 30719 4.65 12874 3.03 12874 3.03 14276 28864 0.93 1533 27871 1.19 1533 27871 1.19 1533 27871 1.18 20283 333227 1.08 20283 33362 <td></td> <td>Most Similar (Top) Hit BLAST E Value</td> <td>3.0E-59</td> <td>3.0E-59</td> <td>3.0E-59</td> <td>3.0E-69</td> <td>3.0E-59></td> <td>3.0E-59</td> <td>3.0E-59</td> <td>3.0E-59 X</td> <td>3.0E-59</td> <td>2.0E-59 B</td> <td>2.0E-59 A</td> <td>2.0E-59 B</td> <td>2.0E-59 A</td> <td>2.0E-59 A</td> <td></td> <td>2.0E-59 H</td> <td>2.0E-59 A</td> <td>2.0E-59 L</td> <td>1.0E-59 B</td> <td>1.0E-59 T</td> <td>1.0E-59 D</td> <td>1.0E-59 D</td> <td>1.0E-59 A</td> <td>1.0E-59 A.</td> <td>1.0E-59 BR</td> <td>1.0E-59 BE</td> <td>1.0E-59</td> <td>1.0E-59</td> <td>1.0E-59</td> <td>.1.0E-59 AJ130894.1</td> <td>8.0E-50 AW977845.</td>		Most Similar (Top) Hit BLAST E Value	3.0E-59	3.0E-59	3.0E-59	3.0E-69	3.0E-59>	3.0E-59	3.0E-59	3.0E-59 X	3.0E-59	2.0E-59 B	2.0E-59 A	2.0E-59 B	2.0E-59 A	2.0E-59 A		2.0E-59 H	2.0E-59 A	2.0E-59 L	1.0E-59 B	1.0E-59 T	1.0E-59 D	1.0E-59 D	1.0E-59 A	1.0E-59 A.	1.0E-59 BR	1.0E-59 BE	1.0E-59	1.0E-59	1.0E-59	.1.0E-59 AJ130894.1	8.0E-50 AW977845.
Exam ORI ID ID ID ID ID ID ID ID ID ID ID ID ID		Expression	1.57	76.0	2.12	1.94	1.16	1.16	0.87	0.87	6.04	0.71	6.32	1.19	2.6	2.8		1.31	2.83	4.65	3.03	0.93	1.19	1.19	2.47	1.08	0.97	76.0	0.86	0.54	0.54	12.88	0.85
0 0000000000000000000000000000000000000		ORF SEQ ID NO:	30143				33663	33654	35794	35795					36663	36664		37274	31126	30719		26964	27870	27871		33227	33392	33383	35210	35337	35338	33227	201/8
100 C C C C C C C C C C C C C C C C C C		<u> </u>		_						_ 1	24746	20357	22190	23071	23421	23421		23970	24595	25263	12974	14276	15133	15133	15335	20135	20283	20283	22039	22157	22157	20135	1350
		Probe SEQ ID NO:	4789	4990	G128	7259	7832	7832	9944	994	12327	7883	9537	10425	10734	10734	-	11311	12091	12605	150	1529	2412	2412	2623	7462	7617	7817	9285	930	8504	10760	(*)

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Describtor
1455	14202	26886	2.65	8.0E-80	4759159 NT	LN	Homo sapiens small nuclear ribonucleoprotein D3 potypeptide (18kD) (SNRPD3) mRNA
2169	14898	27632	3.6	8.0E-60	5174656 NT	TN	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2169	14898	27633	3.6	8.0E-80	5174656 NT	LN.	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
5892	18677	31623	1.12	8.0E-80	8.0E-80 AB029004.1	NT	Hamo sapiens mRNA for KIAA1081 protein, pertial ods
0411	19179	32178	10.1	8.0E-80	8.0E-80 S83182.1	LN	hysiurchan-binding protein=hapathocyte growth factor activator homolog (human, plesma, mRNA, 2408 πt)
7596	20264	33372	1.07	8.0E-80	11420841 NT	L	Homo sepiens phosphate cytidylytransferase 1, choline, beta isoform (PCYT1B), mRNA
7865	20580	33687	2.28	8.0E-80	8.0E-80 X17033.1	L	Human mRNA for integrin alpha-2 subunit
8837	21529	34675	2.6	8.0E-80	11428949 NT	FX	Homo sapiens S-entigen; retine and pineal gland (arrestin) (SAG), mRNA
9371	21946	35118	96'0	8.0E-80	11417118 NT	TN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9371	21946	35119	0.96	8.0E-60	11417118 NT	TN	Homo sepiens KIAA0433 protein (KIAA0433), mRNA
10473	23119	36348	0.59	8.0E-60	TN 7885398	F	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10736	23423	36666	6.38	8.0E-80	8.0E-80 AL163204.2	LΝ	Homo sapiens chromosome 21 segment HS21C004
10736	23423	29987	6.36	8.0E-80	8.0E-80 AL163204.2	L	Hamo sapiens chromosome 21 segment HS21C004
737	13511	20169	3.61	7.0E-50	7.0E-60 AF055006.1	L	Homo sapiens MHC class 1 region
738	13511	26169	17.82	7.0E-60	7.0E-60 AF055068.1	LN.	Homo saplens MHC class 1 region
796	13568	26228	86.0	7.0E-60	4504634 NT	LN	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2124		27584	1.08	7.0E-50	7.0E-60 AF077188.1	LN	Homo septens cullin 4A (CUL4A) mRNA, complete cds
2788	15403	28233	1.53	7.0E-80	7.0E-60 AB011153.1	LN	Homo sapiens mRNA for KIAA0581 probein, partial cds
4158	16898	29627	2.56	7.0E-60	4505488 NT	LX	Homo sapiens omithine decarboxylase 1 (ODC1) mRNA
\$307	21974	35149	4.02	7.0E-80	7.0E-80 H58041.1	EST HUMAN	y/12/04.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element:
							yr12704.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA done IMAGE:205087 5' similer to contains
11337	24027	37331	2.11	7.0E-60	7.0E-60 H58041.1	EST_HUMAN	LTR5 repetitive element;
2177	14908	27639	1.06	6.0E-80	6.0E-80 BE984974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Hamo sepiens cDNA clone IMAGE:388069 3'
							yq78h09.r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:201953 5 similar to contains
8336	21029		10.5	6.0E-00	6.0E-60 H52456.1	EST_HUMAN	OFR repetitive element;
82		25545		5.0E-60	5.0E-60 AI807917.1	EST_HUMAN	wf52c07.x1 Sceres_NFL_T_GBC_S1 Home septems cDNA clone IMAGE:2359212 3:
82	12908	25546	2.29	5.0E-80	5.0E-60 AI807917.1	EST_HUMAN	wf52c07.x1 Soeres_NFL_T_GBC_S1 Homo sapiens.cDNA.clone IMAGE:2359212.37
2972	15738		1.27	4.0E-60	4.0E-60 AA299037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA, 5' end similar to similar to retrovirus-related pol
İ							hr81105.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
1253	- 1	33012	0.88	4.0E-80		EST_HUMAN	CRIDES GIP-KHO BINDING PKO I EIN 1;
9054	- 1		0.68	4.0E-80	4.0E-60 AL163278.2	LN	Homo sapiens chromosome 21 segment HS21C078
11267	23929	37219	1.29	4.0E-00	· 11433597 NT	Ł	Homo sepiens v-raf-1 munhe leukemia vinal oncogene homolog 1 (RAF1), mRNA

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Table 4
Single Exon Probes Expressed in Brain

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Single Exon Probes Expressed in Brain	ORF SEQ Expression (Top) Hit Acession (Top) Hit Acession Signal BLAST E No. Source Source	32757 2.73 2.0E-80 AA311159.1	32758 2.73 2.0E-30 AA311159.1 EST HUMAN		1 EST HUMAN	0.84 2.0E-80 X85597.1 EST_HUMAN	3.01 2.0E-60 [L36033.1 NT Human pre-B cell stirrulating factor homologue (SDF1b) mRNA, complete cds	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA	35725 2.0E-60 11981659 NT (SEMAGA), mRNA	11434729INT	1.8 2.0E-60 BF530674.1 EST HUMAN	EST HUMAN		2.0E-80 AF068757.1 NT	2.34 2.0E-80 11418068 NT Homo sapiler to HSPC0222 protein (H. sapiens) (LOC33504): mRNA	1.77 2.0E-60 AB011399.1 INT	1.13 1.0E-60 BE178586.1 EST HUMAN	1.16 1.0E-60 AU143389.1 EST_HUMAN	1.2 1.0E-60 AL163285.2 NT	33671 0.91 1.0E-60 BE064410.1 EST_HUMAN RC4-BT0311-141199-011-h08 BT0311 Homo septens cDNA	3 48 1 0E-201 A 2 2 4 0 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1.0E-80 AV754081.1 EST HUMAN	9.0E-61 AU119344.1 EST HUMAN	1.16 8.0E-61 AW006478.1 EST HUMAN	28127 1.16 8.0E-61 AW006478-1 EST HUMAN W05b10.x1 NCI CGAP Cost Homo septients cDNA close IMAGE-2506656.3	1.53 8.0E-81 X57147.1 NT	1.05 8.0E-61 AA583968.1 EST HUMAN	1.97 7.0E-61 7706870 NT	1.97 7.0E-61 7708670 NT	2.38 7.0E-61 7706870 NT	
		32757	32758	32880		33729	34608	35724	35725	36448	37732	37733					25925	29271	30245	33671		34517	26463	28126	28127		33614	25583	25584	25583	25584
	Exan SEQ ID NO:	ш	19702	19812			21458	22528	22528	L	24398						_l		_	20543	21345	L	13835	15385		15717	20491	12941			12941
	Probe SEQ ID NO:	7010	7010	7124	7532	7904	8766	9878	9678	11449	11809	11809	12364	12404	12496	12510	200	3882	<u>\$</u>	7848	8853	8681	1077	2676	2678	2951	77.96	124	124	125	125

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	imiter Top Hit Acession Databese Top Hit Descriptor Source Source	0E-61 7706670 NT (Homo sapiens PXR2b protein (PXR2b), mRNA	0E-61 7706670 NT Homo sapiens PXR2b protein (PXR2b), mRNA	6.0E-61 BE409310.1 EST_HUMAN 601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'	EST_HUMAN	INT	6.0E-61 BE257400.1	6.0E-61 ASS6033.1 EST_HUMAN Inn68h09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897.3'	6.0E-61 AY008285.1 NT Homo seplens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product	6.0E-61 AU130889.1 EST_HUMAN AU130689 NT2RP3 Homo septens cDNA clone NT2RP3001263 5		6.0E-61 U24498.1 NT Human autosomal dominant potycystic kidney disease protein 1 (PKD1) gene	6.0E-61 AF035737.1 NT Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, complete cds	6.0E-61 AF090386.1 NT Homo sapiens napsin A mRNA, complete cds	6.0E-81 AF090386.1 NT Homo saplens napsin A mRNA, complete cds	6.0E-61 BE409310.1 EST_HUMAN 601300938F1 NIH_MGC_21 Homo septems cDNA clone IMAGE:3635480 5'	0E-61 4507500 NT Homo sapiens T-cell lymphoma investon and metastasis 1 (TIAM1) mRNA	3008 NT	5.0E-61 AL 163279.2 NT Homo sapiens chromosome 21 segment HS21C079	0E-61 4502166 NT Homo sapiens amykid beta (A4) precursor protein (protease nedn-II, Alzhetmer disease) (APP), mRNA	5.0E-81 AJ229041.1 NT Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3	4507500 NT	0E-61 4502296 NT Homo saplens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1) mRNA	31637 NT	4.0E-61 AV731140.1 EST_HUMAN AV731140 HTF Homo sepiens cDNA clone HTFARB01 6'	EST_HUMAN	3.0E-81 AA301233.1 EST_HUMAN EST14323 Testis tumor Homo septens cDNA 5' end	3.0E-61 AA301233.1 EST_HUMAN EST14323 Tectls tumor Homo septems cDNA 5' end	0E-01 8922829 NT Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA	2.0E-61 BE168410.1 EST_HUMAN QV3-HT0513-060400-147-d01 HT0513 Homo saplens cDNA	2.0E-61 BE168410.1	2.0E-61 N53039.1 EST_HUMAN gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
	Most Similar (Top) Hit BLAST E Value	7.0E-61	7.0E-61	6.0E-81 BE.	6.0E-61 BE.	6.0E-61 AF	6.0E-61 BE	6.0E-61 AA	6.0E-61 AY	6.0E-61 AU	6.0E-61 S78	6.0E-61 U2	8.0E-61 AF	6.0E-61 AF	6.0E-61 AF	8.0E-81 BE	5.0E-61	5.0E-81	5.0E-61 AL:	5.0E-61	5.0E-81 AJ	5.0E-61	5.0E-61	4.0E-81	4.0E-61 AV	3.0E-61 AF	3.0E-61 AA:	3.0E-61 AA:	2.0E-61	2.0E-61 BE	2.0E-61 BE	2.0E-61 NS
-	Expression (1.04	1.04	2.95	1.62	15	26.0	2.63	1.58	9.37	3.37	1.82	1.67	1.35	1.35	1.62	1.73	2.22	2.56	3.27	1.78	1.07	3.38	0.87	3.51	0.69	0.64	0.64	1.52	0.82	0.82	1
	ORF SEQ ID NO:	25583	25584	25705	26226	26719	19072	27078	27.583	28711	31682	33003	33282	37384	37385	26226	25789	27112	28444	28608		25789	30416	31438		34151	34427	34428	25906	28807	80987	27087
	Exen SEQ ID NO:	12941	12941	13067	13565	14047	14372	14389	14854	16063	18723	19927	20189	24075	24075	13565	13149	14419	15798	15956	16712	13149	17799	18517	24582	21013	21288	21288	13271	13942	13942	14408
	Probe SEQ ID NO:	5034	5034	259	783	1298	1626	1643	2123	3301	5941	7242	7518	11474	11474	12265	320	1874	3032	3183	3963	4941	2080	6725	12068	8320	8508	8598	28	1180	1190	1680

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	yy03f11.r1 Soares melanocyle 2NbHM Homo sapiens cDNA clone IMAGE:270189 5'	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA	AV694317 GKC Hamo sapiens cDNA clone GKCELG06 5	Hamo sepiens mRNA for KIAA0538 protein, pertiel cds	UI-HF-BNO-akd-f-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA done IMAGE:3078774 5'	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA	Homo sapiens ribosomal protein L44 (RPL44), mRNA	Homo saplens origin recognition complex, subunit 2 (yeast handog)-like (ORC2L) mRNA	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA	xn11b09.y1 NCI_CGAP_LI5 Homo sepiens cDNA clone IMAGE:2690369 5' similar to contains element MSR1 recettive element:	601273513F1 NIH MGC 20 Homo sepiens cDNA clone IMAGE:3614667 5	Homo saplens KIAA0808 gene product (KIAA0808), mRNA	QV2-HT0577-140300-077-906 HT0577 Homo sepiens cDNA	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA	Homo sapiens TRAF family member-essociated NFKB activator (TANK) mRNA	UI-H-BW0-ett-b-08-0-UI.s1 NCI_CGAP_Sub6 Hamo sepiens cDNA clone IMAGE:27328713'	UI-H-BW0-git-b-08-0-UI.st NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:27328713'	Homo sapiens chromosome 21 segment HS21C010	H.sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA	Homo sapiens growth hormone releasing hormone (GHRH), mRNA	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(UBEZD3) genes, complete ods	MR0-BN0070-040400-010-h01 BN0070 Homo sapiens cDNA	Homo sapiens cadherin 18 (CDH18), mRNA	Homo sapiens KIAA0971 protein (KIAA0971), mRNA	Homo sapiens actirun, alpha 4 (ACTN4), mRNA
e Exoli Plobe	Top Hit Database Source	EST_HUMAN N		T_HUMAN		T_HUMAN						Т	Т,	T_HUMAN			EST_HUMAN U	EST_HUMAN U					H							T_HUMAN			
Billo	Top Hit Acession No.		11428168 NT	2.0E-61 AV694317.1 E		2.0E-61 AW500258.1 E	11421778 NT	11419729 NT	5453829 NT	6005983 NT	1.0E-61 AW827281.1	1.0E-61 BE386363.1 E	7862319IN	1.0E-61 BE174455.1 E	4759249 NT	4759249 NT	1.0E-61 AW298181.1 E	1.0E-61 AW 298181.1 E	1.0E-61 AL163210.2		7662303 NT	11416891 NT		4759171 NT	8923130 NT	8923130 NT	11034840 NT		Ī	1.0E-61 AW989726.1 E	11416280 NT	11428892 NT	11425578 NT
-	Most Similar (Top) Hit BLAST E Value	2.0E-61 N39397.1	2.0E-61	2.0E-61	2.0E-61/	2.0E-61	2.0E-61	20E-61	1.0E-81	1.0E-81	1.0E-61	1.0E-81	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-61 M76423.1	1.0E-61	1.0E-61	1.0E-61 M30135.1	1.0E-61	1.0E-61	1.0E-81	1.0E-61		1.0E-61	1.0E-61	1.0E-61	1.0E-61	1.0E-81
}	Expression Signal	1.04	0.98	0.98	0.99	1.67	2.3	1.81	1.11	3.71	1.42	1.47	0.86	1.2	0.81	0.81	8.11	8.11	0.75	1.62	0.70	1.29	7.11	0.67	1.42	1.42	ဧ		3.06	2.7	7.73	5.24	2.84
-	ORF SEQ ID NO:		32090	34748		35678	36014		26188	27304	27856	28257	28786	29106	29773	29774	30157	30158	30247	30772	31310	31511	32482	32732	32845	32846	33861		34041		35110	35775	36462
	Exan SEQ ID NO:	15357	19102	21604	22012	22473	22798	23482	13528	14580	14922	15607	16128	16468	17144	17144	17535	17535	17632	18114	18398	18584	19461	19684	19780	19780	20728		20906	21852	21836	22578	23228
	Probe SEQ ID NO:	2647	6332	8913	3462	8822	10150	10799	756	1851	2193	2839	3369	3715	4407	4407	4804	4804	4905	2309	5603	5733	0880	6991	7091	7091	8033		8212	9182	9257	8268	10531

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820 ID NO: 820 ID NO:

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Single Exon Probes Expressed in Brain

-			_		_		-	,		_	·		_					_							_				_	_			
	Top Hit Descriptor	Homo sapiens mRNA for KIAA0350 protein, partial cds	Homo sapiens mRNA for KIAA0350 protein, partial cds	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA	Homo sapiens mRNA for PkB kinese	Homo saplens nucleoporth 88kD (NUP88), mRNA	Homo sapiens pyruvate dehydrogenase khase, Isoenzyme 3 (PDK3) mRNA	Homo sapiens Ras association (Ral GDS/AF-8) domain family 2 (RASSF2), mRNA	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA	Homo saplens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein mRNA	Homo sapiens II.2-inducible Total kinase (ITK): mRNA	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Galtus gellus Dach2 protein (Dach2) mRNA, complete cds	Homo sapiens chromosome 21 segment HS21C068	wm55g11.x1 NCI_CGAP_Ut2 Hamo saplens cDNA clone IMAGE:2439908.3/	no83f02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S RIBOSOMAL PROTEIN (HUMAN);	Homo sepiens G protein-coupled receptor 51 (GPR51), mRNA	Homo sapiens chromosome 21 segment HS21 C078	Homo saplens mRNA for KIAA0707 protein, partial cds	Homo sapiens mRNA for KIAA0707 protein, partial cds	CM3-BT0595-190100-072-e09 BT0595 Homo sepiens cDNA	CM3-BT0595-190100-072-e09 BT0595 Homo sapiens cDNA	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA done IMAGE:2712482 3'	UI-H-BI1-ebq-e-02-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA done IMAGE:2712482 3'	EST72607 Ovary II Homo sapiens cONA 5' end similar to similar to zinc finger protein family	Homo sapiens mRNA for KIAA0717 protein, peritial cds	Human Met-tRNA-i gene 1	Homo sapiens zinc finger protein 144 (Met-18) (ZNF144), mRNA	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC83928), mRNA	601485666F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'	801485856F1 NIH_MGC_89 Homo septems cDNA clone IMAGE:3888253 5	Human DNA topolsomerase I mRNA, partial cds
	Top Hit Database Source	N FN	Į.	Į.	F	Į.	۲	¥	Ņ	TN	NT	L	ĮŅ.	NT.	LN.	EST HUMAN	EST_HUMAN	뉟	FN	IN	IN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	F	۲	EST_HUMAN	EST_HUMAN	N
	Top Hit Acession No.	9.0E-63 AB002348.2	9.0E-63 AB002348.2	11418185 NT	/15056.1	11426985 NT	4885544 NT	11421160 NT	7662289 NT	7682289 NT	4557734 NT	5031810 NT	8.0E-63 AF198349.1	8.0E-63 AF198349.1	8.0E-63 AL163268.2	7.0E-63 AI872137.1	6.0E-63 AA420803.1	11526464 NT	4.0E-63 AL163278.2		4.0E-63 AB014607.1	4.0E-63 AW750372.1	4.0E-63 AW 750372.1	4.0E-63 AW134709.1	4.0E-63 AW134709.1		0.1		6005963 NT	11545810 NT			
	Most Similar (Top) Hit BLAST E Value	9.0E-63	9.0E-63	9.0E-83	9.0E-63 Y15056.1	9.0E-83	9.0E-63	9.0E-€3	9.0E-63	9.0E-63	8.0E-63	8.0E-63	8.0E-83	8.0E-63/	8.0E-63	7.0E-63	6.0E-63	5.0E-63	4.0E-63	4.0E-63	4.0E-63 A	4.0E-63 A	4.0E-63	4.0E-63 A	4.0E-63 A	4.0E-83 A	3.0E-63 A	3.0E-63 J00310.1	3.0E-63	3.0E-63	3.0E-63 B	3.0E-63 B	2.0E-63 U07804.1
	Expression Signal	7.42	7.42	3.05	1.63	3.86	0.91	1.38	2.03	2.03	1.32	2.06	3.02	3.02	3.31	2.09	48.05	1.97	0.84	1.16	1.16	3.64	3.64	2.3	2.3	4.32	2.82	2.26	11.81	32.78	1.15	1.15	1.09
	ORF SEQ ID NO:	28385	96868	37798	69808	32837	33501	34055	36736	36737	27803	27834	28861	28862	29600			34612	28726	29174	29175	32115	32116	37021	37022	37771	27377	28225	26636	32150	35444	35445	25639
	Exon SEQ ID NO:	16766	16786	17895	18179	19772	20387	20918	23499	23499	15066	15095	16210	16210	16975	13675	18061	21465	16075	16540	16540	19123	19123	23747	23747	24430	14664	15487	13967	19161	22258	22258	12999
	Probe SEQ ID NO:	4020	4020	5164	5379	7082	7724	8224	10816	10816	2343	2373	3454	3454	4234	808	5255	8773	3315	3788	3788	6353	8223	11077	11077	11846	1928	2782	2824	6382	2008	9805	186

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Oligio Exoli Flores Explessed III Digili	Top Hit Descriptor	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA	Homo sapiens glutamate-cystelne ligase (gamma-glutamylcystelne synthetase), catalytic (72.8kD) (GLCLC) mRNA	Homo saplens Down syndrome candidate region 1 (DSCR1), mRNA	Homo saplens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds	Home sapiens RHCE mRNA for Rh blood CE group entigen polypeptide, complete cds	601301627F1 NIH_MGC_21 Hamo sepiens aDNA clane IMAGE:3636103 5	Homo sapiens amykid beta (A4) precursor protein (protease neatn-II, Alzheimer disease) (APP), mRNA	Homo sapiens chromosome 3 subtelomerto region	Homo saplens polycystic kidney disease associated protein (PKD1) gene, complete cds	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclese) (QPCT), mRNA	Homo sapiens similar to extonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA	QV1-FT0170-040700-265-c05 FT0170 Homo saplens cDNA	QV1-FT0170-040700-265-c05 FT0170 Homo sepiens cDNA	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKARZB), mRNA	Human germiline T-call receptor bata chain Dopernine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV3S1A1N2T, TCRBV3S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S2A1N4T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>	Homo sapiens MIST mRNA, pertial cds	Homo sapiens MIST mRNA, partial cds	Homo sapiens Carbonic anhydrase-raiated protein 10 (LOC56934), mRNA	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA	Homo sapiens mRNA for KIAA 1624 protein, pertial cds	Homo sepiens similar to seme domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphortn) 3A (H. sepiens) (LOC63232), mRNA	Homo sapiens chromosome 21 segment HS210010	Homo saplens kinesin family member 38 (KIF3B), mRNA	Homo sapiens kinesin family member 3B (KIF3B), mRNA
פוב ווסעיו פופ	Top Hit Database Source	Z	Ę	Z	FZ.	F	EST_HUMAN	NT	LZ	TN	TN	N TN	뒫	EST HUMAN	EST_HUMAN	LX LX	TN	<u> </u>	N.	Z	N-	Į.	N L	NT	TN	IN	NT
5	Top Hit Acession No.	4885226 NT	TN 4557824 NT	7657042 NT	2.0E-63 AB030388.1	2.0E-63 AB030388.1	2.0E-63 BE410739.1	4502188 NT	2.0E-63 AF109718.1	39891.1	2.0E-63 AF111167.2	6912617 NT	11419428 NT	2.0E-63 BF373541.1	2.0E-63 BF373541.1	11421940 NT	11421940 NT	J68059.1	2.0E-63 AB032369.1	AB032369.1	9910365 NT	9910365 NT	2.0E-63 AB046844.1	11421514 NT	AL163210.2	11420949 NT	11420949 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-63	2.05-63	20E-83	2.0E-63	2.0E-83	2.0E-63	2.0E-63	2.0E-63	2.0E-63 L39891.1	2.0E-83	2.0E-63	2.0E-83	2.0E-63	2.0E-63	2.0E-63	2.0E-63	2.0E-63 [U68059.1	2.0E-63 /	2.0E-63 /	2.0E-63	2.0E-63	2.0E-63 /	2.0E-83	2.0E-63/	2.0E-63	2.0E-63
	Expression	1.68	2.34	5.57	1.43	1.43	1.1	3.44	2.02	3.74	-	9870	25	2.96	2.96	0.84	0.84	1.67	0.88	0.88	1.45	1.45	0.87	95.0	3.96	1.35	1.35
	ORF SEQ ID NO:	25847		26244		26882	27203	28563		29274	30169	30435	30505	31512	31513	31837	31838	32379	32425	32426	32477	32478	33454	33490	34262	34791	34792
	Exen SEQ ID . NO:	13006	13270	13579	14306	14306	14502	15917	16040	16635	17544	17818	25062	18585	18585	18871	18871	19365	19411	19411	19456	19466	20342	20377	21124	21643	21643
	Probe SEQ ID NO:	183	485	807	1589	1559	. 1760	3154	3279	3885	4813	2036	5181	5794	5794	£60 0	9083	6602	6649	. 6649	9269	6975	7678	7713	8431	8952	8952

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On gle LAOIT FLOORS LADIOSSEU III DIGIII	Exam ORF SEQ Expression (Top) Hit Acession ID NO: Signal BLAST E No. Source Source	22490 35691 1.12 2.0E-63 AL 163218'2 NT Homo sepiens chromosome 21 segment HS21C018	23338 36577 6.43 2.0E-63 N78946.1 EST HUMAN gbtX17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);	36604 2.96 2.0E-63 AF099810.1 NT	36605 2.96 2.0E-63 AF099810.1 NT	30807 5.97 2.0E-63 11418185 NT	28934 1.28 1.0E-63 F08485.1 EST HUMAN	28935 1.28 1.0E-63 F08485.1 EST_HUMAN	29672 2.92 1.0E-63 F08485.1 EST_HUMAN	29673 2.92 1.0E-63 F08485.1 EST_HUMAN	30703 0.8 1.0E-63 AJ271736.1 NT	31394 1.4 1.0E-63 AW 582268.1 EST HUMAN	32055 0.68 1.0E-63 AW451950.1 EST_HUMAN	32056 0.68 1.0E-63 AW 451950.1 EST_HUMAN	2.68 1.0E-63 AL163247.2 NT	4.04 (1.0E-63 AL163207.2 NT	33586 4.36	6.16 8.0E-64 BE280796.1 EST_HUMAN	31792 3.88	7.34 8.0E-64 11418177 NT	1.6 8.0E-64 T80651.1 EST_HUMAN	1.13 7.0E-64 BE394321.1 EST_HUMAN	30052 2.73 7.0E-64 4507490 NT	30053	35779 3.43 7.0E-64 Y07848.1 NT	wb51e07.x1 NCI_CGAP_GC8 Homo septens dDNA done IMAGE:2309220 3' similar to gb:M15182 BETA- 1.63 6.0E-64 Al651892.1 EST_HUMAN GLUCURONIDASE PRECURSOR (H-MAN):		27157 1.63 6.0E-64 AI651992.1 EST_HUMAN	28524 4.39 6.0E-64 AW026445.1 EST_HUMAN	28525 4.39 6.0E-64 AW026445.1 EST_HUMAN	31237 2.46 6.0E-64 Y18933.1 NT	31238 2.46 6.0E-64 Y18933.1 NT	8352 31261 4.08 6.0E-64 M13975.1 NT Homo sepiens probein kinese C beta-li type (PRKCB1) mRNA, complete cds
	Exan ORFS SEQ ID ID N			23363 36	23383 36	25177 30	14248 26	14248 28		17047 29	18074 30	18476 31	19071 32	19071 32	21064				18829 31	24479	24518				22581 35	14459 27							18352 31
	Probe SEQ ID S NO:	6836	10647	10672	10872	12098	1502	1502		4308	5268			Ш								l			8833	1718	l	_[_	\Box		5555

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705); mRNA	Homo sepiens calcitonin receptor (CALCR), mRNA	Homo sapiens calcitionin receptor (CALCR), mRNA	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA	Homo sepiens mesenchyme homeo box 1 (MEOX1), mRNA	Homo sapiens soely-CoA synthetase (LOC55902), mRNA	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds	trkC [human, brain, mRNA, 2715 nt]	Homo sapiens stromal antigen 3 (STAG3), mRNA	Homo sapiens stromel entigen 3 (STAG3), mRNA	wv13e03.x1 NCI_CGAP_Bm23 Home septems cDNA clone IMAGE:2529436 3	wr13e03.x1 NCI_CGAP_Bm23 Homo sepiens cDNA clone IMAGE: 2529436 3'	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens mRNA for KIAA0903 protein, partial cds	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds	Homo septens phosphogkucomutase-releted protein (PGMRP) gene, complete ods	Human (3)mbt protein homolog mRNA, complete cds	Homo sepiens KIAA0618 gene product (KIAA0618), mRNA	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA	Homo sepiens putetive transcription factor CR53 (CR53) mRNA, partial cds	Homo seplens mRNA for KIAA0903 protein, partial cds	801590382F1 NIH_MGC_7 Home septems cDNA clone IMAGE:3944397 6'	RC3-ST0197-120200-015-803 ST0197 Homo saplens cDNA	RC3-ST0197-120200-015-e03 ST0197 Homo saplens cDNA	C18895 Human placenta cDNA (TFujiwara) Homo saplens cDNA clone GEN-569E02 5	001589565F1 NIH_MGC_7 Homo septens cDNA clone IMAGE:3943577 5	AV711714 DCA Homo sepiens aDNA alone DCAAMC01 5	AV711714 DCA Homo expiens cDNA done DCAAMC01 5'	H.sepiers Isoform 1 gene for L-type calclum channel, exon 28	RC8-FN0019-290600-011-G11 FN0019 Homo sepiens cDNA	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
Jie Exon Propes	Top Hit Database Source							PE IN	N FK			EST_HUMAN WY	Г		Ha	NT	N Hot	NT											EST_HUMAN 601	Γ	EST_HUMAN AV7		T_HUMAN	NT
ŽIIO	Top Hit Acession No.	6012461 NT	11422189 NT	11422189 NT	11525879 NT	11525879 NT	11420555 NT	6.0E-64 AF274753.1	6.0E-84 S78475.1	11420197 NT	11420197 NT	6.0E-64 AW026445.1	6.0E-84 AW028445.1	11528198 NT	5.0E-64 AF231919.1	1	5.0E-64 AB020710.1			J82358.1	7862205 NT	7862205 NT	1	1	1	1	3.1		3.0E-64 BE794381.1 E	3.0E-64 AV711714.1	3.0E-64 AV711714.1			3.0E-64 AF248953.1 N
	Most Similar (Top) Hit BLAST E Value	8.0E-64	6.0E-64	6.0E-64	6.0E-64	6.0E-64	6.0E-64	6.0E-64	6.0E-84	6.0E-64	6.0E-64	6.0E-84	6.0E-64	6.0E-64	5.0E-64	5.0E-64	5.0E-64	5.0E-64 L40833.1	5.0E-64 L40933.1	5.0E-64 U89358.1	5.0E-64	5.0E-64	5.0E-64	5.0E-64 /	4.0E-64	4.0E-64	4.0E-84/	3.0E-64 C18895.1	3.0E-64	3.0E-84	3.0E-64 /	3.0E-64 Z26273.1	3.0E-64	3.0E-84/
	Expression Signal	1.26	0.62	0.62	234	2.34	8.78	2.09	2.78	6.01	6.01	1.84	1.84	4.97	2.85	2.85	1.84	1.3	1.3	1.37	4.85	4.85	6.71	1.05	0.58	223	223	5.41	0.89	2.22	222	1.21	3.34	1.83
	ORF SEQ ID NO:	31269	31453	31454	32889	32890	35077	35240	35458	36800	36601	28524	28525	31089	26235	26236	26738	26827	20828	27149	26897	26898	28328	29455	33493	36844	36645	27658	28682	28841	28842	31734	32169	34198
	SEQ ID NO:	18361	18531	18531	19823	19823	21905	22068	22271	23360	23360	15885	15885	24608	13573	13573	14084	14148	14148	14449	14210	14210	16690	16828	2380	23404	23404	14924	16011	16192	16192	18771	19170	21058
	Probe SEQ ID NO:	5564	5739	5739	7136	7136	9228	9708	9618	10669	10689	10941	10941	12/16	8	8	1316	140	<u>\$</u>	178	2829	2820	3940	4085	77.18	10716	10715	2185	3240	3436	3436	2980	§	8365

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Table 4
Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	Most Similer Top Hit Acession I Top Hit Descriptor Source Value	33.0E-84 AF248953.1 NT Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	3.0E-64 BE206521.1 EST_HUMAN PROTEIN HOMOLOG 2 (HUMAN);	3.0E-84 BE206521.1		3.0E-64 AL163246	3.0E-64 AW977384.1 EST_HUMAN	3.0E-64 AW977384.1 EST_HUMAN	3.0E-64 AL163227.2 NT	2.0E-64 AA609040.1 EST_HUMAN	4 2.0E-64 4757701 NT Homo sepiens elF4E-ilike cap-binding protein (4EHP) mRNA		2.0E-64 Al927030.1 EST_HUMAN	15 2.0E-64/AL163246.2 NT Homo sepiens chromosome 21 segment HS21C046	2.0E-64 AL163246	Homo sepiens glutamic-oxeloacetic transaminase 2, mitochondrial (aspertate aminotransferase 2) (GOT2),	2 OF OF A WESS1451 FOT HIMAN	2.0E-64 AW958145.1 EST HUMAN	2.0E-64 AU124387.1 EST_HUMAN	2.0E-64 AF113708.1	2.0E-64 BF668537.1 EST_HUMAN	2.0E-64 A1078387.1 EST_HUMAN	4 2.0E-64 M77185.1 NT H.sepiers dopamine receptor D5 pseudogene 1, pertial cds	2.0E-64 11431054 NT	2.0E-64 AW606785.1 EST_HUMAN	3 2.0E-64 11434008 NT Homo sepiens lymphocyte cytosolio protein 1 (L-plestin) (LCP1), mRNA	2.0E-64 11434008 NT	2.0E-64 1.1423508 NT	2.0E-84 AU132570.1 EST_HUMAN	2.0E-64 T06397.1 EST_HUMAN	2.0E-84 T06397.1 EST_HUMAN	2 2.0E-64 BF528114.1 EST_HUMAN 60204288ZF1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4180556 5'
בה 	Top Hit Acession No.	AF248953.1	BE208521.1	BE206521.1	AL163246.2	AL163246.2	AW977384.1	AW977384.1	AL163227.2	AA609940.1	4757701		AI927030.1	AL163246.2	AL163246.2	9907087	AW958145 1	AW958145.1	AU124387.1	AF113708.1	BF688537.1	AI078387.1	M77185.1	11431054	AW606785.1	11434008	11434008	1.1423508	AU132570.1	T06397.1	T06397.1	BF528114.1
	Most Similar (Top) Hit BLASTE Value	3.0E-64	3.05-64	3.0E-84	3.0E-64	3.0E-64	3.0E-64	3.0E-84	3.0E-64	2.0E-64	2.0E-64		2.0E-64	2.0E-84	2.0E-64	78 30 C	2.0F.04	20E-84	2.0E-64	2.0E-64	2.0E-64	2.0E-84	2.0E-64	2.0E-64	2.0E-84	2.0E-84	2.0E-64	2.0E-84	2.0E-64	2.0E-64	2.0E-84	20E-64
	Expression Signal	1.93	3.69	3.69	1.54	1.54	9.0	9.0	1.8	1.64	1.54		1.82	2.05	2.05	1.40	0 78	0.78	2.78	1.47	5.21	1.18	4.54	0.7	0.65	0.73	0.73	0.56	0.97	0.59	0.59	3.72
	ORF SEQ ID NO:	34199	34220	34221	35165						26799				27988	20548	L		31655									_	34984			36592
	Exon SEQ ID NO:	21058	21086	21086	21994					13824	14125		_[15248	15001		L	18701			19283	18364	20371	20396	21259	21259	21728	21818	22529	22629	23353
	Probe EQ ID NO:	8365	8393	8393	8327	9327	9414	9414	11691	1066	1377	3	2528	2533	2533	2127	3767	3787	5918	6148	6394	6497	6601	7077	7732	8567	8567	88 88 88	9130	9879	6286	10682

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	wn81b06.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone IMAGE:2452211 3'	wn81b06.x1 NCL_CGAP_Utf Homo sapiens cDNA clone IMAGE:2452211 3'	PM2-SN0018-220300-002-e12 SN0018 Homo sepiens cDNA	Homo sapiens period (Drosophile) hamolog 3 (PER3), mRNA	CHR220101 Chromosome 22 exon Homo sepiens cDNA done C22_132 5	Homo sepiens chromosome 21 unknown mRNA	au00c01x1 Schneider fetal brain 00004 Homo septens cDNA ctone IMAGE:2519136 3' similer to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN);contains element MSR1 repetitive element;	Homo seplens syneptojenin 1 (SYNJ1), mRNA	Homo septens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, trible LIM domain protein 6, and synaptophysin genes.	complete cds; and L-type calcium channel a>	Homo sapiens TRIAD3 mRNA, partial cds	Homo sapiens TRIAD3 mRNA, partiel cds	Homo sepiens hypothedoal protein FLJ11028 (FLJ11026), mRNA	zk53f08.s1 Soares_pregnant_uterus_NbHPU Homo septens cDNA clone IMAGE:486567 3'	Homo saplens chromosome 21 segment HS210045	H.saplens DNA for endogenous retroviral like element	H. sapiens DNA for endogenous retroviral like element	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA	au68h07.x1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE:25190053' similar to SW-RL21 HUMAN P46778 60S RIBOSOMAL PROTEIN L21.	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA	HSAAAEAWO TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test346 (b)	AV721898 HTB Homo septens cONA clane HTBBZC06 5	nj88d10.s1 NCI_CGAP_Pr11 Home sepiens cDNA clone IMAGE:898379 similar to gb:K03002.60S RIBOSOMAL PROTEIN 132 (HUMAN)	nh37b07.s1 NCI. CGAP Pr6 Homo sapiens cDNA clone IMAGE:954517	xx07b09.x1 NCL_CGAP_Co21 Homo sepiens cDNA clone IMAGE:2883545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S, ;contains L1.b2 L1 repetitive element :	zw53b06.s1 Soares total fetus_Nb2HF8_9w Homo septems cDNA clone IMAGE:773747 3'	zw53b06.81 Soares_total_fetus_Nb2HF8_9w Homo sepiens cDNA clone IMAGE:773747 3'	qf18h05.xf NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:1750425 3'
ile Exon Probe	Top Hit Database Source	EST_HUMAN W	EST_HUMAN W	Г		EST_HUMAN C	F	EST_HUMAN 9		17	<u>8</u>	E	F		EST_HUMAN Z	H		NT	EST_HUMAN O	EST HUMAN S	Π	EST_HUMAN H	EST_HUMAN A	EST HIMAN R	Т	EST HUMAN L	EST_HUMAN D	EST_HUMAN 2	EST HUMAN
Sing	Top Hit Acession No.	2.0E-64 AI922911.1	2.0E-64 AI922911.1	2.0E-84 AW864773.1	37387		1.0E-64 AF231919.1	1.0E-84 Al929419.1	07334		1.0E-64 AF198779.1	1.0E-64 AF228527.1		8922829 NT	1.0E-64 AA042975.1	3.2			9.0E-65 BF330676.1	8.0E-65 AI928244.1	_		6.0E-65 AV721898.1	6.0F-65 AA550229.1		6.0E-85 AW083252.1 E	6.0E-65 AA427878.1 E		6.0E-65 Al085314.1 E
	Most Similar (Top) Hit BLAST E Value	2.0E-84	2.0E-64	2.0E-84 /	2.0E-64	2.0E-64 H55162.1	1.0E-64/	1.0E-84	1.0E-64		1.0E-04	1.0E-64 /	1.0E-64/	1.0E-84	1.0E-64	1.0E-64	9.0E-65 X89211.1	9.0E-65 X89211.1	9.0E-85	8.0E-65	7.0E-65	7.0E-65 Z21378.1	6.0E-65	6.0F-65	6.0E-65.A	6.0E-65.A	6.0E-85	6.0E-65	9.0E-65
	Expression Signal	5.97	5.97	1.78	1.55	4.85	2.94	10.45	0.79		5.74	1.27	1.27	0.79	1.07	1.81	1.53	1.53	10.43	10.87	201	1.27	3.59	4.73	0.62	23	3.46	3.48	0.81
	ORF SEQ ID NO:	36909	36910	37149	31114		25698	27214	28426		28912	28974	28975	29270	35816		27738	27739		37405	35921	37731	26454		32242	34481	34742	34743	34814
	Exen SEQ ID NO:	23656	23656	23863	24562	24834	13060		15776		16257	18327	16327	16631	22812	24545	- 1		24123	24094	22703	24397	13794	14652	19242	21337	21600	21600	21663
	Probe SEQ ID NO:	10981	10981	11198	12039	12468	251	1772	3010		3501	3572	3572	3881	9964	12012	2274	2274	11523	11403	10055	11807	1034	1915	6475	8645	8000	6068	8973

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Supplementary Control			NO: No: Noise																														
Secondary Control Co		Top Hit Descriptor	ARER124F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5	01568124F1 NIH MGC 21 Hamp septents CONA done THYRO1000366 5	(U141295 THYRUT from semiens cDNA clone THYRO1000350 5	(U141295 THYROT HOUSE CONA CONA CONA CONE IMAGE: 4283010	302126239F1 NIH_MGC_56 Harris conversion NT2RP2004714 5	AU128040 NT2KPZ FMIN CONA clone NT2RP2004/14 9	AU129040 NT2RP2 Home sappens receptor, type 1 (ITPR1), mixwh	Homo sepients income in the product (KIAA0656), miking CE-1733450 3 similar to gb: M29581 Line	Homo sapiers rund heafs NHT Homo sapiens cDNA clone living.	qd56g02X1 Somes (HUMAN); contains MER19.11 MEX 19 19 19 19 19 19 19 19 19 19 19 19 19	AU163793 NT2RP3 Homo septens cDNA clone NI 200 Cone IMAGE:382734 5	275e04.r1 Soares, princes, princed partial cds	Homo septents mixed a variation 1 (PF4var1) gene, complete cus	Human platera laces and brodein L7a (RPL7A) mRNA	Home septens index 56 Home septens con A clone in Act 37 similar to gb:L15533 man	602126239F1 MILL TO CAP GC6 Home septens cDNA done IMAGE. 223	ta/6a05x1 NG COSCIATED PROTEIN 1 PRECONSOL	PANCASEA 1110 The Inductible protein CG12-1 (CG12-1), Illinois TNF-Inductible protein	Homo sapiens cadherin EGF LAG seven-pass G-ryps racon. Homo sapiens cadherin EGF LAG seven-pass (SULTX3), mRNA	Homo sapiens sulfotransferase-relation pro-	Novel human gene marphing 22	Novel human gane mapping to contracted pad1 homolog (POH1) mixture.	Homo septiens 202 in comme associated ped1 homotog (FUR1) in company	Homo sapiens 205 processor:	Human transposorting down or Homo sapiens cDNA clone IMAGE.		7		\neg	- 1	
Exon ORF SEQ Expression (Top) Hit Acer Top Hit Acer NO: Signal Value No. NO: 34006 0.56 1.0E-65 BE732118.1 20872 34007 0.56 1.0E-65 BE732118.1 20872 34047 2.03 1.0E-65 BE732118.1 20872 34047 2.03 1.0E-65 BE732118.1 20872 34047 2.03 1.0E-65 BE732118.1 20872 34048 2.03 1.0E-65 BE732118.1 20872 34048 2.03 1.0E-65 BE732118.1 20872 34048 2.03 1.0E-65 BU14123040. 8 21609 34752 2.62 1.0E-65 BU14123040. 9 21607 34753 2.62 1.0E-65 BU14102040. 17 21607 34753 2.62 1.0E-65 BU14102040. 17 234848 1.01 1.0E-65 BU162040. 1.0E-65 BU162040. 17 23484 1.01 1.0E-65 BU162040. 1.0E-65 BU162040. 17 23542	Xon Floues		atabase	HUMAN	Π	Т	T	١	T				ST HUMAN	ST HUMAN	5	5	LZ.	EST HUMAN		EST HUMAN	E	Z EZ		12/2	IN C	TNIC	LN	EST HUMA	EST HUMA	_	EST HUM	EST HUM	
Exon ORF SEQ Expression (Top) Hit Acer Top Hit Acer NO: Signal Value No. NO: 34006 0.56 1.0E-65 BE732118.1 20872 34007 0.56 1.0E-65 BE732118.1 20872 34047 2.03 1.0E-65 BE732118.1 20872 34047 2.03 1.0E-65 BE732118.1 20872 34047 2.03 1.0E-65 BE732118.1 20872 34048 2.03 1.0E-65 BE732118.1 20872 34048 2.03 1.0E-65 BE732118.1 2088 2.1659 3.4753 2.62 1.0E-65 BE732118.1 2089 2.1659 3.4753 2.62 1.0E-65 BE732118.1 2080 2.1659 3.4753 2.62 1.0E-65 BL129040.1 21 2.1659 3.4753 2.62 1.0E-65 BL129040.1 21 2.1659 3.4753 2.62 1.0E-65 BL129040.1 21 2.244 1.0E-65 BL2040.1 3.6244 3.6244 3.6244 3.6244	ingle E			ES	3/2			1		1997	NICCO	-				T	508880		T		18041	1418322	1418240	= :	١è	n lo		-	19.1		53.1	143 1	3
Exam ORF SEQ Expression Moet Similar SEQ ID ID NO: Signal Value NO: 20872 34006 0.56 1.0E-40e 1. 20872 34007 0.56 1.0E-40e 1.0E-40e 2. 20872 34007 0.56 1.0E-40e 1.0E-40e 2. 20872 34047 2.03 1.0E-50e 1.0E-50e 2. 20872 34047 2.03 1.0E-50e 1.0E-50e 2. 20872 34047 2.03 1.0E-50e 1.0E-50e 2. 20876 34752 2.62 1.0E-50e 1.0E-50e 2. 20876 34752 2.62 1.0E-50e 1.0E-50e 2. 20846 3646 1.0F-7 1.0F-7 1.0F-7 2. 20847 3640 1.0F-7 1.0F-7 1.0F-7 2. 20846 37122 2.24 1.0F-7 2. 20846 37018 8.53 1.0F-7 2. 20847 38640 1.8F-7 1.8F-7 2. 20840 1.2897 <td>(C)</td> <td></td> <td>Ht Acess No.</td> <td>12118.1</td> <td>32118.1</td> <td>41295.1</td> <td>41295.1</td> <td>98707.1</td> <td>29040.1</td> <td>444</td> <td>- 18</td> <td>2</td> <td>1917161</td> <td>1153793.</td> <td>.acce00</td> <td>303/832</td> <td>7,0107</td> <td>707007</td> <td></td> <td>710747</td> <td>100</td> <td></td> <td></td> <td>AL 18031</td> <td>AL16031</td> <td></td> <td></td> <td>W87289</td> <td>DECOM</td> <td></td> <td>S A19246</td> <td>41000</td> <td>BAINE</td>	(C)		Ht Acess No.	12118.1	32118.1	41295.1	41295.1	98707.1	29040.1	444	- 18	2	1917161	1153793.	.acce00	303/832	7,0107	707007		710747	100			AL 18031	AL16031			W87289	DECOM		S A19246	41000	BAINE
Exam ORF SEQ Expression (Top) Hill SEQ ID ID NO: Signal Value NO: 20872 34007 0.56 1.0E 1.20872 34047 2.03 1.0E 1.0E 2.0872 34047 2.03 1.0E 1.0E 2.20872 34048 2.03 1.0E 1.0E 2.20872 34048 2.03 1.0E 1.0E 2.2092 34753 2.6E2 1.0E 1.0E 2.2093 34753 2.6E2 1.0E 1.0E 2.2096 3.7122 2.2A 1.0E 1.0E 2.709 3.7122 2.2A 1.0F 1.0F 2.709 3.7122 2.2A 1.0F 1.0F 2.709 1.2897 2.2A		-		65 BE73	65 BE7	85 AU1	-85 AU1	-85 BF6	.65 AU	92 AC	8	E-65	E-05 AI	E-65 AL	E-85 №	E-05 A	R-85 M	8			10 10 10 10 10 10 10 10 10 10 10 10 10 1	0E-05	1.0E-85	9.0E-88	9.0E-86	9.0E-86	9.0E-88	9.0E-08	8.01-00	20.5	6.0E-0		8.0E-8
Exam ORF SEQ Expression SEQ ID ID NO: Signed NO: 1D NO: Signed NO: 20872 34006 0.56 120872 34007 0.56 0.56 120872 34047 2.03 120872 34047 2.03 120872 34048 2.03 120872 34048 1.23 120872 34752 2.55 120872 34648 1.24 12092 34752 2.55 12093 34752 2.55 12094 34752 2.55 12095 34752 2.55 12096 3772 1.1 177 23446 1.28 177 23897 3610 173 24804 31086 173 14081 2653 1332 14081 2653 1332 14081 26757 1487 14214 30009			ost coming (Top) Hit BLAST E	1.0E	1.06	- B	1.08	lo.	F. 0	1.0	0.1	5.																.51	E	8	1.15	-	1.15
Evan ORF SEQ SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		+		98.0	92.0	200	203	7	782	262	238	1.96	5.05	1.1	90	1.01	1.58	8.5	22		27	2 2			-		-	9					
Exam ORF SEQ ID ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:			Expres Sign						010	100	-	100	-	\$ 6	2 2	1 44		100	1850	-	122		8	+	1000	7222	2/2/2	1	8000	1	1 8	282	29699
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						<u> </u>		1	Ш	8918	8918	8328	2008	7758	9785	10200	10470	10546	10676	11075	44472	18913	1210	1251	6	0	133	뚌	*	\$	=	₹	_

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Single Exon Probes Expressed in Brain	Тор Hit Descriptor	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' slmiler to WP:F15G9.4A CE18595;	PM2-HT0604-030300-001-b06 HT0604 Homo sapiens cDNA	H.seplens mRNA for ribosomal protein L31	RC4-BT0311-141199-011-h06 BT0311 Homo septens cDNA	601681592F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3931791 5	601681592F1 NIH_MGC_9 Homo eapliens cDNA clone IMAGE:3951791 5	Home septens thyroid hormone receptor binding protein (AIB3), mKNA	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mKNA	RC1-NN0063-100500-022-e02 NN0063 Homo sepiens cDNA	H. sapiens DNA for endogenous retroviral like element	Homo sapiens germ-line DNA upstream of Jkappa locus	Human endogenous retrovirus, complete genome	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate	cyclohydrdase (MTHFD2), mRNA	QV1-DT0069-110200-067-g10 DT0069 Homo saplens cDNA	EST377546 MAGE resequences, MAGI Homo sapiens cDNA	Homo sepiens cAMP-regulated guenine nucleatide exchange factor I (cAMP-GEFI) mRNA, complete ads	Homo sapiens methylane tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate	cyclohydrolese (MTHFD2), mRNA	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA	Humen endogenous retrovirus pHE.1 (ERV9)	UI-H-BW1-emr-e-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:30/0/4/ 3	Homo sapiens mRNA for KIAA0998 protein, partial cds	Homo sapiens solute cerrier family 25 (mitochondrial cerrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	yz27g12.r1 Sogres_multiple_acterosis_ZNIbHMSP Homo sapiens dDNA clone IMAGE:284326 5' similar to	SW. TAZE I I GOAL FOUND I I ST. OF THE CONTROL OF T	yZ/g12.r1 Scarces_multiple_sciencess_ZNDHMSP* Homo septents curvis content invalce_zosts25.5 similar to SW:H2B1_TIGCA_P36068 HISTONE H2B.1/H2B.2. [2] PIR:B56612;
Jie Exon Prot	Top Hit Database Source	EST HUMAN	EST_HUMAN	NT ,	EST HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	EST HUMAN	NT	IN	LN.		Ā	EST_HUMAN	EST_HUMAN	5		NT	TN	TN	EST_HUMAN	TN	FX	Į.		ESI HUMAN	EST_HUMAN
Sinc	Top Hit Acession No.	6.0E-66 Al924653.1	6.0E-66 BE178563.1	K69181.1	5.0E-88 BE064410.1	5.0E-66 BE898644.1	5.0E-66 BE898644.1	11420557 NT	6879816 NT	4.0E-66 AW897798.1	X89211.1	4.0E-68 AJ223364.1	9635487 NT		11428643 NT	4.0E-66 AW939119.1	4.0E-66 AW965473.1	4 0F-86 U78168.1		11428643 NT	11421638 NT	4.0E-86 X57147.1	4.0E-86 BF507493.1	4.0E-86 AB023215.1	4502098 NT	TN RECOOR		3.0E-66 N55323.1	3.0E-66 N55323.1
	Most Similar (Top) Hit BLAST E Vakue	8.08-66	6.0E-68	6.0E-86 X69181.1	5.0E-88	5.0E-86	5.0E-88	5.0E-68	4.0E-68	4.0E-98	4.0E-66 X89211.1	4.0E-68	4.0E-66		4.0E-88	4.0E-88	4.0E-66	4.05-86		4.0E-06	4.0E-66	4.0E-86	4.0E-86	4.0E-88	3.0E-88	3 OF 98		3.0E-86	
	Expression Signal	4.55	0.48	3.14	1.45	0.74	0.74	16.11	96.0	1.14	1.83	3.02	10.89		3.73	1.15	4.83	7 83		0.72	6.63	0.73	1.97	1.28	10.96	6		1.18	1.18
	ORF SEQ ID NO:	00200		37052	26769	30382	30383	35028	26206	27170	27744				31153			32770	0,1130	31153								27429	27430
	Exon SEQ ID NO:	12021	21028	23778	14094	17765	17765	21864	13545	14471	15004	15195	17465		18262	<u> </u> _	17928	l	1	18262	1_	L	_	L	1	1		14711	14741
	Probe SEQ ID NO:	4330	8333	11108	1346	5048	8048	25	133	1720	2278	2477	4733		5463	2992	6757	7024	3	7529	7976	8034	10556	11351	1407		è	1975	1975

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Table 4
Exon Probes Expressed

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		_				_	1	_	-	-		-					_			_			_							
Top Hit Descriptor	bs/2205.y1 NIH_MGC_20 Homo sapiens oDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892 KIAA0708 PROTEIN.:	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 094892 KIAA07pa PROTEIN	Home series brotheficel protein of 14820020 of 14920020 of	Hamp septens hypothesical protein 4 (492022.2 (D.402023.2), mKNA	Homo secients KRAB zinc finate protein 7500 mbNA	Homo sapients develormentally new ideal CTD birding	2191001.81 Sogress theaths NHT Horns cardians DNA Acres NACE: 245000.01	Homo sablens chronosome 21 segment HS24C300	Novel human gene mapping to chomosome 13	801875351F1 NIH MGC 55 Homo senione china characteristics en	Homo sapiens mRNA for NADPH-cytochrome P.450 radiuctases complete add	Home sablens mRNA for NADDH-cyto-browne D. 450 reduces, conjugate cus	DKFZp781A229 r1 761 (sunovum hemy) Home exclana chair All All DKFZ-701 and All All DKFZ-701 and All All DKFZ-701 and All All DKFZ-701 and All All DKFZ-701 and All All DKFZ-701 and All All DKFZ-701 and All DKFZ-	EST38850 Embryo, 9 week Horno seniens Child 5' and similar to similar to similar to	EST38850 Embro: 9 week Home septemble Control State Similar to Similar to Control Similar	RC4-BT0568-170100-011-07 BT0668 Homo serviens CDNA	RC4-BT0569-170100-011-07 BT0596 Home semilana CDNA	AV731333 HTF Home senience CONA Cone HTEADOGS R	UIH-BIZ-shn-#-10-0-UI 81 NCI CGAP Suba Home service - DNA -1 - 114 ST GENERAL -	601455262F1 NIH MGC 98 Hym septem - DNA Alone 144 CC And BINACE 27 27 283 3	Homo septems KIAA0985 romain (KIAAnose) - DNA	801175782F1 NIH MGC 17 Home septems of NA About MA OF 2521759 FT	PM2-TN0103-040900-001-002 TN0103 Home service management of the service of the se	Homo sapiens thyroid authantions 70kD (Ku antivers (7.2004)	Homo egolens demma-dithematemas 4 (CCT4)		months equally adjusted (A4) precured protein (proteins natural, Alzheimer disease) (APP), mRNA	WASSALD ON NOT COAD COAD COAD COAD COAD COAD COAD COAD	MOUNT INCLUDENT GOOD HOME SEIDENT GOOD IN A GENERAL WAS SEED OF THE WAY A SEED OF THE WAY OF THE WA	2982h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07500 SAV PROTEIN;
Top Hit Database Source	EST HUMAN	EST HUMAN	LN	Į.	Į.	Į	EST HUMAN	Į.	TN	EST HUMAN	NT	F	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	¥	EST HUMAN	EST HUMAN	1	Ę	5	FOT LIEMAN	FOT LIMAN	EST HUMAN	EST_HUMAN
Top Hit Acession No.	2.0E-67 BE303037.1	2.0E-87 BE303037,1	11422946 NT	11422946 NT	2.0E-67 AF309581.1	4758795 NT	2.0E-67 AA625755.1	2.0E-67 AL163300.2	2.0E-87 AL049784.1	2.0E-67 BF240758.1	20E-67 AB051763.1	2.0E-67 AB051763.1	20E-67 AL120542.1	2.0E-67 AA334609.1	2.0E-67 AA334609.1	2.0E-67 AW602835.1	2.0E-67 AW602635.1	2.0E-67 AV731333.1		2.0E-67 BF034485.1	11436448 NT		2.0E-67 BF377169.1	8189	11417877 NT	4502486 NT	1.0F-87 AA202794 1			
Most Similar (Top) Hit BLAST E Value	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-87	2.0E-87	2.0E-67	2.0E-67	2.0E-67	20E-67	2.0E-67	20E-67	2.0E-67	2.0E-87	2.0E-67	20E-87	2.0E-87	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	2.0E-67	1.0E-67	1 0F-87 /	1.0E-67	8.0E-68	8.0E-68
Expression Signal	1.36	1.36	1.3	1.3	1.09	1.28	3.8	3.03	0.0	5.54	2.46	2.46	0.76	0.82	0.82	1.21	1.21	0.83	0.97	3.72	.4.67	211	1.86	1.36	2.05	9.34	1.01	8.58	. 2.13	86.4
ORF SEQ ID NO:	27325	27326	27702	27703		27887	28870	28366	31726	31774	31966	31967	32315	34290	34291	34724	34725	35248	35447	36889		37145	36433	30819	31018	25695	26114	37770	27636	29238
Exan SEQ ID NO:	14814	14614	14963		15105	15163	16216	16732	18782	18814	18978	18978	19310	21148	21148	21586	21586	22076	22281	23646	25433	23868	23201	25231	24874	13055	13467	24420	14903	16601
Probe SEQ ID NO:	1877	1877	2235	2235	2384	2432	3480	3984	508	88	6203	88	8545	8438	8456	8895	8895	8	8098	10970	10988	11183	- - - - - - - - - - - - - - - - - - -	12235	12527	240	692	11845	2174	3861

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Table 4
Single Exon Probes Exurasse

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[T	Т	Τ	Τ	Τ	Т	Τ	Τ	Т	T	Τ	Τ	Τ	Τ	Τ	Т	Т	Т	Τ	Τ	Τ	T	7	Г	Т	Т	Т	Τ	Т	Т	Т	Τ	Т	T
	Top Hit Descriptor	HSPD18178 HM3 Homo sepiens cDNA clone s3000023D09	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds	Homo sapiens gene for activin receptor type IIB, complete cds	yg38g04.s1 Sceres infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 3'	801458514F1 NIH_MGC_66 Homo sepiens aDNA dane IMAGE:3882034 5	IL3-CT0534-180900-273-A01 CT0534 Homo saplens cDNA	FORMIN 4 (LIMB DEFORMITY PROTEIN)	yz78d07,r1 Soares_multiple_solerosis_2NbHMSP Homo septens cDNA clone IMAGE:289165 5	QV0-BT0074-130999-014-g04 BT0074 Homo sepiens cDNA	Homo saplens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	QV4-ST0234-181199-037-f05 ST0234 Homo septens dDNA	Homo saplens mRNA for KIAA0577 protein, complete ods	Homo saplens mRNA for KIAA0577 protein, complete cds	601177002F1 NIH_MGC_17 Homo sepiens aDNA dane IMAGE:3532344 5'	al47g12.s1 Soeres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:14805183'	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA	Homo saplens sentrin/SUMO-specific protesse (SENP1), mRNA	zw74d02.r1 Soares_tests_NHT Homo sepiens cDNA clone IMAGE:781923 5	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA	Homo saplens phosphodesterase 78 (PDE7B), mRNA	Homo sapiens MIF2 suppressor (HSMT3) mRNA, complete cds	Homo sapiens myosin IC (MYO1C), mRNA	Homo sapiens interfeukin-7 receptor precursor (IL7R) gene, exons 7 and 8 and complete cds	Human protein kinase C substrate 80KH (PRKC3H) gene, exon 4-5	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5	Homo eaplens CGI-76 protein (LOC51632), mRNA	Homo seplens CGI-78 protein (LOC51632), mRNA	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	Homo sapiens 26S protessome-associated pad1 homolog (POH1) mRNA	Homo saplens 26S probasome associated pad1 homolog (POH1) mRNA	Homo saplens EphA4 (EPHA4) mRNA
	Top Hit Database Source	EST_HUMAN	Į,	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	TN	EST_HUMAN	NT	ZI.	EST HUMAN	EST_HUMAN	l.	Þ	EST_HUMAN	דא	LZ	NT	T		L	TN		Ę	Þ						
	Top Hit Acession No.	F28784.1	00522.1	AB008681.1	345088.1	2.0E-68 BF035316.1	JF336745.1	305859	178483.1	3F330594.1	4505222	1	1.0E-68 AB011149.1	1.0E-68 AB011149.1	1.0E-68 BE296032.1	1.0E-68 AA897343.1	7662340 NT	11436716 NT	1.0E-68 AA429538.1	11418860 NT	11418869 NT		11433277 NT	1			11418431 NT	11418431 NT	4505222 NT	11430460 NT	5031976 NT	5031976 NT	5031980	5031980 NT	4758279
	Most Similar (Top) Hit BLAST E Value	3.0E-68	2.0E-68 D00522.1	2.0E-68 AB008681	2.0E-68 R45088.1	2.0E-68	2.0E-68 BF336745	2.0E-68 Q05859	2.0E-68 N78483.1	2.0E-68 BF330594.	1.0E-68	1.0E-88	1.0E-68	1.0E-68	1.0E-68	1.0E-68	1.0E-88	1.0E-68	1.0E-68 A	1.0E-88	1.0E-68	1.0E-68 L76416.1	1.0E-68	1.0E-68 AF043129.	1.0E-68 U50319.1	1.0E-68 U50319.1	1.0E-68	1.0E-68	1.0E-68	1.0E-88	9.0E-69	9.0E-09	9.0E-89	9.0E-89	9.0E-09
	Expression Signal	1.23	15.31	1.38	9.54	5.38	0.73	0.63	0.75	1.66	1	13	1.03	1.03	0.95	0.92	1.37	1	9.0	1.85	1.85	3.5	1.71	1.62	128	1.26	1.48	1.48	2.66	2.11	1.16	1.18	1.41	1.41	1.15
	ORF SEQ ID NO:	36261		30004		32462	33030	34685	36376	37160	25541	25737	27715	27718	29373	30302	30674	33350	36235	36685	36686	36741	37098	37178	37223	37224	37584	37585	25541	30712	25460	25401	26426	26427	27740
	Exan SEQ ID NO:		17883	17368	19520	19445		21539	23151	23873	12903		14977	14977	16739	17694	18045	20245	23019			23502	23815	23880	23831	23831	24281	24261	12903	25322	12847	12847	13766	13766	15001
	Probe SEQ ID NO:	10399	2865	4633	6778	කුණ	7270	8848	10505	11210	77	288	2249	2240	3991	4969	6239	7578	10373	10756	10756	10819	11148	11228	11270	11270	11688	11666	12511	12719	19	2	1006	1006	2275

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Table 4
Single Exon Probes Expressed

Single Exon Probes Expressed in Brain	Most Similar Top Hit Accession Top Hit Accession Top Hit Accession Top Hit Descriptor Signal BLAST E No. Source Source	1.15 9.0E-89 4758270 NT HAMP SANIONE ELLA (PER 14.1) ENTA	9.0E-89 4757867 NT	9.0E-69 AU117241.1 FST HI MAN	8.0E-69 AJ237744.1	966912 NT	9.09 6.0E-69 A1192764.1 EST HUMAN doi:11566 60S RIROSONAL PROTEIN 149 Auto sapions cDNA clone IMAGE:1743601 3' similar to	EST HIMAN	5.0E-69 AA826039.1 FST HIMAN		4.0E-80 BE561063.1 EST HUMAN	EST HUMAN	57732 NT	4.0E-69 4557732 NT	0.52 4.0E-99 AU119634.1 EST HUMAN AU119634 HEMBA HOME CONTACT HUMAN AU119634 HOME CONTACT HUMAN AU119634 HEMBA HOME CONTACT HUMAN AU119634 HEMBA HOME CONTACT HUMAN AU119634 HEMBA HOME CONTACT HUMAN AU119634 HEMBA HOME CONTACT HUMAN AU119634 HEMBA HOME CONTACT HUMAN AU119634 HEMBA HOME CONTACT HUMAN AU119634 HEMBA HOME CONTACT HUMAN AU119634	EST HUMAN	3.0E-69 AF221712.1 NT	H	3.0E-69 11418185	AJ277557.1 NT		7. FX	Į.		1 EST HUMAN	3.0E-69 AA376399.1 EST_HUMAN	ΓN
	E E								ŀ																		
	SEQ ID ORF SEQ NO:	15001 27741	16852 29479	23488	16140	19033 32008	20458 33581	20458 33582		13291	25073 31384	18545 31467	19297 32301				13376 26006	14284	304 37797	OZ.	30563	33032			84 34106		80 35152
	Probe Ex SEQ ID SEC NO: NG		4109 16			6259 19	7762 20	7762 20-			5674 25(_		598 133		5163 17894		6759 17928			_		\perp	9313 21980

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Table 4
Single Exon Probes Expressed in Brain

Top Hit Acession Detablese Top Hit Descriptor	3.0E-99 X06233.1 NT (MIF)-related protein	5730036 NT Homo septems SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA	11432120 NT	AA376399.1 EST_HUMAN	11419157 NT	TN	TN	2.0E-69 AF160252.1 NT Homo sapiens KIAA0553 protein gene, complete ods, and alphalib protein gene, partial cds	2.0E-99 AF160252.1 N.T Homo saplens KIAA0553 protein gene, complete ods, and alphallip protein cene, partial cds	20E-69 BE257857.1 EST_HUMAN 801109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'	EST HUMAN	EST_HUMAN	LN L	1.0E-89 BE409084.1 EST_HUMAN 801301284F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3635781 51	Г	1.0E-99 BE902501.1 EST_HUMAN 601675788F1 NIH MGC_21 Homo septens cDNA clone IMAGE:3958532 6	AW393969.1 EST_HUMAN	7062263 NT	7882283 NT	TN	TN	EST_HUMAN	1.0E-69 BE631007.1 [EST_HUMAN 601278532F1 NIH_MGC_39 Homo sapiens cDNA done IMAGE:3610814 6'	1.0E-69 BE245070.1 FST HUMAN ICDNA clone TCRAP2678		EST HUMAN	1.0E-69 AB014607.1 NT Homo sepiens mRNA for KIAA0707 protein, partial ods	1.0E-89 BF528429.1 EST_HUMAN 602043782F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181325 5'	4504918 NT	1.0E-69 BF125887.1 EST_HUMAN 601762902F1 NIH_MGC_20 Hamo septens aDNA clane IMAGE:4025785 5	1.0E-69 A1809894.1 EST_HUMAN repetitive element contains element MIR repetitive element;
Top Hit Acession De		5730036 NT	11432120 NT	EST	19157 NT					EST	EST	EST	호				1	7062263 NT	7862263 NT	3032973.1 NT									4504918 NT		
Most Similar (Top) Hit BLAST E Value	3.0E-89	3.0E-89	3.0E-69	3.0E-89 A	3.0E-69	2.0E-69 A	20E-69 A	2.0E-89 A	2.0E-69 A	20E-69B	2.0E-69 A	2.0E-69 A	1.0E-80 A	1.0E-89 B	1.0E-69 B	1.0E-89 B	1.0E-89 A	1.0E-69	1.0E-89	1.0E-89 A	1.0E-69 A	1.0E-69 BI	1.0E-69 Bi	1.0E-69 BI		1.0E-69 Bi	1.0E-69 AF	1.0E-69 BI	1.0E-69	1.0E-89 BF	1.0E-69 AI
Expression Signal	2.03	0.75	1.44	7.81	5.17	1.64	1.84	10.33	10.33	2.08	3.16	1.08	1.08	0.74	0.87	0.87	4.37	1,28	1.28	3.01	3.01	1.14	1.14	4.91		4.91	1.38	0.57	10.52	1.74	4.45
ORF SEQ ID NO:	35286	35582	36468						25828				27139		31700	31701	32274			32803			32555	35837		35938	38034	36177		37261	
Exan SEQ ID NO:	22111		23235			_[13180	13180	14615	15618	21144	14441	17687	18741	18741	19273	19636	19636	19571	19571	19526	19528	22721	1	22721	22816	22961	23465	24512	24769
Probe SEQ ID NO:	9433	9729	10538	10745	12024	138	138	395	395	1878	2848	8452	1698	4962	6963	2929	8208	6721	8721	6737	6737	6782	6782	10073	0.007	100/3	10168	10314	10782	11964	12366

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Table 4
Single Exon Probes Expressed in Brain

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Cirgo Exol rioda Explassed in Brain	Top Hit Descriptor	nc13d12.r1 NCI CGAP Pri Homo serviens aDNA close IMAGE-11008022	Homo sapiens DGS-I mRNA, 3' end	tm89f01.x1 NCL CGAP Bm25 Homo contens cDNA class MAADE: sacesses at	THROUGHT INC. CGAP Brost Home severe contact and a contact	#15h04.1 NCI CGAP GCB1 Home servers contact that CE-7100303 3	Homo sapiens tumor suppressor deleted in oral concernational 4 /DOC 401	Homo saplens adenyate cyclese 3 (ADCY3) mRNA	Harro sapiens MIST mRNA partiel exte	Homo sablens MIST mRNA partial cde	Homo sabiens dene encoding splicing factor SE1 extra 2.9	Homo saplens mRNA for KIAA1294 profein partial cds.	Homo sapiens mRNA for KIAA1204 protein pertial cde	Human displacement protein (CCAAT) mRNA	Human displacement protein (CCAAT) mRNA	Human PBX3 mRNA	Human PBX3 mRNA	Homo sanjens niverbylinid accemblase 4 cess	Homo sablens kervanherin hele 25 transmentin (TDNs)DxxA	Homo sapiens karusuharin heta 2h transmetta (TDN2), IIIntien	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.84D) (GLCLC) mRNA	Homo sabiens NDST4 mBNA for N channel for N	Iomo seniens NIDSTA mRNA for N Jean-of-Jean-N. 1864	Homo saplens specific persularia 4 (autremed deniment	Homo sapiens spastic paraplegia 4 (autosomal dominant spastin) (SPCA) mBNA	Homo sapiens HIR (histone cell cycle requigition defective. S. cerawkiae) homology a (HIDA) and NA	Homo sabiens HIR (histone cell cycle requireffor defeather S. persession) have a pure at the contract of the c	irmn certains emitted hate (A.).	Himan Kii (h2n/han) silvarit m DNA	Homo saciens (MP-N-exchine reminity end month and constant	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
מום דייסיין פוס	Top Hit Database Source	EST HUMAN	N.	EST HUMAN	EST HUMAN	EST HUMAN	-1	N	Į.	N													Į.								
)	Top Hit Acession No.	8.0E-70 AA230303.1	8.0E-70 L77508.1	7.0E-70 AI497807.1	7.0E-70 AH97807.1		31668	4757723 NT	7.0E-70 AB032369.1		7.0E-70 AJ000052.1		5.1	7.0E-70 M74099.1				7.0E-70 AF153715.1	25964	11525984 NT	4567624 NT	7.0E-70 AB036429.1		29885	11429685 NT	11526319 NT	11526319 NT	4502166 NT	30938.1	8923899 N	7682307 NT
	Most Similar (Top) Hit BLAST E Value	8.0E-70	8.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70 M74099.1	7.0E-70 X59841.1	7.0E-70 X59841.1	7.0E-70	7.0E-70	7.0E-70	7.0E-70	7.0E-70/	7.0E-70/	7.0E-70	7.0E-70	7.0E-70	7.0E-70	6.0E-70	6.0E-70 M30938.1	6.0E-70	5.0E-70
	Expression Signal	2.08	1.93	1.01	1.01	1.96	2.92	3.67	4.88	4.88	2.16	22	2.2	3.58	3.58	3.8	3.8	3.43	2.69	2.69	0.57	0.62	0.62	1.54	1.54	1.65	1.65	1.77	121	1.22	2.18
	ORF SEQ ID NO:			27260		27371			30888	30880	32509	34159	34160	34457	34458	34902	34903	33522	33551	33552	35394	38058	36059	36941	36942	37515	37516	20291	27593	27970	28003
	Exen SEQ ID NO:								_1			21023	21023	21314	21314	21744	21744	20406	20431	20431	22200	22844	22844	23682	23682	24196	24196	13021	14863	15230	15598
	Probe SEQ ID NO:	2334	85 85 85	1806	1806	1923	2056	4199	5395	5395	828	8830	88	8622	8822	8025	8055	8335	8861	9361	9656	10196	10196	11010	199	11597	11597	851	2133	2513	2555

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		Т	T	Т	T	T	Т	\top	Т	Т	1	Т	T	Т	Т	T^-	7	Г	Т	T	T	Т	Т	⋖	Т	Т	П	7	T	7	Т	_	-
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens KIAA0792 gene product (KIAA0792) mRNA	MR3-HT0487-150200-115-806 HT0487 Homo sapiens CDNA	EST03928 Fetal brain, Strategene (cet#838206) Homo seniens cDNA clone HERDNISE	CM4-UM0003-010300-105-008 UM0003 Homo seniens cDNA	CM4-UM0003-010300-105-008 UM0003 Homo serviens cDNA	RC0-BT0522-071290-011-812 BT0522 Homo semisor CDNA	RCo-BT0522-071299-011-e12 BT0522 Homo septems cDNA	Homo sapiens plakophilin 4 (PKP4), mRNA	Homo saciens diskophilin 4 (PKP4), mRNA	WH80403.X NCI CGAP CLI 1 Home serving CDNA close IMACE 2388005.31	802141561F1 NIH MGC 46 Hamp september CDNA chame IMAGE-4202808 5	802141561F1 NIH MGC 46 Homo sepiens CDNA clone IMAGE-4302808 5	hz81h02.x1 NCI CGAP Lu24 Home septems abna close IMAGE 321440 31	Homo eaplens phosphetidylinosital 4-kinase 230 (p4K230) mRNA complete ods	yy07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 6' similar to	SW.LJSHI_KA I PZBZ66 3-HYDKOXYISOBUTYRATE DEHYDROGENASE PRECURSOR;	1990/810.rd Scares metanocyte 2NbHM Homo saptens cDNA clone IMAGE:270522 5' similar to SW:D3HI RAT P29266 3-HYDROXYISORUTYRATE DEHYDROGENASE DDEC IDSOD .	451h01x1 NCI CGAP Pant Homo eaplens cDNA clone IMAGE-2004043.3	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA	Homo saplens KIAA0183 gene product (KIAA0193), mRNA	Homo sapiens KIAA0163 gene product (KIAA0193), mRNA	Homo saplens chromosome 21 segment HS21C002	2/48g04.r1 Sceres retina N2b4HR Homo septens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A	W68MA of Sorge folds I have endern 4NIO 5 Lives - 100 Comment of the comment of t	Himen normiscle muse's heavy she's B (ANDAM) - DNA	Harrier From the Art Republic (MTC) MICHAL DE COS	Heaplans date for echusanomin (CO)	Homo series NAI P4 mPNA complete cuts	Himen many for NET and inform (Homo sabiens cytrolesmic dynain intermediate wheir 4 minut America.	Homo sepiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds	
Jie Exon Pro	Top Hit Database Source	L	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	١.	NT.	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT	1454	ES! HOMAN	EST HUMAN	EST HUMAN	5	5	T.	LN L	EST HIMAN	EST HIMAN		LZ.	- L2	Į.		Z	L'A	
	Top Hit Accession No.	7662307 NT	5.0E-70 BE188034.1	4.0E-70 T06037.1	4.0E-70 AW 783226.1	5	3.0E-70 BE071796.1		11430988 NT	11430988 NT	3.0E-70 AI831975.1		L	3.0E-70 BE502973.1	1				2.0E-70 AI246899.1	8923689 NT	7661983 NT	7661983 NT	2.0E-70 AL163202.2	2.0E-70 AA054010.1					5.1		5	П	
	Most Similar (Top) Hit BLAST E Value	5.0E-70	5.0E-70	4.0E-70	4.0E-70	4.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	2.0E-70	2 OF 70 MA2464 4	Z.VE-70	2.0E-70 N42161.1	2.0E-70	2.0E-70	20E-70	20E-70	2.0E-70 /	2.0E-70	2.0E-70 H37988 1	2.0E-701M69181.1	20E-70 X72862 1	2.0E-70 X72882 1	2.0E-70	2.0E-70 D12825 1	2.0E-70	20E-70	
	Expression Signal	2.18	2.75	1.03	1.78	1.78	1.23	1.23	0.65	0.65	1.8	1.85	1.65	0.58	1.2	44.00	2	14.09	1.7	1.56	3.05	3.05	1.86	5.32	0.78	5.06	8.7	8.7	127	1.75	12.14	12.14	
	ORF SEQ ID NO:	28004		32431			27016			31235	31581	32031			25484	26080		26080	26113	28421	26578	28579	27177		29011	29404	30839	30040	31867	32307	32342	32343	
	SEQ ID NO:	15598	24519	19417					_	18330		19053	19053	22856	12865	13440		13449	13464	13760	13915	13915	14478	15043	16368	16772	18227	18227	18888	18303	19333	19333	
	Probe SEQ ID NO:	2555	11974	8656	9699	9696	1584	1684	5532	5532	5855	6280	6280 6280	10008	37	673		673	88	<u>6</u>	118	1181	1/36	2318	3815	4027	\$28	5,28	6111	8238	6999	6293	

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo septens statytransferase 6 (N-ecetytlacosaminide albha 2.3-statytransferase) (SIAT6), mRNA	Homo sepiens cysteiny-tRNA synthetase mRNA, complete cds, alternatively spliced	Human guanine nucleotide-binding protein abha-subunit gene (G-s-abha), exons 4 and 5	Homo sapiens amylo-1.8-glucosidase, 4-eipha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA	yp70g02.r1 Soares fetal liver splean 1NFLS Homo septens cDNA clone IMAGE:193682 6	Homo saplens dynactin p62 subunit (LOC51164), mRNA	Homo sepiens calclum-binding transporter mRNA, partial cds	Homo sapiens mRNA for KIAA1216 protein, partial cds	Homo sepiens hypothetical protein FLJ20450 (FLJ20450), mRNA	Homo saplens hypothetical protein FLJ20450 (FLJ20450), mRNA	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EiF3S6) mRNA	Homo sapiens low density lipoprobein-related protein 2 (LRP2), mRNA	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo saplens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA	2755005 rt Soares fetal Iver scheen 1NF S St Homo serviers cDNA closes NAACE 446004 Rt	WASACIS II Scarpe bastle NHT Home september DNA close (IAA CESTAALE)	AV738538 CB Hamo septems cDNA clone CBL BGB10 6	9904f01x1 Soares, testas, NHT Hamo sapiens cDNA clone IMAGE:1738009 3' similar to TR:014045 014045 PHOSPHOTRANSFERASE.:	9604f01.x1 Sourse, thethe. NHT Homo saplens cDNA clone IMAGE:1738009 3' similar to TR:014045 O14045 HOSPHOTRANSFERASE;	wb52c05x1 NCL CGAP_GC6 Homo septens cDNA clone IMAGE:2308288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES	wb62c06xf NCI_CGAP_GC8 Homo septens cDNA clone INAGE:2309288 3' similer to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GFNFS	2p21d11.r1 Strategene neurospithelium (#837231) Homo sapiens cDNA done IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL.	2x80h08.r1 Sogres testis NHT Homo sepiens cDNA clone IMAGE-758075.51	291a06.s1 Soares fetal liver spicen 1NFLS S1 Hamo sapiens cDNA clone IMAGE-462226 31	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens SP100-HMG nuclear autoentigen (SP100) mRNA, complete cds
jle Exon Prob	Top Hit Database Source		- La	TA L		T HUMAN										T HUMAN	Т	Т	EST HUMAN O	EST_HUMAN C	EST HUMAN O			Τ	П		H
Sing	Top Hit Acession No.	11422842 NT	2.0E-70 AF288207.1	2.0E-70 M21741.1	11423599 NT	2.0E-70 H47959.1	11526355 NT	20E-70 AF123303.1	2.0E-70 AB033042.1	8923420 NT	8923420 NT	4503520 NT	11430460 NT	11430460 NT	4507476 NT	1.0E-70 W85795.1	-	T	9.0E-71 AI143870.1	9.0E-71 AI143870.1	9.0E-71 AI854003.1	9.0E-71 AI654903.1	8.0E-71 AA171451.1				5.0E-71 AF056322.1 IN
	Most Similar (Top) Hit BLAST E Value	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	2.0E-70	1.0E-70	1.0E-70	1 0E-70 /	1.0E-70	9.0E-71	9.0E-71	9.0E-71	9.0E-71	8.0E-71	7.0E-71	7.0E-71	7.0E-71	5.0E-71 A
	Expression Signal	1.68	0.76	9.02	0.5	0.8	96'0	1.46	0.47	3.75	3.75	7.32	3.06	3.06	2.63	08.0	0.65	7.13	7.05	7.05	2.23	4.79	5.03	8.9	1.02	2.07	2.97
-	ORF SEQ ID NO:	30530		33639	33951		34918	35904	36373	36933	36934	37559	31058	31059			-	36777	31579	31580	32714	32714		33036	34408	37262	27673
	Exen SEQ ID NO:	17973		20514	20815	21250	21756	22686	23146	23677	23677	24236	24767	24757	16147	21850	22349	23532	18641	18641	19668	19668	21658	19959	21270	23961	14835
	Probe SEQ ID NO:	6897	7303	7819	8121	8558	29067	10038	10500	11005	11005	11639	12353	12353	3388	9180	8696	10852	5854	5854	6832	11508	8968	7275	8578	11302	2207

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Single Exoll riobes Expressed in Brain	Top Hit Descriptor	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete ods	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds.	bb81a06.y1 NIH_MGC_10 Home septens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMAN OG B	Tmul022 Human Epidermal Keratinocyte Subtraction Library-Upregulated Transcripts Homo sapiens cDNA similar to gi 6598881	Tmul022 Human Epidermal Keratinocyte Subtraction Library-Upregulated Transcripts Homo sapiens cDNA similar to oi 659884	W/7011.11 Sogres breest 2NNHRst Home sentens ADNA Alone 1148 ACC 454772 FT	ye/3e09.r1 Soares fetal liver spieon 1NFI S Homo services CONA Alone 14/4 CE 1704700 ET	oy/15e03.s1 Source_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1685916.3' similar to contains I OR1 to 1 O	Homo sablens nauronal cell death-nelated material (1 0054546)	Conn sanisms dischard 2 mens 2 through 4 K - 1 - 1 - 1	Homo service unactions general Authority Autho	Homo saplens PMS2I,16 mRNA, partial cds	Homo septens PMS2_16 mRNA, pertial cds	Homo saplens hair/enhancer-of-solit halsed with YRPW motifulue (HEV.)DNIA	Homo sapiens frordenic pyrophosphatase mRNA commisse ode	Homo sapiens SNARE profein kinase SNAK mRNA commissionals	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	02_15 Human Epidermial Keratinocyle Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5's similer to Homo sapiens chromosome 19	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo saplens oDNA	Homo sarians affraction premisers (ATDM) and 10	Human mRNA for KIAAAAA Sone complete ode	VITS6110.11 Scenes Infant brain 1NIR Home services child close MAACE space of	D GOOD CAND THE COURT WAS A COURT OF THE COU	Homo seriens mRNA for MA Antico matter and synthesis, yeast, homolog). If the 2 (GCN5L2), mRNA	Homo septents (III) NA Property parties cds Homo septents CAC 70 mRNA martiel At-	Sold and the second of the sec
GIB EXUIT FIUL	Top Hit Database Source	LN LN	IN	EST_HUMAN	EST_HUMAN	EST HUMAN	T	Т								Į.	- L	±N.	EST_HUMAN o	EST HIMAN			T HUMAN				
5	Top Hit Acession No.	2.0E-71 AF095703.1	2.0E-71 AF095703.1	2.0E-71 BE018477.1	2.0E-71 BF149173.1	2.0E-71 BF149173.1			1.0E-71 AI077927 1	1828	1.0E-71 AF206890.1	Ī			7867153 NT		1.0E-71 AF246219.1	1.0E-71 AF246219.1	1.0E-71 BE122850.1	1.0E-71 BE122850 1				428182			
	Most Similar (Top) Hit BLAST E Value	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71	2.0E-71 R55626.1	2.0E-71 T95489.1	1.0E-71	1.0E-71	1.0E-71 /	1.0E-71	1.0E-71	1.0E-71	1.0E-71	1.0E-71 A	1.0E-71	1.0E-71 A	1.0E-71	1.0E-71	1.0E-71 AF218904.1	1.0E-71 D28476.1	1.0E-71 H23178.1	1.06-71	1.0E-71 AB011131.1	1.0E-71 U80753.1	
	Expression Signal	3.88	3.88	3.21	1.36	1.38	2.35	8.43	1.83	2.37	6.15	11.71	1.38	1.38	3.91	2.53	5.88	5.88	0.98	86.0	2	1.92	96.0	1.07	1.39	13.35	
	ORF SEQ ID NO:	36357	36358	36524	37463	37464	37490		26037	28351	26494	28740	27536	27537	28142	28903	28982	28983	29031	29032	29114	29801	29916	32420	32726	32971	
_	Exan SEQ ID NO:	23131	23131	23287	24151			24561	13402	13687	13836	14066	14808	14806	15407	16249	16338	1838	16392	16392	16477	17173	17287	19405	19679	19896	
	Probe SEQ ID NO:	10485	10485	10583	11552	11552	11576	12038	623	920	1078	1317	2074	2074	888	8883	3583	3583	3639	3639	3724	4437	4552	6643	9869	7211	

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Oligio Exoli Flores Explored III Diani	Top Hit Descriptor	Human chondroitin suifate proteoglycan versican V0 splice-vertant precursor peptide mRNA, complete cds	Human chondroitin sulfate proteoglycan versican V0 spikoe-variant precursor peptide mRNA, complete cds	Human gamma-aminobutyric acid transaminase mRNA, partial cds	Human gamma-aminobutyric acid transaminase mRNA, partial cds	TCAAP1E1252 Pediatric scuts myslogenous leukennia celi (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1252	Homo sepiens 959 Ido cartig between AML1 and CBR1 on chromosome 21q22, segment 3/3	Homo saplens hypothetical protein FLJ20585 (FLJ20585), mRNA	TCR V detta 2-C aipha ≖T-cell receptor detta and C alpha fusion gene {atternatively spliced, splice junction} [human, precursor B-cell line REH, mRNA Partial, 211 nt]	Homo sepiens hypothetical probth (FLJ11127), mRNA	Homo sepiens protein methyttransferase (JBP1) mRNA, complete cds	Homo sapiens protein methytransferase (JBP1) mRNA, complete cds	wb31a08.x1 NCI_CGAP_GC6 Harro saplens cDNA clane IMAGE:2307254 3'	Homo sapiens semephorin W (SEMAW) mRNA	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, excn 5	Homo sapiens mRNA for KIAA1081 protein, pertial cds	Homo sapiens mRNA for KIAA1081 protein, pertial ods	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA	Homo sepiens basic transcription factor 2 p44 (bt/2p44) gene, partial cds, neuronal apoptosis inhibitory profesi (nato) and sundval motor nation profesi (smr) dense, completa cos	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and Johned cds	Homo sepiens solute carrier family 13 (sodkum-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA	801890419F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:4131461 5	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'	aj28b09.s1 Soeres_testie_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02067 H.sepiens mRNA for 7SL RNA pseudogene (HUMAN);	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds	al83d02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395.3'
	Top Hit Database Source	Į.	<u> </u>	TN	Z	EST_HUMAN 8			L L		F		EST_HUMAN W		± L	1 LN	TN TN	± LN	,					EST_HUMAN 6	EST_HUMAN O	EST_HUMAN n		EST_HUMAN
Sillo I	Top Hit Acession No.					Σ	3.0E-72 AJ228043.1	8923548 NT		1416196	3.0E-72 AF167572.1		3.0E-72 AI654337.1	4759093 NT	3.0E-72 AF073367.1			3.0E-72 AB029004.1	4826987 NT		5031892		11428871 NT	2.0E-72 BF308560.1		2.0E-72 AA789277.1		1.0E-72 AA846225.1
	Most Similar (Top) Hit BLAST E Value	3.0E-72 U16306.1	3.0E-72 U16308.1	3.0E-72 U80228.1	3.0E-72 U80228.1	3.0E-72 E	3.0E-72	3.0E-72	3.0E-72 S77589.1	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3.0E-72 /	3.0E-72	3.0E-72	3.0E-72	3.0E-72	3 0E-72 ISON17 1	3.0E-72	3.0E-72 X98289.1	2.0E-72	2.0E-72	2.0E-72	2.0E-72	2.0E-72	1.0E-72
	Expression Signal	6.64	20.0	0.72	0.72	1.24	11.45	2.17	2.69	3.12	1.07	1.07	0.95	1.27	2.1	2.1	4.82	4.82	3.63	2.15	96.0	12	<u>2</u>	0.71	0.71	2.47	5.75	1.19
	ORF SEQ ID NO:	26546		26587		26042	28481	28684	29186	29876	30079	30080	30215		31621	31622	31819	31820	32284	33240			31597	34832	34833	36589		27527
	Exen SEQ ID NO:	13888	13888	13925	13925	14256	15838	16034	18555	17243	17447	17447	17591	18232	18678	18676	18853	18853	19281	20457	20769	22978	18656	21683	21683	23331	24819	14800
	Probe SEQ ID NO:	1132	1132	1171	1171	1510	3072	3273	3803	4508	4715	4715	4862	5433	5891	5891	8074	6074	8516	7485	8075	10331	2889	8983	8983	10840	12449	2068

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The state of the second in pigning the secon	Top Hit Descriptor	Homo sablens vacuolar protein sorting 41 (vesst homolon) (VPS41) mRNA	Homo sabiens myosin, heavy polypeptide 13, skeletel mysole APA13, mDNA	Homo septens myosin, heavy polynemine 13, skeletel mysole (AVAL13), month	AV751818 NPD Home sapiens CONA clane NPDAIE11 F	RC4-HT0578-170300-012-002 HT0578 Homo expises CDNA	RC4-H70578-170300-012-002 H70578 Homo seniens cDNA	Homo saplens synaptic divocorden SC2 (SC2) mRNA complete city	Homo sablens synaptic divocardain SC2 (SC2) mRNA remilate ode	MR0-CT0063-071099-002-h11 CT0063 Homo sepients CDNA	Homo septens ribosomal protein L13a (RPL13A), mRNA	W#55c08.x1 NCI_CGAP_Bm25 Homo sapiens CDNA clone INAGE:2501098 3' similer to TR:Q59050 Q59050 HYPOTHETICAL PROTEIN M MARK	Homo sabians phosphathchinosthal Juhnese class 2 alche actionness (Divocos)	Horne conjugate hazargan construction of the conjugate of	The separate specification (LOCS/19), MINNA	nomo sapiena vecudar A I Pase isotom VA68 mRNA, complete cds	bb62a06.y1 NIH_MGC_9 Homo septens cDNA clone IMAGE:3030034 5' similer to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN): ab:M21495 Marise completed a parma and made and a constant and a con	Homo saplens interfered in 12 recently here 1 (11 12 PB 1). The PB 1 (11 12 PB 1) in the PB 1 (1	Homo sapiens interfeudin 12 receptor, beta 1 (II 12RB1) mRNA	Homo saplens transition protein 1 (during histone to protein pendagement) (TNP4) mRNA	Homo sapiens DEAD-box protein (HAGE), mRNA	Homo saplens thyroid autoentigen 70kD (Ku antigen) (G22P1), mRNA	Homo sepiens hypothetical protein FLJ20309 (FLJ20309); mRNA	Homo seplens chromosome 21 segment HS21C008	Homo suplens chromosome 21 segment HS21 C082	Homo septens chromosome 21 segment HS21C018	QV0+T10684-020300-137-403 HT0494 Homo septems cDNA	Homo seglene HELG protein (FAM4A1) mRNA	CMO-CNEESE 280100-164-108 CN0044 Homo sepiens cDNA	2005e04.e1 Stategene fetal retine 937202 Homo sapiens cDNA clone IMAGE:565950 3' similar to	AV720428 HTC Home seniors CONA Alma HTCA ARA74 EL	AV729428 HTC Home septens cDNA clone HTCAAF671 5'	
פום באסון ביוס	Top Hit Database Source	Ę	F	Ļγ	EST HUMAN	EST HUMAN	EST HUMAN		F	EST HUMAN	FN	EST HUMAN	LN	TN	LIA.	Z	EST HUMAN	L	M	N	F	NT	NT	NT	NT	TN	EST_HUMAN	•	T_HUMAN	FST HIMAN	Т	EST HUMAN	
5	Top Hit Acesslon No.	7657676 NT	11321578 NT	11321578 NT	1.0E-72 AV751818.1	1.0E-72 BE175434.1	1.0E-72 BE175434.1	1.0E-72 AF222742.1	1.0E-72 AF222742.1	9.0E-73 AW374968.1	11424099 NT	8.0E-73 AW071756.1	4505798 NT	1142848D NT	8 0E 73 AE413430 4	113128.1	8.0E-73 BE019900.1	11528037 NT	11528037 NT	4507628 NT	11418786 NT	11418189 NT	8923290 NT	2	2	2	8.0E-73 BE166574.1	11422159 NT	3.0E-73 AW843789.1	-			
	Most Similar (Top) Hit BLAST E Value	1.0E-72	1.0E-72	1.0E-72	1.0E-72	1.0E-72	1.0E-72	1.0E-72	1.0E-72	9.0E-73	9.0E-73	8.0E-73	8.0E-73	8.0F-73	A OF 72	S.C13	8.0E-73	8.0E-73	8.0E-73	8.0E-73	8.0E-73	8.0E-73	7.0E-73	7.0E-73/	7.0E-73 /	6.0E-73	6.0E-73	4.0E-73	3.0E-73	3.0E-73 AA136403	3.0E-73 AV729428	3.0E-73 AV729428.	
	Expression Signal	3.63	1.31	1.31	12	3.7	3.7	10.25	10.25	1.35	15.11	2.29	F	5.16	287		6.25	1.92	1.92	0.45	1.28	3.31	0.83	1.18	1.35	3.07	3.48	2.2	2.77	0.71	0.65	0.65	
	ORF SEQ ID NO:	31390	32231	32232	32305	33304			35325	26875		26434	31180	32245	33817	+	35105	35484	35485	36379	37488	31012	26528	28705			32827	30497	28741	32374	34482	34463	
	Exon SEQ ID NO:		19231		25093	20207	20207	22144	22144	14191	23551	13774	18292	19245	20689		21932	22232	22232	23153	24172	24859	13869	16058	17818	12869	19783	17982	14067	19361	21348	21348	
	Probe SEQ ID NO:	2680	6464	6464	9239	7537	7537	9491	9491	144	10871	1015	5493	6478	ğ		8253	9640	9840	10507	11673	12506	1112	328	\$	호	7072	5173	1318	9699	9656	9856	

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	ou11d02x1 Sogres_NFL_T_GBC_S1 Hamp sepiens cDNA clone IMAGE:16259553'	Homo sapiens chromosome 21 segment HS21C046	RC3-NN0068-270400-011-c04 NN0066 Homo sepiens cDNA	Homo sapiens BASS1 (BASS1) mRNA, pertial cds	RC3-NN0066-270400-011-c04 NN0066 Homo sepiens cDNA	Human beta globin region on chromosome 11	Homo sapiens caspase 8, apoptosis-related cysteine protesse (CASP8) mRNA	Homo saplens Parkinson disease (autosomal recessive, Juvenile) 2, parkin (PARK2), transcript variant 3, mRNA	Homo sapiens Parkinson disease (autosomal recessive, Juvenile) 2, parkin (PARK2), transcript variant 3, mRNA	Homo sapiens chromosome 21 segment HS21 C083	Mus musculus rhofrac-Interacting citron kinase (Crik) mRNA, complete cds	Mus musculus rhorac-interacting citron kinase (Crit) mRNA, complete cds	Homo sapiens mRNA for KIAA1591 protein, partial cds	Homo saplens interleukin 4 receptor (IL4R), mRNA	Homo sepiens Interleukin 4 receptor (IL4R), mRNA	Human peripheral myelin protein 22 mRNA, complete cds	Homo sapiens mRNA for KIAA1329 protein, partial cds	Gallus gellus Dech2 protein (Dech2) mRNA, complete cds	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	Homo sapiens glutathione synthetase (GSS) mRNA	Homo sapiens supervilla (SVIL), transcript varient 1, mRNA	Homo sapiens supervilin (SVIL), transcript vertant 1, mRNA	Homo saplens galactosyceramidase (Khabbe disease) (GALC), mRNA	Homo sapiens galactosyceramidase (Krabbe disease) (GALC), mRNA	Homo sapiens mRNA for KIÁA1059 protein, partial cds	RC3-NN0066-270400-011-c04 NN0066 Homo seplens cDNA	AU121585 MAMMA1 Homo sepiens cDNA cione MAMMA1000490 5	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	CM1-HT0282-111199-042-h10 HT0282 Homo sapiens cDNA	og61b07.r1 Sceree_testis_NHT Homo eaplens cDNA clone IMAGE:1839637.5' similar to contains element. MER22 repetitive element;	001276071F1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE:3617105 5
ופ באטוו רוטטב	Top Hit Detabase Source	EST_HUMAN	± LN	EST_HUMAN F		EST_HUMAN F	TA L				- L		N L	TZ TZ				4 LN	D IN					,		H IN	EST_HUMAN R	-HUMAN	NT	HUMAN	EST_HUMAN N	EST_HUMAN 0
Billo	Top Hit Acession No.	3.0E-73 AI004040.1	3.0E-73 AL163246.2	3.0E-73 AW 898081.1	2.0E-73 AF139897.1	2.0E-73 AW898081.1	,	4502582 NT	7669539 NT	7689539 NT	2.0E-73 AL163283.2		2.0E-73 AF096824.1	2.0E-73 AB048811.1	11431471 NT	11431471 NT			2.0E-73 AF198349.1	2.0E-73 AF198349.1	4504168 NT	11496980 NT	11496980 NT	4557612 NT	4657612 NT	2.0E-73 AB028982.1	2.0E-73 AW898081.1 E	1.0E-73 AU121585.1 E	1.0E-73 AF198349.1 N	1.0E-73 BE151283,1	1.0E-73 AI147427.1 E	1.0E-73 BE385477.1 E
	Most Similar (Top) Hit BLAST E Value	3.0E-73	3.0E-73	3.0E-73	2.0E-73	2.0E-73	2.0E-73 U01317.1	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73 /	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73 M94048.1	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	2.0E-73	1.0E-73 A	1.0E-73	1.0E-73 B	1.0E-73	1.0E-73B
	Expression Signal	1.61	1.5	1.54	1.43	1.78	1.3	3.99	P.0	19 :0	1.03	0.89	0.89	6.27	1.27	1.27	0.09	0.73	0.62	0.52	1.21	1.31	1.31	3.37	3.37	1.82	1.83	1.71	1.12	1.07	1.37	2.85
-	ORF SEQ ID NO:				28271			28590	28943	28944		32102	32103	32159	32376	32377	33476	33478	35284	35285	36189	36257	36258	36917	36918	30955		27221	27946	32015	35230	36426
	Exen SEQ ID NO:	24209	25003					15940	16294	16294	17138	19114	19114	19158	19363	19363	20362	20364	22110	22110	22969	23040	23040	23662	23662	23692	14674	14518	15205	19039	22061	23195
	Probe SEQ ID NO:	11611	12734	12738	831	1939	2296	3177	3538	3538	4401	6344	6344	6388	9800	9800	7699	7701	9432	9432	10322	10394	10394	10987	10987	11020	12293	1776	2488	6286	9399	11428

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ongo the control of t	Top Hit Descriptor	Homo sapiens CD39-like 4 (CD39L4) mRNA	Ca2+/calmodulin-dependent protein Idnase IV Idnase Isoform [rats, brain, mRNA, 3429 nt]	Ce2+/calmodulin-dependent protein Idnase IV Idnase Isoform (rets, brain, mRNA, 3429 nt)	yw48g10.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:245826 3'	Homo sapiens NKG2D gane, exan 10	Homo saplens chromosome 21 segment HS21C046	601649284F1 NIH_MGC_73 Homo sepiens cDNA done IMAGE:3632997 5'	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 57	Homo seplens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene,	partial cds	801283521F1 NIH_MGC_44 Homo seplens cDNA clone IMAGE:3605453 5	801283521F1 NIH_MGC_44 Homo saplens cDNA claim IMAGE:3605453 5'	UI-H-BI0-earth-03-0-UI.s1 NCI_CGAP_Sub1 Homo sepiens cDNA clone IMAGE:2709365 3'	UHH-BI0-eeh-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sepiens cDNA clone IMAGE::2709365 3'	hr54e11.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3132332 3'	hr54e11.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3132332 3'	Homo sapiens ectin filament associated protein (AFAP), mRNA	df17c09.y1 Morton Fetal Cochilea Homo sapiens cDNA clone IMAGE.2483704 5'	PMA-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA	Homo sapiens phoephatidylinositol glycem, class L (PIGL), mRNA	H.saplens mRNA for TPCR16 protein	Homo septens VAMP (vestcle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA,	Minns endens Interded Lin A recomptor (II AD)	Homo saplens interferidin 4 recentor (11.4R) mRNA	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo saplens hypothetical protein FLJ13222 (FLJ13222), mRNA	H.seplens mRNA for HIP-I	H.sepiens mRNA for HIP-I	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of 1.1) (CHL1) mRNA	Homo saplens DNA for emyloid precursor protein, complete cds	Homo sapiens mRNA for KIAA1019 protein, partial cds
פון ווווסעד פון	Top Hit Detabase Source	F	F	F	EST_HUMAN	뉟	LN TN	EST_HUMAN	EST_HUMAN		L	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	EST_HUMAN	EST_HUMAN	NT	NT	ţ	2 2	5	Z	LN LN	Z	NT	LN LN	 	Į,	¥
	Top Hit Acession No.	4557426 NT	383194.1	583194.1	V52239.1	7.0E-74 AJ001689.1	7.0E-74 AL163246.2	7.0E-74 BE967432.1	7.0E-74 BE266305.1		1	.1	6.0E-74 BE388260.1	6.0E-74 AW014039.1	6.0E-74 AW014039.1	6.0E-74 BE048846.1	8.0E-74 BE048846.1	11058013 NT	5.0E-74 AW020986.1	5.0E-74 AW362756.1	11425417 NT		0001037	400/000 N	11431471 NT	7862263 NT	7882263 NT	11345483 NT	09420.1		5729788 NT	ı	-
	Most Similar (Top) Hit BLAST E Value	8.0E-74	8.0E-74 S83194.1	8.0E-74 S83194.1	8.0E-74 N52239.1	7.0E-74	7.0E-74	7.0E-74	7.0E-74		6.0E-74 /	8.0E-74	6.0E-74	6.0E-74	6.0E-74	6.0E-74	6.0E-74	6.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74 XB9670.1	10 4	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74 Y09420.1	5.0E-74 Y09420.1	5.0E-74	4.0E-74 D87675.1	4.0E-74
	Expression Signet	1.06	2.2	2.2	1.36	2.59	1.08	2.83	5.51		2.4	11.78	11.78	1.32	1.32	1.34	1.34	3.02	7.33	2.62	1.86	12.98	77 1	1 84	18	6.98	0.6	2.78	2.56	2.56	2.68	1.79	5.15
	ORF SEQ ID NO:	26150	31544	31545		27390	28732	35038	31011			27776	27777	28279	28280	29082	29093	30744	26322		30784	31419	24.46	31530	31537	32567	32567	33758	36565	36566	38687	26723	26272
	Exon SEQ ID NO:	13407		18613		14677	16082					15039	15039	15634	15634	16453	16453	18086	13854	15413	18125	18497	40540	18908	18608	19539	19539	20631	23328	23328	23442	13080	13602
	Probe SEQ ID NO:	723	5824	5824	10791	1942	3322	0142	12505		138	2314	2314	2867	2867	3700	3700	5281	882	2706	6322	5703	E740	5840	5819	6795	7569	7836	10836	10636	10757	273	832

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	T	T	T	Т	Т	Τ	Т	Т	Т	Т	Т	T	T	T	T	T	Т	T	Т	Т	Т	\top	Τ	T	T	Т	Т	Т	7	Т	Т	Т	1	Τ-
Top Hit Descriptor	Human patielet alvooprotein IIb mRNA 3' end	RC8-HT0678-220500-011-C03 HT0678 Homo saciens cDNA	Homo saplens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	Homo sepiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	Homo saplens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA	801557524F1 NIH MGC 58 Homo septiens cDNA done IMAGE: 3827549 5	Homo sapiens mRNA for KIAA1395 protein, pertial cds	Homo sapiens chromosome 21 segment HS210004	zp90e06.s1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA	Homo sepiens hypothetical protein FLJ11026 (FLJ11026), mRNA	Homo sapiens beta 2 gene	Homo saplens zinc finger protein 259 (ZNF259) mRNA	Homo sepiens mRNA for KIAA0833 protein, pertial cds	Homo sapiens chromosome 21 segment HS21C048	Homo sapiens DNA for Human P2XM, complete cds	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA	2780c01.r1 Source, NhHMPu, S1 Homo sepiens aDNA clone IMAGE: 667776 5	2760c01.r1 Source_NhHMPu_S1 Hamo septems cDNA clone IMAGE:867776 57	Homo eapiene giutamate receptor, fonotropio, kainate 1 (GRIK1) mRNA	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA	Home saplens chromosome 21 segment HS21 0088	RC2-BT0642-270300-019-f06 BT0642 Homo equiens oDNA	Human neurofibromin (NF1) gene, complete cds	Homo sapiens KIAA0852 protein (KIAA0852), mRNA	601070088F1 NIH_MGC_12 Hamo sapiens cDNA dane IMAGE:3456260 5	801070088F1 NIH_MGC_12 Hamo septems cDNA clane (WAGE:3456260 5)	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds	MR0-HT0559-230500-021-e03 HT0559 Homo sapiens cDNA	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS	Homo sapiens partial AK155 gene for AK155 protein, excris 1-3 and joined CDS	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
Top Hit Database Source	F	EST HUMAN	F	F	Ę	노	EST_HUMAN	Ε	Z	EST HUMAN	TN	EST_HUMAN	Ę	卜	¥	TN	FN.	Z	5	EST_HUMAN	EST_HUMAN	エフ	LZ	TN	EST_HUMAN	LN LN	TN	EST_HUMAN	EST_HUMAN	¥	EST_HUMAN	NT	Z	۲,
Top Hit Acessian No.	2.0E-74 J02963.1	2.0E-74 BE711134.1	11439587	11439587 NT	11439587 NT	11439587 NT	2.0E-74 BF030788.1	2.0E-74 AB037816.1	2.0E-74 AL163204.2	AA196181.1	7657334 NT	1.0E-74 AW816405.1	8922829 NT	1.0E-74 X02344.1	4508020 NT	1		1.0E-74 AB002059.1	4758697 NT	1.0E-74 AA258549.1	1.0E-74 AA258549.1	4504116 NT	4504116 NT	,	.1	1.0E-74 M89914.1	417977	1	1.0E-74 BE549105.1	1.0E-74 AF214562.1	1.0E-74 BF351951.1 E		1.0E-74 AJ251550.1	11420540 NT
Most Similar (Top) Hit BLAST E Value	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	2.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74	1.0E-74
Expression Signal	1.11	2.5	1.89	1.89	2.78	2.78	0.92	1.29	90.9	3.95	1.89	5.02	1.05	13.6	1.47	1.81	2.27	4.39	3.66	6.0	6:0	0.86	0.86	4.81	1.15	1.86	1.15	1.13	1.13	4.82	99.0	0.55	0.55	1.38
ORF SEQ .ID NO:	98708	31424	31521	31522	31521	31522	32748	33863	35208		25509	25764	25907	25912	25995	26197	26406	27690	28545	28782	28783	28282	29293	29338	29415	32380	33291	33773	33774	34543	34571	36001	36002	36241
Exam SEQ ID NO:	17676	25074	25077	25077			19695			24687	12881	13129	13272	13277	13367	13538	13744	14951	15900	16125	16125	18851	16851	16700	16787	19368	20197	20650	20650	21396	21425	22788	22788	23028
Probe SEQ ID NO:	4949	5709	2806	2806	5876	5876	7003	7841	9282	12234	32	328	487	\$ \$	287	785	979	2223	3136	3366	3366	38	3901	98 88	4042	9002	7528	7965	7955	8704	8733	10140	10140	10380

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Cingra Exort Probes Expressed in Brain	Top Hit Descriptor	Homo serviers clintathione S. transferment Hope 2/OCTTON	One server a rightfloor S. tensfer at 1.0 (2011.2), INCAA	Homo seciens DNA for Himan POXM American Adv.	Homo seplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	Homo saniene DNA cutreine & mathrithmas and Amilians	Homo sabiens chronosome 21 segment HS24 Cho.	W438408.x1 NCI_CGAP_Pr22 Home september 20NA done IMAGE:2417654 3' similar to gb:M14123_cds4	INCOMENCE OF THE PROPERTY OF T	INGONIS STANCI CIGAP CAS Light appeals CONA CIGAR INVOCATIONS 33	601128068F1 NIH MAC 9 Home section Child Act 11 (20)	20 7 F08 r1 Strategies why (403 7004) House and Park Anna Park	601348909F1 NIH MGC 8 Home seelen folks date in 11 of control of the control of t	601346909F1 NIH MICC 8 Home series COINA JOHN NO CONTROLL CONTROL	602186616T1 NIH MGC 49 Homes enters con A constitution of the cons	#31c12x1 NCI_CGAP_CE Homo septens CDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 HYPOTHETICAL 20 4 KP DECETTION	OVI-BTD832-210-200-200-200-200-200-200-200-200-20	WORLD Come molecular Children	CMO-NINORS7-15040N-335-614 NINORS7 U	601303866F1 NIH MGC 21 Home explane 2014 also be the Common and th	Homo saciens hypothetical protein E. 140747 (El. 140747) - ENIA	Homo sapiens NIPSNAP C. elegans homology 1 (NIPSNADA) DNA	Homo sapiens NIPSNAP C elegans homology (NIDSNADA) TONA	Homo seplens etilervotis transferior initiative forby 2 and the 10 through transferior initiative forby 3 and the 10 through transferior initiative forby 3 and the 10 through transferior initiative forby 3 and the 10 through transferior initiative forby 3 and the 10 through t	Homo saplens NIPSNAP C secrets homology (Alice Advisor	Homo seplens NIPSNAP, C. eferans homology (Virt. Crypt.), mileyon	Ono saplens mussin heavy redynamical a spatial and the saplens mussin heavy redynamids 4 spatial and 11 th 1	Homo septens HTRA serine professor (DRSC41) and All All All All All All All All All Al	Homo septens HTRA series protected (PRSSA1) com-	Homo sections mRNA for KIAAA581 provision martial water	Homo sepiens syneotoienin 1 (SYALI1) mRNA	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
מום בייטון בווסיין פול	Top Hit Database Source	LN	LN	N	5	Ę	Z	HENT HIMAN	EST HI IMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN		Т	Т	7	Т												
5	Top Hit Acession No.	11417856 NT	11417856INT	1.0E-74 AB002059.1	1.0E-74 AF240788.1	-	2	6.0E-75 AI817415.1								5.0E-75 AI638623.1			20		72837	11417946 NT	11417946 NT	5579457 NT	11417946 NT	11417946 NT	7669505 NT	3.0E-75 AF157623.1			4507334 N	4759153 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-74	1.0E-74	1.0E-74	1.0E-74	8.0E-75	8.0E-75	6.0E-75	5.0E-75/	5.0E-75	5.0E-75	6.0E-75	5.0E-75	5.0E-75	5.0E-75	5.0E-75 A	4.0E-75 B	4.0E-75 N36757.1	4.0E-75	4.0E-75 B	4.0E-75	4.0E-75	4.0E-75	4.0E-75	4.0E-75	4.0E-75	4.0E-75	3.0E-75 A	3.0E-75 AF157623.1	3.0E-75 AB011153.1	3.0E-75	3.0E-75
	Expression Signer	292	5.01	1.58	1.53	3.68	1.86	1.47	0.61	0.61	19. 0	9.0	0.78	0.78	1.53	2.39	2.18	1.02	1.5	4.80	0.94	0.56	0.56	5.78	2.26	2.26	18.12	3.72	2.41	2.78	1.11	5.86
	ORF SEQ ID NO:	37800		27690				27781	33466	33467	34643	34855	34946	34947	35197	35993	25568		27202	28266	28802	31128	31129	31926	32436	32437	36517	26409	26409	27279	27570	27876
	SEQ ID NO:		24513	14951	24897		24700	15044	20352	20352	21498	21705	21782	21782	22027	22782	12831	13232	14501	15621	16248	18241	18241	28 28 28 28	<u>\$</u>	19421	23270	13747	13747	14567	14836	15143
	Probe SEQ ID NO:	11885	11965	12103	12567	2650	12254	2319	7688	7688	8808	9015	8083	9083	8273	10134	110	446	1759	2853	3402	5442	2442	6176	883	8	15584	883	88	1828	2106	2422

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Table 4
Single Exon Probes Expressed in Brain

									\Box		\top		Γ		T	T	T	Ι		8					П		Г		\rac{1}{>}	-
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Home employe of the second of	Home series month 6- VIA Account.	Himen address and the NAAA0301 protein, partiel ods	Human delication and the spholipid-binding protein (PLA2) mRNA, complete cds	Home seriors DNA for sun 12-4	Home explans MIVA for annivoral precursor protein, complete edis	Homo serviers advotor all the control of the contro	Homo saciens adentir-related protein complex 1 strains 2 subunit (AP1S2), mRNA	Homo saplens HIR (histone cell curie remitation defeature c	Home senters till Acid.	Home sections (1) A A Constant Cert Cycle regulation defective, S. cerevisies) hamalog A (HIRA), mRNA	Home contact VIA Access	Hours experis NAAU022 gene product (KIAA0623), mRNA	Homo sapiens Oncogene TIM (TIM) mRNA	Homo sapiens Oncogene TIM (TIM) mRNA	Homo saptens snall 1 (drosophila homolog), zinc finger protein (SNAI1), mRNA	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA	Homo sapiens synuclein, alpha (non A4 component of emyloid precursor) (SNCA), mRNA	qo91e02.x1 NCI_CGAP_KId5 Homo sepiens cDNA done IMAGE:1915898 3' similar to TR:Q66386 Q69386	Home evaluation of the contract of the contrac	Homo earliens hardels have been placed that the property of the polypeptide 1 (PTPRZ1) mRNA	2900402.XI NCI_CGAP_Ut4 Home septems cDNA done IMAGE:2032707.3' similar to contains PTR7.tt	H. Saplens FR(7) none anno 1 g 3 / main	ZETROS st Sceres thesis NHT Home sepiens cDNA done IMAGE:726485 3' similar to gb:M13932 40S	SHOWS STANDING STANDI	CO (SUCZETT I NIT _MCC_19 Framo septens CDNA clone IMAGE:4129678 5	8077h08 s1 Strateges I mod (#027348) U.S.	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	
gle Exon Pro	Top Hit Detabase Source	FZ	ΙZ	12	5 5	Į.	5	5	Ę	5		5			Z	Z		ž	EST HIMAN	ECT LIBIAN	101	<u> </u>	EST HIMAN	NT.	ERT LINAM	EST LINAN	EST HIMAN	EST HUMAN	NT	
	Top Hit Acession No.	3.0E-75 AL163201.2			3.0E-75 M72393 1	3.0E-75 D87675.1	7882421 NT	11420958 NT	11420956 NT	11526319 NT	1152631D	TM62200INT	002200	TIM COMMENT	700004	IN COMMENT	IN STREET	N 22202011	3		8683	4506328 NT	1.0E-75 AW 188135 1		;	T				
	Most Similar (Top) Hit BLAST E Value	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-76	3 0F-75	2 00 75	3.0E-73	2000	3.0E-75	2.0E-75/	2.0E-75	1.0E-75	1.0E-75	1.0E-75 A	1.0E-75 X52221.1	1 0F-75 A	1.0E-75 B	1.0E-75 BF313845 1	1.0E-75A	1.0E-75 A	
	Expression	76.0	1.32	0.75	0.75	3.27	0.73	0.83	0.83	1.68	88	4.56	4.56	2.52	250	- 2	0.41	238	14.	2.45	1.12	1.12	6.68	3.27	4.27	3.75	3.75	10.83	2.56	
	ORF SEQ ID NO:	28434	28597		28758		29769	30493	30494	32623	32624	32783	32784	33284	33285	34717	35414	36314		34484	27539	27540	27.762	28366		35167	35168		36972	
	Exon SEQ ID NO:	15787	15947	16104	16104	L	17141		17980	19588	19588	19727	19727	20183	20183	21574	22230	23088	18384	21340	14808	14808	15026	15713	21008	21995	21995	23480	23704	
	Probe SEQ ID NO:	3021	3184	3345	3345	4147	4404	5171	6171	9671	6671	7035	7035	7622	7522	8883	1258	10440	5587	8648	2078	2078	2301	2047	8313	8328	8288	10797	11033	

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Cingra Lyon Flores Expressed in Brain	Most Similar Top Hit Acession (Top) Hit Descriptor Top Hit Descriptor	6.42 4.0E-76 D81625 1 EST HIMAN HIMAROMAB Himme 644 half /TE	3.0E-76/BF5162621 FST HIMAN	3.0E-76 BF516262.1 EST HIMAN	3.0E-76 4503478	3.0E-76 4503476 NT	3.0E-78 BF375889.1 EST HUMAN	3.0E-76 BF375689.1 EST HUMAN	3.0E-76 BE348993.1 EST HUMAN	3.0E-76 Z41314.1 EST HUMAN	3.0E-76 AA190611 1 EST HIMAN	3.0E-78 AF286598.1 NT	3.0E-76 N42871.1 EST HUMAN	3.0E-76 AW 299353 1 FST HIMAN	3.0E-78 AA442309.1 EST HUMAN	3.0E-76 AA442309.1	3.0E-78 AW967984.1 EST HUMAN	3.0E-78 AW956455.1 EST HUMAN	2.0E-76 D84295.1 NT	2.0E-76 D84295.1 NT	2:0E-76 D84295.1 NT	2.0E-76 4557862 NT	2.0E-76 4503944 NT	2.0E-76 4758053 NT	2.0E-76 4504028 NT	2.0E-76 4504028 NT	2.0E-76 AA253954.1 EST HUMAN	2.0E-76 P23286 SWISSPROT	2.0E-78 AA445992.1 EST HUMAN	2.0E-78 AA445902.1 EST_HUMAN
		4.0E-76 D	3.0E-76.BI	3.0E-76 BI	3.0E-78	3.0E-76	3.0E-78 BF	3.0E-76 BF	3.0E-76 BE	3.0E-78 Z4	3.0E-76 AA	3.0E-78 AF	3.0E-78 N4	3.0E-76 AV	3.0E-78 AA	3.0E-78 AA	3.0E-78 AV	3.0E-78 AV	2.0E-78 D8	2.0E-76 D8	2:0E-76 D8	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-76 AA	2.0E-78 P2:	2.0E-76 AA	2.0E-76 AA
	Expression Signal	6.42	3.2	3.2	3.28	3.26	4.96	4.96	1.07	207	1.09	9.57	0.88	3.34	0.99	0.99	2 8:	4.86	1.50	4.39	4.39	1.19	1.08	-	<u>و</u> .	1.91	16:0	3.34	2.06	2.08
	ORF SEQ ID NO:	35769		3 26027	27029		28828	28829	28434	37796	31354	32025	33877	35456	35486	35487	30812	30602			25769			26430			27369	28261	28701	28702
	SEQ ID	3 22571	13393	13393	14340			16179	16803	17891	18441	19048	20744	22269	22283	22293	25191			13134	13134	13234	13368	13/68	14273	14273	14658	15614	16052	16052
	Probe SEQ ID NO:	9923	615	615	1594	1594	3422	3422	4058	5158	5646	6275	8050	9616	9641	9641	11876	11979	275	333	SS SS	\$	9/9	3	1528	1526	1921	2846	3291	3291

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Table 4
Single Exon Probes Expressed in Brain

	Top Hit Descriptor	ac83b02.y5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:014591 014591 SIMILARITY TO P22059:	State TPRDII complete cole	1 OT0028 Homo serviens cDNA	ts and discoldin Hike domains 3 (FDII 3) mRNA	r (GG018) gene, pertial cds	V1081 protein, partial cds	A) enchar protein 10 (AKAP10), mRNA	n (HSTPCR86P), mRNA	what protein S26 (H. sepiens) (LOC83150) mRNA	g protein 4 (dna Liike) (HIRIPA), mRNA	Trolete cds	molete cds	omo sapiens cDNA clone IMAGE 3944302 5	lomo sapiens cDNA 5' end	forno septens cDNA clone IMAGE:3913737 5	Tomo septens cDNA clone IMAGE:3638753 57	yp11h02.r1 Scares breast 3NbHBst Home sapiens cDNA cione IMAGE:187155 5' similar to SP-ANKB HIMAN OD1484 ANKYPIN BRAIN VADIANT 4	formo sepiens cDNA clone IMAGE:4109503 5	Homo sapiens professome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA	HR Homo sections CDNA close 1MACE seasons F	HR Homo saplens cDNA clone IMAGE:363578.5	ye89f04.s1 Soures fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:123007 3' similar to contains MER10 reportition alement.	T Homo earlane (ANIA alone MIA OF: 745000 pt	Homo sepiens polymerase (RNA) II (DNA dimeded) polymentide E (2500) (DNI DOE) DNIA	Homo sapiens polymerase (RNA) (DNA directed) notweenide E (25KD) (DNI DOE) DNA	Libeta and creecal recentor 2 (FNARD) mDNA	9977h12x1 Sogres fetal lung NbHL19W Homo servens CDNA clare IMAGE-1745net 2	3CK) gene, exon 2	netalloprotease domain 10 (ADAM10) mRNA	Se 1 (TLK1) mRNA. complete cds
Onligie Lyon Flobes Lypresed in Drain	Top Ht Des	ac83b02.y5 Strategene lung (#837210) Homo sapiens cDi 014591 SIMILARITY TO P22059	Human mRNA for possible profein TPRDII complete cds	QV3-OT0028-220300-132-b11 OT0028 Home series	Homo sepiens EGF-Ike repeats and discolute Hike domeins 3 (FDII 3) mRNA	Gorille gorille offectory receptor (GGO18) gene, pertial cds	Homo sapiens mRNA for KIAA1081 protein, partial cds	Homo sepiens A kinase (PRKA) anchor protein 10 (AKAP10) mBNA	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC83150) mRNA	Homo sapiens HIRA Interacting protein 4 (dna Lilke) (HIRIP4), mRNA	Human mRNA for HMG-1, complete cds	Human mRNA for HMG-1, complete cds	601589896F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE 3944302 5	EST37301 Embryo, 8 week I Homo seplens cDNA 5' end	601512435F1 NIH_MGC_71 Homo septems cDNA done IMAGE:3913737 5	601302333F1 NIH MGC 21 Homo septens cDNA clone IMAGE:3638753 5	99/1h02.r1 Soares breast 3NbHBst Homo septens cDNA ck SP-ANKB HI MAN OD1484 ANKYPIN RPAIN VAPIANT	601866926F1 NIH MGC 17 Homo sapiens oDNA done IMAGE 4109503 5	sapiens professome (prosome, macropain) 26S sub	2962e02.rd Soares retina N254HR Homo sections cDNA clone IMAGE-363578 5	ze62e02.r1 Soures retina N2b4HR Homo sapiens cDNA clone IMAGE:363578.57	ye89f04.s1 Source fetal liver spleen 1NFLS Homo sepiens MER10 repetitive element	210/1001.91 Source thefie NHT Homo earliers ADNA along 1944 CE:745300.91	Sepiens bolymerase (RNA) II (DNA directed) polyce	sapiens polymerasa (RNA) II (DNA directed) polymer	Homo sablens interferon (sloha, beta and omeda) recentor 2 (IENAR2) mBNA	12.x1 Sogres fetal lung NbHL19W Hamp septens	7 Homo sapiens glucoldinase (GCK) gene, exon 2	Homo sepiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA	Homo seplens tousled-like kinese 1 (TLK1) mRNA, complete cds
אום דייטוו ביוחדים פול	Top Hit Database Source	EST HUMAN 014	T	T HUMAN			NT						Hum.	EST HUMAN 6015	EST_HUMAN EST3	EST_HUMAN 6015	EST_HUMAN 60130	ST HUMAN SP.A	T		T HUMAN	П		Т				T HUMAN			NT
	Top Hit Acession No.	2.0E-76 AI821149.1		8.1	31660		2.0E-76 AB029004.1	11426908 NT		11437211 NT			1.0E-76 D63874.1	1.0E-76 BE798537.1	1.0E-76 AA333207.1		9.0E-77 BE410354.1 E	8.0E-77 R83144.1		4506230 NT			8.0E-77 R00245.1	-	594	4505944 NT	4504600 NT	Al204066.1	AF041015.1	5.0E-77 4557250 NT	
	Most Similar (Top) Hit BLAST E Value	2.0E-76	2.0E-78	2.0E-78	2.0E-78	2.0E-76	2.0E-76	2.0E-76	2.0E-76	2.0E-78	2.0E-78	1.0E-76	1.0E-78	1.0E-78	1.0E-78	9.0E-77	9.0E-77	8.0E-77	8.0E-77	8.0E-77	8.0E-77	8.0E-77	8.0E-77	7.0E-77	7.0E-77	7.0E-77	6.0E-77	6.0E-77	5.0E-77	5.0E-77	5.0E-77
	Expression Signal	0.97	1.23	6.21	1.40	1.6	6.47	0.75	1.91	3.53	3.58	2.38	2.38	6.12	0.72	4.53	1.4	0.92	1.09	1.74	1.91	1.91	4.02	2.4	252	2.52	8.53	3.22	2.11	1.77	96.0
	ORF SEQ ID NO:	28879	25725	30240	30390		31233	33094	33333	36045	36763	29638	29639	30849		32508		25633	29849	30854	37351	37352	31008	27370	27868	27869	25703	26969	28631	26763	28139
	Exan SEQ ID NO:	16225	13082	17622	† 2221		18329	20016	20230	22830	23521	17008	17008	18164	18927	19486	24941	12994	17221	18168	24048	24048	24925	14659	15132	15132	13064	14281	13964	14087	15400
	Probe SEQ ID NO:	3469	4114	4895	2005	5228	5531	7334	7580	10182	10839	4285	4265	5362	9150	6825	12844	182	4486	5366	11360	1380	12620	1922	2411	2411	256	1534	1214	1339	2691

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									T												T			1						T	
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens cullin 1 (CIII 1) mRNA	Homo sablens unfatility smallers and its control and its contr	Homo saplens EGF-like recedts and discordin Like domains 3 /EDit 27Dh.l.s	Homo sapiens EGF-like recents and discordin Like domeine 3 (EDLS), months	DKFZp434G1728 r1 434 (sworwn: hees) Home senions cDNA close DKFZp434G1729 F	Homo sapiens protein kinase C beta-II troe (PRKCB1) mRNA commissions	Homo sapiens hypothetical protein FL/20343 (FL/20343) mRNA	Homo saplens 3-hydroxylsobuthryl-Coenzyma A hydrolese (HIRCH) mDNA	Homo sapiens 3-hydroxylsobutyry-Coenzyma A hydrolese (HIRCH)	Homo sepiens sorting needn 5 (SNX5) mRNA	Homo sapiens sorting neeth 5 (SNX5) mRNA	Human mRNA for KIAA0209 cers, partial cds	Human mRNA for KIAA0299 gene partial ods	Human (INC-104, and KIE14 and KIE14 and KIE14 and KIE14	Human UNC-104- and KIF1A-nalated revision mRNA parent out	Home content of domein and an arrangement of the content of the co	Home series SET density and literated designations of the Carlotte (SET) MAR) mRNA	M84001.1 Weizmann Olfactory Entheline Home engine only Appendix Ap	SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY265.	9464901.11 Wetzmann Olfactory Epithelium Homo sapiens cDNA cione IMAGE:238808 5' similar to SP:S17447 S17447 PROBABI E I I CAND DINIDAN DISCENSIONAL CIONAL DINIDAN DI	PM3-MT0078-080800-005-003 MT0078 Home seniors ANA	AV784817 MDS Homo serviene CDNA About MOSDIFFA F	RC3-BN0053-170200-011-h01 RN0053 Home enters CONIA	Homo saplens CYP17 gans, 51 and	Homo sapiens CGI-79 protein (LOCS/RS4) mRNA	Homo sepiens mRNA for KIAA1415 mother cate	Homo sapiens mRNA for KIAA1415 protein, partial ods	ho43b05.x1 Soures_NPL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:3040113.3' similar to SW:GAG2 HUMAN P10264 RETROVIRIS-RFI ATED GAG POLIVED CTELLI.	tw22g02.x1 NG_CGAP_Bm52 Homo eaplens oDNA done IMAGE:2280486 3' similar to TR:065245 065245 F21E10.7 PROTEIN:	tw22g02.x1 NG_CGAP_Bm52 Homo septens cDNA done IMAGE:2260486 3' similar to TR:065245 065245 F21E10.7 PROTEIN.;
gie Exori Pro	Top Hit Dafabase Source	L	Į.	TN	LX.	EST HUMAN	NT	닏	Z	Z	Z	ΙΝ	Į.	F	Į.	LN LN	5	F		EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	L	Ę	NT	LN	EST_HUMAN	EST HUMAN	
	Top Hit Acession No.	4503160 NT	8394518 NT	5031680 NT	6031660 NT	5.0E-77 ALD43953.1	5.0E-77 M13975.1	8923319 NT	11428849 NT	11428840 NT	11421928 NT		5.0E-77 AB002297.1		5.0E-77 U37194.1		5730038	5730038 NT				-	2.0E-77 AV764617.1	_		7706315 NT		2.0E-77 AB037836.1	2.0E-77 BE044316.1	2.0E-77 AI813519.1	
	Most Similar (Top) Hit BLAST E Value	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	5.0E-77	3.0E-77	3.0E-77		3.0E-77 H65167.1	3.0E-77 H65167.1	3.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	20E-77	20E-77	20E-77	2.0E-77 A	2.0E-77 AI813519.1
	Expression Signal	0.80	0.89	2.47	2.47	2.96	0.57	0.60	128	1.28	2.48	2.48	122	1.22	3.12	3.12	1.00	1.09		0.79	0.79	3.58	1.4	1.91	1.13	5.23	1.92	1.92	1.96	0.74	0.74
	ORF SEQ ID NO:	28214	28923	30022	30023							35250	36249	36250	37716	37717	27417	27418		36050	36051	36709	26753	26844	27548	27560	28053	28054	28396	28740	29750
	Exen SEQ ID NO:	15472					19603	20393	20800	20960	22078	22078	23034	23034	24384	24384	14701	14701		22836	22836	23468	14079	14160	14816	14827	15569	15590	16758	17116	17116
	Probe SEQ ID NO:	2787	3512	4655	4655	4884	988	99	828	8288	2692	2	10388	10388	11794	11794	1965	1965		10188	10188	10785	3 30	1412	8	88	2002	200 2	4012	4370	4379

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Exon ORF SEQ Expression M NO: ID NO: Signal ID NO: 17282 0.96 0.96 17282 0.82 1.59 18652 31593 1.9 18859 31826 1.73 18859 31826 1.74 22106 35280 5.05 22106 35280 0.47 22106 35280 0.47 22106 35280 0.47 22545 35739 0.47 22545 35739 0.47 12870 25480 1.03 12870 25480 1.03 13074 25714 7.19 1554 26716 7.19 1554 26297 1.731 14649 27362 0.9 1566 28451 1.731 16806 28451 1.72 17723 29867 2.29 17732 29867 1.641 </th <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th>_</th> <th></th> <th></th> <th></th> <th></th> <th>_</th> <th>_</th> <th>_</th> <th>_</th> <th></th>							_					_	_	_	_															
Exon ORF SEQ Expression of Figures Most Similar of Log Hit Acession of Figures Most Similar of Value	bes Expressed in Brain	Top Hit Descriptor	Homo saptiens glubanic-oxaloscedic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear name amorphism misches della company of the	Series encounty minocatonatrial protein, mRNA	INSB212.51 NCI_CGAP_P12 Homo saplens cDNA clone IMAGE:1188838 similar to SW:RL29 HUMAN	P4/914 00S RIBOSOMAL PROTEIN L29. [1] :contains element MSR1 repetitive element;	601119632F1 NIH MGC 17 Homo sepiens cDNA clone IMAGE:3029436 57	at74a09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311	4770c09x1 NOI_COAP_Bm25 Homo sepiens cDNA clone IMAGE:2017360 3' similar to WP:F29011.1	CEUSTOS LOW DENSITY LIPID RECEPTOR-RLATED PROTEIN;	numan protein kinase C substrate 80K-H (PRKCSH) gene, exch 7	numan protein kinase C substrate 80K-H (PRKCSH) gene, exon 7	SOLOSO IOST TINIH MGC_19 Homo saplens cDNA clone IMAGE:4124541 5	ou loss tour 1 NIH MGC 19 Homo sapiens cDNA clone IMAGE:4124541 6	Turno septems mixiva for KIAA 1276 protein, pertial cds	remo especie minuto de Nutor 12/0 protein, pertei cds	none septens amyloid beta (A4) precursor protein (protease nextn-ll, Alzheimer disease) (APP), mRNA	formo sapiens amyloid beta (A4) precursor protein (protease nextn-II, Alzheimer disease) (APP), mRNA	forno sabiens amykirid bets (A4) was insec module (A4).	(Notes a redirect A ATRICHER (ISSES) (APP), mRNA	notive septents arrived beta (A4) precursor protein (protesse nextra-II, Alzheimer disesse) (APP), mRNA	research Sogreg_thymus_NHFTh Hamo sapiens cDNA clone IMAGE:2536160 3'	iumo supiens mitura for KIAA1101 protein, complete cds	iomo sapiens 2,4-dienoyi CoA reductase 1, mitochondriai (DECR1), mRNA	Unio saparita Col-su protein (LOC51626), mRNA	United supremises your Kild contrigues to the Care of	omo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-excry, mRNA	unio sapiens NiAA0005 gene product (KIAA0005), mRNA	Homo sapiens N/A40005 gene product (K/AA0005), mRNA Homo sapiens dynactin 1 (DCTN4) name arms 27 mul 20	DO DATE IT OWNER TO THE TOTAL
Exon No.: ORF SEQ Expression No.: Expression Signal Top Hit Top Hit Access No. 17282 0.96 2.0E-77 4504 17282 0.96 2.0E-77 4504 17282 1.59 2.0E-77 4504 17282 1.69 2.0E-77 4504 17282 1.69 2.0E-77 4504 18652 314593 1.73 2.0E-77 4804 18765 31826 1.73 2.0E-77 4803203.1 22106 35280 5.05 2.0E-77 480321.1 22106 35280 5.05 2.0E-77 480321.1 22546 36739 0.47 2.0E-77 480321.1 22545 36739 0.47 2.0E-77 4803102.1 12870 25489 1.03 1.0E-77 45021.1 13074 25714 7.19 1.0E-77 45021.1 13074 25716 7.13 1.0E-77 45021.1 15584 2629 1.02 <	gie Exon Pro	Top Hit Database Source			EST LITERAL	EST CITATA	EST HIMAN	POT LIMAN	TOWN TO LO	NAMOR 161		TOT LETANAN	TOWAN	NOW DE LE							100000	NAMA!								
Exon ORF SEQ Expression MA NO: ID NO: Signal B 17292 0.96 0.96 17282 0.96 0.96 17292 0.96 0.96 17292 0.96 0.96 17292 0.96 0.96 18652 31593 1.69 18859 31826 1.73 18859 31826 1.73 22106 35280 5.05 22106 35280 0.47 22106 35280 0.47 22545 35739 0.47 12870 25480 1.03 12870 25490 1.03 13074 25716 7.19 1554 26716 7.19 1554 26716 7.19 1554 26716 7.19 1564 2730 1.03 1566 28451 1.731 16806 28451 1.72 <t< td=""><td>uio</td><td>Top Hit Acession No.</td><td>4504088</td><td></td><td>AARSOOS 1</td><td></td><td>-</td><td></td><td></td><td></td><td></td><td>T</td><td>T</td><td>T</td><td>T</td><td>24.88</td><td>701</td><td>4502166 N</td><td>4502166 N</td><td>450246610</td><td>3</td><td>T</td><td>330</td><td>N DOCUM</td><td></td><td>3333</td><td>ZAR1840 N</td><td>7881840 N</td><td>086944.1</td><td></td></t<>	uio	Top Hit Acession No.	4504088		AARSOOS 1		-					T	T	T	T	24.88	701	4502166 N	4502166 N	45024 66 10	3	T	330	N DOCUM		3333	ZAR1840 N	7881840 N	086944.1	
Exon SEQ 1D ID NO: Signa NO: 17292 17292 17292 17292 17292 17292 17292 17292 17292 17292 17292 17223 18554 17223 18606 172870 17223 18606 172870 17223		Most Similar (Top) Hit BLAST E Value	2.0E-77		2.0E-77	2.0E-77	2.0E-77	2.0E-77	2.0E-77	2 OF-77	2.0E-77	2.0E-77	2.0E-77	1.0E-77	1.0E-77	1.0E-77	Į,	1.05-77	1.0E-77	1.05-77	1 0F-77 A	1.0E-77.A	1.0E-77	1.06-77		7	1.0E-77	1.0E-77	1.0E-77 AF086944.1	
Exon SEQ 1D NO: 17282 17282 17282 18859 18652 18859 18765 17876 17876 17870 17870 17870 17872 17873 1870 17732 1870 17732 1870 17732 17732 1870 17732 17732 17732 17732 17733		Expression Signal	0.96		.59	19	1.73	15.45	0.82	5.05	5.05	0.47	0.47	1.03	1.03	7.19	4	2	17.31	17.31	0.9	1.32	1.72	3.37	18.41	229	-	-	2.45	
		ORF SEQ ID NO:				31593	31826	32829	34259	35280	35281	36738	35739	25489	25490	25714	25745	01103	26296	26297	27360	27902	28451	29684	29851	29967	30337	30338	31561	
						L		19765	21120	22108	22108	22545	22545	12870	12870	13074	13074		15554	15554	14649	15184	15806	17059	17223	17338	17732	17732	18627	
Probe SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		Probe SEQ ID NO:	4557		4717	5865	6080	7074	8427	9428	9428	9805	9895	42	42	200	268		855	855	1912	2445	3040	4320	4488	4603	5010	5010	5839	

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Table 4
Single Exon Probes Expresse

													T			T	T	Τ												T	Γ	П
Top Hit Descriptor	Home contact of Control of Contro	Himse von Willebrand (July 1971) gene, excris 27 and 28	Home sections distill	Home sections of the Consorting, noncing 1 (DIAPH1), mRNA	Home sections called 4 (All 14), mRNA	Human mand for kidney and down a second seco	Histories DNA for Cone could be a contract (EGF) precursor	Haspiens DNA for Come caMP-DDE can	Homo saplens ful-GloAT-P mRNA for niltramference	Homo sepiens hu-GicAT-P mRNA for clina manufacture.	RC3-CT0254-280989-011-b05 CT0254 Homo sapiens cDNA	RC2-ET0023-080500-012-e05 ET0023 Homo saniens cDNA	RC2-ET0023-080500-012-e05 ET0023 Homo sepiens cDNA	AU118789 HEMBA1 Homo septens cDNA clone HEMBA1004354 5	AU118789 HEMBA1 Homo septiens cDNA clone HEMBA1002354 5	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA	Homo septens hypothetical protein FLJ11316 (FLJ11316), mRNA	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y4886A.6	Himen collection than N/O CA	Home samene Back's manifer of the Control of the Co	Homo saviens transforming a manufactured by the protein mRNA, partial cds	EST366120 MAGE resemble of MACE 11	Human haccomal alpha mamoral flows (2007)	601648061F1 NIH MGC 62 Homesenins chiva Accessing F1	OKFZ0434NR322 -1 424 (Among Huma) 11	Novel human date manching to chomesome 22	wr97b12.x1 NCI_CGAP_Kid11 Homo septens cDNA clone IMAGE:2495615 3' similar to SW:WAP PIG	United ACIDIC PROTEIN PRECURSOR;	Home separate pre-mitting splicing factor (SFRS3) mRNA, complete cds	Home septical Land (LOCAUSTB), mRNA	Home septems pricephendylmostical 4-kinase, catalytic, alpha potypeptide (PIK4CA) mRNA	Homo septens SFRS profein kinese, 2/SRBK2) — But A
Top Hit Database Source	Į.	Ę	Į	Ę	1	Ę	Ę	Ę	Z.	Ę	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	님	F	H. H.	NT	L.		EST HUMAN	LN	T HUMAN	Т	LN	T	T				
Top Hit Acession No.	1.0E-77 AF086944.1	1.0E-77 M25844.1	4885182 NT	5881412 NT	11420159 NT	1.0E-77 X04571.1	1.0E-77 X94354.1	1.0E-77 X94354.1	1.0E-77 AB029396.1	1.0E-77 AB029396.1	9.0E-78 AW753302.1	8.0E-78 AW947061.1	8.0E-78 AW947061.1		6.0E-78 AU118789.1	11432710 NT	11422486 NT	5.0E-78 AW873424.1		2	6585	T			4.0E-78 AL043314.2	4.0E-78 AL355841.1			58778	4505806 NT	4505808 NT	11420732 NT
Most Similar (Top) Hit BLAST E Value	1.0E-77	1.06-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	1.0E-77	9.0E-78	8.0E-78	8.0E-78	6.0E-78	6.0E-78/	6.0E-78	3.0E-78	5.0E-78	5.0E-78 M55586.1	5.0E-78	5.0E-78	5.0E-78	5.0E-78 U60889.1	5.0E-78	4.0E-78	4.0E-78 A	4.0E-78 Algasno4.1	4.0E-78 A	4.0E-78	4.0E-78	4.0E-78	4.0E-78
Expression Signal	2.45	4.1	0.82	21.7	1.05	0.69	0.62	0.62	3.1	3.1	2.55	3.11	3.11	1.87	1.8/	254	0.72	5.53	3.81	2.33	11.12	223	6.78	3.31	1.07	1.78	60.	2.08	1.73	2.61	2.61	1.41
ORF SEQ ID NO:	31562	31697	32120	32450	33338	33437	35000	35001	36288	36289	36328	371176	32118	20040	84007	25,050	2000	28019	28797	30789	31183	32808	34821	34822	28531	28940	27079	27779	29652	30088	30080	31391
Exen SEQ ID NO:	18627	l				20327	21835	21835	23067	23067	23032	17101	42040	2 66	2000	13024		15281	16139	18130	18287	19745	21671	21672	13872	14254	14390	15041	17027	17454	17454	18474
Probe SEQ ID NO:	5839	5956	6356	6953	7564	288	98	9165	10421	10421	3 2	200	3 3	2	RARE	222	+	2567	3380	5327	2488	7054	8981	8982	113	1508	1644	2316	4288			5681

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Single Exon Probes Expressed in Brain	Top Hit Detabase Source Top Hit Descriptor	F08773 0 1TT	1N 00 /07	Z	Z									T HIMAN	1000			T LI 164461	T	7	H MAN	Т	Т	广	Ť	Г	1		丁	HOMAN			THE INVENT	EST_HUMAN AU122163 MAMMA1 Homo saplens cDNA clone MAMMA1001786 5:	
Singl	Top Hit Acession No.	45087208181	40E-78 AE012872 4		T	11417251 NT	11580151 NT	11580151INT	4.0E-78 AF169148 1		-				07334	4507334 NT	450A328 NT	3	T	T	T		_							1507000	4507098 NT	11417304 NT		П	
	Most Similar (Top) Hit BLAST E Value	4.0F-78	4 0F-78	4 0F-78		4.0E-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78 X05844 1	4.0E-78/	3.0E-78	3.0E-78 AF095901	3.0E-78 AU140604.	3.0E-78	3.0E-78	3.0E-78	3.0E-78 BE144758 1	3.0E-78 BE156318 1	2.0E-78 LI04480 4	2.0E-78 AA311872.1	2.0E-78 AW 402306.	2.0E-78 AW 402306.	2.0E-78 BF689800.1	2.0E-78 AV714177.1	2.0E-78 AI557509.1	2.0E-78 AJ557509.1	2 0F-78 A1107837 4	2.0F-78 NA9054 4	1.0E-78	1.0E-78	1.0E-78	1.0E-78 AV648699 1	1.0E-78 AU122163.1	
	Expression Signal	0.58	2.88	286		0.6	1.96	1.96	5.18	215	3.57	1.39	1.39	86.0	0.72	96.0	0.93	5.14	1.97	2.17	1.87	1.54	1.54	3.99	2.33	1.4	4.	3.27	3.89	3.07	3.07	2.83	0.76	0.55	
	ORF SEQ ID NO:	33148		34592		35192	.36206	36207	37305	37456	31016	25810	25611		29181	29181	30430		36832			33126	33127	33405	33762	34100	34181	36952	37012	29491	29492	30655	30570	33517	
	SEQ ID NO:		21444	21444		\bot		_	┚	24146	24868	12972	12872	16460	18548	16548	17813	22834	23582	15884	16743	20047	20047	78202	25002	1700	E	23689	23738	16865	16865	18020	17934	20401	
	Probe SEQ ID NO:	7390	8752	8752		9268	10342	10342	138	11547	12517	2	19/	3/48	8	8	8 8	19186	10802	3119	3895	7367	è i	2 5	73.54 Z	38.4	+	11017	11068	4123	4123	4		1730	

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Single Exon Probes Expressed in Brain		Top Hit	n.	Source 1 op hit Descriptor		Human serine/threonine kinase MNB (mmb) mRNA complete and		EST_HUMAN wa20b08.x1 NCI_CGAP_KId11 Homo septiens cDNA clare NATE consers at	\neg	EST_HUMAN RC2-BN0074-090300-014-c12 BN0074 Homo septems cDNA	Homo sapiens mRNA for activator of S phase Kinase, complete cds	Homo sepiens ubiquitin-conjugating enzyme F2F 3 (homolooming to a conjugating enzyme F2F 3 (homolooming enzyme F2F 3	Homo septems hypothetical protein FL/20345 (FL/20345) FBNA	Homo sapiers cAMP response element-binding protein CRE ABOUT Course 120.	Homo explers cAMP response element-binding protein CRE RD- (U. DOZETI 4.5.), mKNA	Homo sapiens threony-tRNA synthetise (TARS), mRNA	Homo sepiers threony-tRNA synthetise (TARS): mRNA	Homo sepiers case'n linese il alpha subunit mRNA complete ode	Homo sepiers case'n kinase II apha subunit mRNA rampirate cus	Homo sepiens DNA for amyloid precursor profein, complete cite	Homo sepiens hypothetical protein FL 20536 (FL 1978; m. B.N.	Homo sepiens zinc finger protein 216 splice variant 1 (ZNE216) mBNA	Homo sapiens zinc finger protein 216 spiles variant 1 (ZNE216) mBNA	Homo septens TRAF6-regulated IKK activator 1 beta Uerra myn a complete cas	Homo sepiens suppressor of white epitot homolog 2 (SWAP2) mRNA	Homo saplens euppressor of white apricot homolog 2 (SWAP2); mRNA	Home seplens of noncoone 21 segment HS21C010	FOT LIMAN ANA TOTAL TOTAL (Drosophile) hamolog 3 (PER3), mRNA	Т	EST HUMAN TR:015408 Q15408 NFITTRAI DENTEASE I Anno septems CDNA done IMAGE:462558 3' similar to	Homo saplens chromosome 21 segment LECATORS	Homo saplens throughester growing II Japan Fr Japan	Homo seplents intersecting the hort Letters, mRNA	Homo septens celline to a one of the complete cds	Human since finder and the control of the complete ods	Homo seniene MSTD0.6 / Acts. 2	Home equals in St 1016 (MS1016) mRNA, complete cds	Common septents minny for KIAA0892 protein, pertiel cds
Sin		Top Hit Agestion	No.		4 OE 70 JEOUTH 4	032373.1	1.0E-78 11430460 NT	_	25891	. ,		5454145 NT	11424427 NT	11421735NT	IN 65/1/24/1	1141/260 NT	141/260			- 13	38643			11000Z/3.1	11423827 NT	8 0F-79 At 183210 2	PRETOCT LE	7.0E-79 BE619648 1			-163282.2 NT	22325	114488.1 NT	3.1	19410.1 NT			
	Moet Similar	(Top) Hit	BLASTE	Value	4 OF 70	1.00-70	1.0E-78	20.0	8/-UC.8	9.0F-79		9.05-79	8.0-1-8 20 de 1	9.0E-70	0.00	0.0E-70	0 OF 70 MODES 4	18/200	9.0E-79.30Z833.1	9.UE-/9/U8/6/5.1	9.00	9.0E-79 AF062346	0.0E-70 AV000036	9.0E-79.0	9.0E-70	8.0F-79.A	8.0F-79	7.0E-79 B		6.0E-79 AA699829.1	5.0E-79 AL163282.2	4.0E-79	3.0E-79 AF114488.1	3.0E-79 AF232708.1	3.0E-79 U09410.1	3.0E-79 AF110322.1	3.0E-79 AB020699.1	
		Expression	Signal		3 28	7 20	1 88	4 05	805	16.87	000	000	07.0	0.79	040	0.49	5.1	8.4	58	0.30	-	173	3 13	3.55	3.55	0.91	1.82	26.39		4.32	7.97	24.	1.28	3.85	1.51	5.24	1.24	
			Ö Ö			31117		30016	30166	30829	31004		33230	33240	34074	34075	34802	34803	35206	36121	36182	38183	36930	37410	37411	29115	30596	28660		37300	08515	25740	2 103	20208	L0097	30738	31345	
	i L	<u> </u>	_		20753	24565	L	17384	17542		19022	L	20148	20148	20938	20038	21652	21652	22034	22911	22985	22965	23674	24098	24098	16478	17910	16009	24400	24079	15936	13100	13735	15Ben	2000	18082	18432	
	- G	SEQ ID	Ö		8020	12045	12477	4650	4811	5346	6248	7251	7473	7473	8244	8244	8961	8961	9280	10263	10318	10318	11001	11497	11497	3725	11800	3247	11890	11478	3173	305	128	3005	1	┸	╝	
												_								<u></u>		ليا				_				Ц_	<u>_</u>	_	<u></u>		1		J	

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Table 4
Single Exon Probes Expressed in F

Single Exon Probes Expressed in Brain	Top Hit Descriptor	192143E4 NIU MCC 49 U	601489143F1 NIH MCC 68 Home Sapiens CLINA GOTE IMAGE:3884554 5	Homo serient raths 4 (NTN4) TODAY	Homo series patin 1 (NTM1) month	80112055F1 NIH MGC 16 Home section CAIA 11 CE 2010	HOTO SEMENE MRNA for KIAAAROO profess and semental and se	Homo sepiens mRNA for KIAANSOn prodein parties cos	Homo secions attended to the contract of the c	Homo septems Bci-2-associated transcription factor about 5	Homo sablens tetratricoversities repeat domain 2 (TTPs) DNIA	AV698115 GKC Homo smolens cDNA chara CKCAHE11 K	Homo saplans Bd-2-associated transcription factor about 501.4	Homo saplens Bid-2-associated transcription factor where the positive and the participants an	W4803.81 Scenes feels liver sales along the State of Stat	80158415F2 NIH MGC 63 Home emisse contact and the Contact and	Homo sapiens BCI-2-Ike 2 (BCI 2I 2) mRNA	H18h07 XI NG CGAP P/3 Home seeling DNA sign MAACE CALLEGE SI	Homo saplens Dickcoof gene 4 (DKK-4) mRNA	Homo saplens Dickoof owne 4 (DKK-4) mRNA	Homo saplans phosphordestars & CAAP specific and such Consess.	Homo sapiens phosphodiesterase BA CGMP-enevitic and either (DDEA).	Homo saplens mRNA for Fas-associated factor EAE4 (Factoring) (Control of Samuel Control of Samuel Cont	Homo expiens mRNA for KIAA0837 profession persial cyle	Homo saplens chloride channel C. C4 (CIC4) mRNA.	Homo septens mRNA for Fee-associated factor FAE1 (Feft canal)	EST182928 Jurket T-cells VI Homo sepiens cDNA 5' end similar to Similar to C. elegens hypothetical protein,	Homo sanlans X transcorder produits 9 (VTS)	Homo saviens mRNA for KIAA020 Section 2.	sanians areaches	forms seniors Bho CTBase and Carter of American Complete ods	Homo sections Rho GTDeep authorities and a Anti-CAPS), transcript variant 4, mRNA	Chicago and a second of the second of AMHGAP (1), transcript variant 4, mRNA
Single Ex	Sion Top Hit Detabase Source	FST HIMAN	EST HUMAN	11428770 NT	11426770 NT	EST HUMAN	Ł	Σ	6012455 NT	Z	10835036 NT	EST HUMAN	뉟	ž	EST HUMAN	EST HUMAN	4757841 NT	EST HUMAN	7857024 NT	724 NT	SS3 NT	4585863 NT	Ę	۲	N	١	EST HIMAN	1789 NT	Z	Ę	TN 87	IZ Q	11.4
	Top Hit Acession No.	3.0E-79 BE789470.1	3.0E-79 BE789470.1	11426	11426	3.0E-79 BE256803.1	3.0E-79 AB014520.1	3.0E-79 AB014520.1	6012	3.0E-79 AF249273.1	108350	3.0E-79 AV608115.1	3.0E-79 AF249273.1	3.0E-79 AF249273.1	163129.1	2.0E-79 BE379926.1	47578	2.0E-79 AI523747.1	78570	76570	45858	45858	2.0E-79 AJ271408.1	2.0E-79 AB023154.1	F170492.1	2.0E-79 AJ271408.1	20E-70 AA312223.1		2.0E-79 AB020637.1	F263613.1	7382479 NT	7382479 NT	
	Most Similar (Top) Hit BLAST E Value	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79	3.0E-79 /	3.0E-79	2.0E-79 H63129.1	2.0E-79 E	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79	2.0E-79 A	2.0E-79 A	2.0E-79 A	2.0E-79 A	20E-79	2.0E-79	2.0E-79 A	2.0E-79 AF263613.1	2.0E-79	2.0E-79	200
	Expression	0.83	0.93	3.58	3.56	0.67	3.35	3.35	0.78	1.61	1.33	1.24	1.62	1.52	0.99	1.6	2.28	2.09	1.12	1.12	5.93	5.83	1.07	1.09	0.83	1.09	12	0.8	1.14	0.80	1.7	1.7	90,
	ORF SEQ ID NO:	31371	31372	31392	31393	32422	32467	32458	33503	33887	35144		36694	36695		26033	26339		27228	27227	27607	27608	27852	28166	20283	29517	 -	31348	31896	30577	32822	32823	22024
-	Exen SEQ ID NO:	18457	18457	18475	18475	19408	19442	19442	20389	20758	21970	22893	23452	23462	13088	13308	13674	13772	14522	14622	14874	14874	14918	15428	10843	16886	18382	18435	18926	17041	19758	19758	NOON.
	Probe SEQ ID NO:	5662	5002	5682	5682	6646	9000	8880	7720	8084	883	10245	10768	10768	<u>ş</u>	919	8	1012	1781	1781	2144	44	7 88	2721	23	444			6149	6864		7907	L

Page 375 of 536 Table 4 Single Exon Probes Expressed In Brain

Single Exon Probes Expressed in Brain	Most Similar Top Hit Acession (Top) Hit Top Hit Acession ORF SEQ Expression (Top) Hit Top Hit Acession ORF SEQ Signal BLASTE No. Source	1108 34247 2.25 2.0E-79 11427428 NT Homo sapiens involtatical profesh Fl. 111006 (Fl. 111006), mBNA	34503 0.58 2.0E-79 8923248 NT	34504 0.58 2.0E-79 8923248 NT	34734 1.65 2.0E-79 11432184 NT	35850 1.44 2.0E-79 S72869.1 NT	35851 1.44 2.0E-79 S72869.1 NT	36627 12.34 2.0E-79 U07819.1 NT	36880 4.05 2.0E-79 BE064386.1 EST HUMAN	36881 4.05 2.0E-79 BE084386.1 EST HUMAN	30594 2.16 2.0E-79 7662357 NT	31108 5.19 2.0E-79 AB020640.1 NT	31075 2.89 2.0E-79 11418322 NT	3.76 1.0E-79 BF383071.1 EST HUMAN	33969 0.78 1.0E-78 BE394211.1 EST HUMAN	37543 2.05 1.0E-79 BF087405.1 EST HUMAN	1.8 1.0E-79 A1480115.1 EST HUMAN	28551 2.35 9.0E-80 AA725848.1 EST HUMAN	28552 2.35 9.0E-80 AA725848.1 EST HUMAN	35757 1.14 9.0E-80 BE798603.1 EST HUMAN	37199 8.68 9.0E-80 11433924 NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA	1.31 8.0E-90 U94387.1 NT Homo seplens Y chromosome snormathonness of conditions and conditions and conditions and conditions and conditions are conditions and conditions and conditions are conditions and conditions and conditions are conditions and conditions and conditions are conditions and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditions are conditional and conditional and conditions are conditional and conditional an	33268 3.07 8.0E-80 11422647 NT	33269 3.07 8.0E-80	35142 1.13 8.0E-80 6005921 NT	35143 1.13 8.0E-80 6005921 NT	26318 1.12 6.0E-80 AM22197.1 EST HUMAN	27071 2.22 6.0E-80 U64898.1 NT
																											35143	26318	27071
	Exon SEQ ID NO:	21108	21356	21356	21593	22640	22840	23389	23632	23632	17908	24548	24690	25091	20837	24220	25333	15907	15907	22561	23907	23907	16342	20175	20175	21969	21969	13640	14384
	Probe SEQ ID NO:	8415	8664	8864	8902	9882	9002	10696	10956	10956	11836	12018	12238	6492	8143	11823	12047	3143	3143	9912	11245	11245	3588	7504	7504	8302	6302	880	1638

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Single Exon Probes Expressed in Brain	Top Hit Descriptor		Homo septens mRNA for Klabattes models	Homo septems mRNA for KIAA4456 model.	Office analysis males described to the control of t	Homo seniere mRNA (* * * * * * * * * * * * * * * * * * *	Home seeing take in dynem heavy chain (DNAH9 gene)	Homo envisors (1) And	Home service that Life (All Alogar), mRNA	Homo services Committee of the Complete of the	House equals is protein-coupled receiptor 51 (GPR51), mRNA	Color explores G protein coupled receptor 61 (GPR51), mRNA	nomo sepiens cinomosome 21 segment HS21C101	riomo septens HSPC146 mRNA, complete ods	Human cone photoreceptor cGMP-phosphodiesterase alphe arbunit nessea 24	Homo seplens brefeldin A-Anhibited guantine nucleotide-exchange make 170001.21	Homo saplens Cytl9 mRNA, complete cds	Human percedsome tergeting signal 2 receptor (Perc?) mRNA committee	Homo sapiens N-acety/glucosamine-phosphate murites — Days	Homo sapiens mRNA for KIAAA747	Homo seplens mRNA for KIAA0717 protein, partial cds	8002.xf NC CGAP Bm23 Home series CONTA 42	Q16796 NADH-UBIQUINONE OXIDOREDUCTASE 39 KP STRINIT PERSONAL SW.:NUEM_HUMA	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and nitrathiums S	tes, complete cds	Homo sapiens CST gene for cerebroside suitotransferese acces 1 2 2 4 5	Homo sapiens mRNA for sodium-gluoose cotransporter (SQLT2 gens)	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and outrathione S-transfer	ves. complete cds	Homo sapiens proteasome (prosome, macropain) 26S surhanif non A Thank a Andreas	Homo septens serine-threonine protein kinasse (MNRH) mRNA	Homo sepiens serine-threoning protein kiness (ANBE) but a complete cos	H.sepiens noot gene (exon 12)	Homo sepiens chromosome 21 sectment HS21 Chbs	Human (3) mbt protein homolog mRNA	Homo saplens mRNA for KIAA 1424 mmsin	SDO BIN INCIDENT PROPERTY OF THE COS.
gle Exon Prob	Top Hit Database Source	- 1	N						Z														EST HUMAN Q1														
Sin	Top Hit Acessian No.		2981.1	2981.1	11421462 NT	A.J4044	11436736 NT	7862393 NT	6.0E-80 M18533.1	528484	11526464 INT	ĮΫ	495 1	-	44407000	6.0F-80 AF228730 4	_	T		0.0E-60/AB018260.1	6.0E-80 AB018280.1 NT			-240788 4 AIT	T	422402 .	7.7	240786.1 NT	9		100000.1	;;	T			337855.1 NT	
	Most Similar (Top) Hit BLAST E Value		9.0	6.0E-80 AB03	6.0E-80		6.0E-80	6.0E-80	6.0E-80	6.0E-80	8.0E-80	6.0E-80 AL16;	6.0E-801AF16	6.0E-8011202	6.0E-80	8.0F-80.4	6.0F-80 1.78560.4	A OF SO	9.0E-90.A	0.0E-80.A	6.0E-80 A	L	0.0E-00 A1422197.1	6.0E-80 AF240788 4	6 0F-80 AB02000	R OF BO A 14224		6.0E-80 AF240786 1	50F-80	50F-80 AE408000 4	5 0E-80 AE10820 4	5 OF 50 X	5.0C-00 A81047	5.0E-80 AL163283.2	0.0E-00 US	3.0E-80 AB037855.1	
	Expression	90,	3	80.	2/5	3.37	4.60	1.17	0.96	3.22	3.22	1.61	0.83	1.48	2.83	26.56	1.50	4	5,00		8	9	3	2.42	5.78	18		1.35	0.74	1.97	197	230	30.0	2 4	80.4	8	
	ORF SEQ ID NO:	20620	2000	24427	77.00	87/15	31882		0380	34558	34559	34761	35113	35619	36788	37138	37623	37677	37725	277726	8715	26318	+			_		30828	25983	28253	28254	-		27821	27886	223	
	SEQ ID NO:	16993	L		1	1	2 20	200	2444	C1412	21412	27008	21938	22412	23541	23862	24297	24347	24392	24392		13649	-	25217	24679	25341		25051	13354	13586	13586	13920	14186	15083	15152		
	SEQ ID NO:	4252	4252	5712	5084	8135	27.75	2330	8733	8773	27.50	8 8	ROZA	9761	10861	11187	11702	11756	11802	11802		11906	 	12028	┙	12707		┙				1100	1439	2361	2431	J	

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Single Exon Probes Expressed in Brain	Most Similar (Top) Hit Acession Database BLASTE No. Source Source	7 5.0E-80 4504292 NT Homo sapiens H3 histone family member 1 (H3E1) mRNA	5.0E-80 AB019038.1 NT	5.0E-80 AB019038.1 NT	5.0E-80 AL163268.2 NT	5.0E-80 8910233 NT	4.0E-80 F25915.1 EST HUMAN	3.0E-80 AL163210.2 NT	3.0E-80 BF085009.1 EST HUMAN	3.0E-80 BE817465.1 EST HUMAN	3.0E-80 A1081675.1 EST HUMAN	2.0E-80 R35321.1 EST HUMAN	2.0E-80 AI444821.1 EST HUMAN	2.0E-80 AL043116.2 EST HUMAN	2.0E-80 AA582952.1 EST HUMAN	2.0E-80 11421930 NT	2.0E-80 175215.1	2.0E-80 AW964270.1 EST HUMAN	Т	2.0E-80 AA393362.1 EST HUMAN	1.0E-80 AL163303.2 NT	1.0E-80 AF231920.1 NT	1.0E-80 A1732866 1 FST HIMAN	1.0E-80 4557810 NT	1.0E-80 BE386615.1 EST HUMAN	1.0E-80 L10347.1 NT	1.0E-80 5174540 NT	1.0E-80 AJ224172.1 NT	1.0E-80 A1948731.1 EST HUMAN	1.0E-80 A1948731.1 EST HUMAN
Single Exc		4504292 NT	-	-	Γ	0233	EST	NT	L		_			2	-	421930 NT		-		_	Γ		FST	57810 NT			5174540 NT	2.1 NT		
			AB0190	AB0190	AL1632		F25915.	AL1632	BF08500	BE8174	A109167	R35321	AI44482	AL04311	AA5829		175215.	AW9842	AJ00737	AA39336	AL16330	AF23192	A1732856		BE38661	L10347.1		AJ22417	Al948731	Al948731
	Most Simila (Top) Hit BLAST E Value								3.0E-90					2.0E-80	2.0E-80	2.0E-80	2.0E-80	2.0E-80	2.0E-80	2.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.05-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80
	Expression Signal	1.67	1.37	1.37	1.28	1.04	8.77	8.96	1.7	3.77	2.68	5.08	1.19	5.82	0.93	1.71	1.46	1.41	1	4.49	2.25	1.37	2.44	0.99	6.43	6.58	1.36	96.0	2.53	2.53
	ORF SEQ ID NO:		28393	29394	30244		35056		30030		31443	27238	27307	27509	32067	32496	32908	34905	35516	36705		26215		30397		31608	32174	32859	33237	33238
	Exan SEQ (D NO:	15502	16764	16764	17627	20949	21888	13023	17395	17580	18522	14530	14591	14782	19623	19474	19838	21748	22320	23463	13132	13554	14682	17778	18050	18867	19175	19794	20145	20145
	Probe SEQ ID NO:	2797	4018	4018	4900	8255	9157	211	4881	4850	6730	1790	1853	2049	8228	8813	7151	2505	8886	10780	331	8	1947	2060	5244	5881	9400	7106	7472	7472

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III DIGILI INCONTRA CARINO	D ORF SEQ Expression (Top) Hit Acession ID NO: Signal BLASTE No. Source Source	24 33960 2.84 1.0E-80 11421211 Homo sapiens protein throsine phosphatase, recentor type A (PTPRA) mRNA	34435 1.72 1.0E-80 11421211NT	34436 1.72 1.0E-80 11421211 NT	35019 1.21 1.0E-80 AF246219.1 NT	35020 1.21 1.0E-80 AF245219.1 NT	36192 0.95 1.0E-80 D63479.2 NT	38479 5.25 1.0E-80 11841278 NT	36480 5.25 1.0E-80 11641276 NT .	31051 1.57 1.0E-80 11417901 NT	31034 3.08 1.0E-80 AB020640.1 NT	36515 1.46 8.0E-81 AI251752.1 EST_HUMAN	36516 1.46 8.0E-81 AI251752.1 EST HUMAN	37048 8.46 8.0E-81 BE394525.1 EST_HUMAN	32909 3.58 7.0E-81 AI822115.1 EST HUMAN	29726 5.26 6.0E-81 BE256829.1 EST HUMAN	29727 5.26 6.0E-81 BE256829.1 EST_HUMAN	30630 2.1 6.0E-81 4501848 NT	30631 2.1 6.0E-81 4501848 NT	33253 0.97 6.0E-81 AF038660.1 NT	34989 1.36 6.0E-81 AA360017.1 EST HUMAN	37723 1.61 6.0E-81 BE396092.1 EST_HUMAN	31041 2.29 6.0E-81 BF679022.1 EST_HUMAN	31042 2.29 6.0E-81 BF679022.1 EST_HUMAN	27882 2.8 5.0E-81 BE288042.1 EST_HUMAN	34143 1.83 5.0E-81 AB007923.1 NT	34144 1.83 5.0E-81 AB007923.1 NT	35383 0.77 5.0E-81 M60316.1 NT	35384 0.77 5.0E-81 M60316.1 NT	37491 2.23 5.0E-81 9506634 NT	37784 1.3 6.0E-81 11526341 NT	26109 2.03 4.0E-81 AI521435.1 EST HUMAN	27270 1.31 4.0E-81/AW779612.1 EST HUMAN P53620 COATOMER GAMMA SI IRI INIT
		33960	34435	34436	35019	35020	36192	36479	36480	31051	31034	36515	36516	37048	32909	29726	29727	30630	30631	33253	34989	37723	31041	31042	27682	34143	34144	35383	35384	37491	37764	26109	27270
	Exon SEQ ID NO:	0 20824	1 21293]			l		\perp											l	┙		21005		_1			24423	13461	14555
	Probe SEQ ID NO:	8130	9601	8801	9185	9185	10325	10548	10548	12289	12498	10583	10583	11102	7162	4354	4354	6201	5201	7489	9136	11800	12430	12430	2214	8311	8311	9548	9548	11577	11839	686	1815

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Top Hit Descriptor	Homo sapiens mRNA for KIAA1345 protein partial Ad-	ws90h03.x1 NCI_CGAP_Co3 Hamo sepiens cDNA done IMAGE:2505269 3' similar to TR:O43815 O43815 STRIATIN	Home conduct mb3 Information	Homo services and interacting proven variant 2 mkn/A, pertial cds	Homo sacients hypothetical protein FT 120220 (FT 120220) TENNA	Home gentleme and the manual and the second	Homo saciens are varient cone 4 (ETX/4) — DATA	Human mRNA for smaked AA/7521 = -1-	Human cone choloraceator collections	Human cone photoscardor (2008) should be a supple subclinity gette, except 3.	Homo saplens mRNA for Death-sessional strain Land	Homo septeme Insteal OMA A TD described OCS	Homo seplens and Company A dehindroness ().	Homo seplens each Chentume & dehighnessees family, member 8 (ACADS), mRNA	OND SEDIENT WEST-IN FORTH SECURITY HER INTERIOR OF ALADS), THENA	Homo sepiens vesicle trafficking protein except (SECZED) mRNA	GIND SEPTIONS CALLING FROM 1 (ALCAZED) INTUNA	Homo seplens calcinetrin hading protein 1/2/AA0320/ Thrad	Homo sapiens bela-ureidomonimase (1 OC54723) mbNA	Homo seplens beta-unidornomionaes (LOCAT223), militario	Homo saplens transcobalamin II: macroculic anamie (TCNO) mDNA	Homo saplens NF2 gene	Homo seplens NF2 gene	Homo septens cullin 4A (Clil 4A) mRNA commission cole	down analysis also the first of the second s	control operator of the period	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurile growth-promoting factor 1) (PTN) mBNA	301474072F1 NIH MGC 68 Homo sepiens aDNA done IMAGE:3877121 5	301474072F1 NIH, MGC 68 Homo septems cDNA done IMAGE:3877121 5	98501.XT NCI CGAP Kid11 Homo sepiens CDNA circus IMA GE-2052324 2	Homo sapiens hypothetical protein (LOC55586), mRNA
Top Hit Defabase Source	LN LN	FST HIMAN		L	N L	<u> </u>	L	L	Ę	۶	<u> </u>	Į	5		Ę	 		5	F	5										T_HUMAN	
Top Hit Acession No.	AB037766.1	AW004608.1	AF263308 1		23209	4767893	11420544					5281	11439065	11439065	4759085	4759085	11417862	11417862	11417871	11417871	141				080		06280				8923839 NT
Most Similar (Top) Hit BLAST E Value	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	4.0E-81	3.0E-81	3.0E-81	3.0E-81	3.0E-81	L C	3.05-81	2.0E-81 E	2.0E-81 B	2.0E-81	2.0E-81
Expression Signal	3.58	0.98	228	226	1.33	1.11	0.57	3.59	3.43	3.43	6.1	1.53	0.71	0.71	3.2	3.2	3.63	3.63	1.53	1.53	4.82	12.36	12.36	1.23	5.83	8	20.0	2.87	2.87	0.71	0.8
ORF SEQ ID NO:	28580	29013	29509	29510	29733	32034	33058	34016	34271	34272	34980	35861	36935	35836	37086	37087	30731	30732	31030	31031	31004	28858	26659	27832	28400	28404	1200	20204	00707	29144	33678
Exem SEQ ID NO:	15931	16372	16881			19863	19982	1	21135			22649	22718	22718	23807	23807	25280	25280	24831	24831	24011	13003	13983	15083	15755	15755	1,500,5	15005	COC	16507	20552
Probe SEQ ID NO:	3168	3619	4139	4139	4360	7177	7299	8185	8443	843	9120	10001	10070	10070	11140	11140	11928	11928	12463	12463	12597	124	124	2371	2989	2980	7697	7627		3/30	/85/
	SEQ ID ID NO: Signal Acadesian No. Signal Value No. Signal Acadesian Value	Exch SEQ ID NO:ORF SEQ SignelExpression Signel(Top) Hit Acession ValueTop Hit Acession No.Top Hit Acession SourceTop Hit Acession SourceTop Hit Acession Source15931285803.584.0E-81 AB037768.1NTHomo sabiens mRNA for KIAA/1345 prometring Homo sabiens mRNA for KIAA/1345 prometring	SEQ ID ORF SEQ Expression Top Hit Acession Detabase Signal BLASTE No. Source So	Exon SEQ ID NO: ORF SEQ Signal ID NO: Expression Signal Signal Signal (Top) Hit BLASTE Value Top Hit Acession No: Source Source Top Hit Acession Source Source 15831 28580 3.58 4.0E-81 AB037768.1 NT 16372 29013 0.98 4.0E-81 AW004608.1 EST_HUMAN 16881 29509 2.26 4.0E-81 AF263308.1 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit BLAST E Value Top Hit Acession No: Top Hit Acession Source 15x31 28580 3.58 4.0E-81 AB037768.1 NT 16x372 29013 0.98 4.0E-81 AW004608.1 EST_HUMAN 16881 29509 2.26 4.0E-81 AF263308.1 NT 16884 29510 2.26 4.0E-81 AF263308.1 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit IBAST E Top Hit Acession No: Top Hit Acession Source Top Hit Acession Source 15831 28580 3.58 4.0E-81 AB037768.1 NT 16372 29013 0.98 4.0E-81 AW004608.1 EST_HUMAN 16881 29509 2.26 4.0E-81 AF263308.1 NT 17098 29733 1.33 4.0E-81 AF263308.1 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit BLAST E Value Top Hit Acession No: Top Hit Acession Source 15831 28580 3.58 4.0E-81 AB037768.1 NT 16837 29013 0.98 4.0E-81 AF265308.1 NT 16881 29509 2.26 4.0E-81 AF265308.1 NT 17098 2973 1.33 4.0E-81 AF265309.1 NT 19863 32934 1.11 4.0E-81 AF268308.1 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit BLAST E Value Top Hit Acession No: Top Hit Acession Source 15831 28580 3.58 4.0E-81 AB037768.1 NT 16837 29013 0.98 4.0E-81 AW004608.1 EST_HUMAN 16881 29509 2.26 4.0E-81 AF263308.1 NT 17098 29733 1.33 4.0E-81 AF263308.1 NT 19863 32934 1.11 4.0E-81 A767893 NT 19862 33058 0.67 4.0E-81 A767893 NT	Exon NO: ORF SEQ ID NO: Expression Signal (Top) Hit BLAST E 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2.26 4.0E-81 AF263308.1 NT 16882 29733 1.33 4.0E-81 AF263308.1 NT 17088 29733 1.33 4.0E-81 AF263308.1 NT 19862 33058 4.0E-81 AF263308.1 NT 20879 34016 3.59 4.0E-81 AF263308.1 NT 21135 34271 3.43 4.0E-81 AF263308.1 NT 21144 34016 3.59 4.0E-81 AF263308.1 NT 2114 34271 3.43 4.0E-81 AF263308.1 NT 2114 34272 3.43 4.0E-81 AF263308.1 NT 22649 35861 <	Exon NO: ORF SEQ ID Signal Most Similar BLASTE Signal Top Hit Acession BLASTE No: Top Hit Acession Source Source A.0E-81 Top Hit Acession A.0E-81 Top Hit Acession Source Source Source A.0E-81 Top Hit Acession Source A.0E-81 Top Hit Acession A.0E-81 Top	Exon NO: ORF SEQ Signal Expression Signal Top Hit Aceseson Acide Top Hit Aceseson Source Top Hit Aceseson Accesson Accessor Accesso	Exon NO:- ORF SEQ ID NO:- Expression Signet (Top) Hit Pub. Top Hit Accession Veliue Top Hit Accession Source Top Hit Accession Source 15831 28580 3.58 4.0E-81 4.0E-81 4.0E-81 4.0E-81 AW004608.1 AV0046	Exon NO:- 1562 ID ORF SEQ ID NO:- 1563 ID Expression Signel (Top) Hit PLASTE Value Top Hit Accession Publication Top Hit Accession Source Top Hit Accession Source 15631 22650 3.58 4.0E-81 AB037768.1 NT 16881 22650 2.26 4.0E-81 AF263306.1 NT 16881 22650 2.26 4.0E-81 AF263306.1 NT 17088 29733 1.33 4.0E-81 AF263306.1 NT 17088 29733 1.11 4.0E-81 AF263306.1 NT 17088 29733 1.33 4.0E-81 AF263306.1 NT 17088 29733 1.11 4.0E-81 AF263306.1 NT 20135 3.4016 3.58 4.0E-81 AF263306.1 NT 2135 3.4271 3.43 4.0E-81 AF263306.1 NT 2136 3.4271 3.43 4.0E-81 AF263306.1 NT 2136 3.4272 3.43 4.0E-81 AF263306.1 NT 22136 3.43 4.0E-81 AF26306.1 NT 22718 3.4683	Exon No.: ORF SEQ ID ID NO: Expression Signal Signal ID NO: Most Similar Signal Signal ID NO: Top Hit Aceesen Signal Signal ID NO: Top Hit Aceesen Signal Signal ID NO: Top Hit Aceesen Signal Signal ID NO: Top Hit Aceesen Signal Signal ID NO: Top Hit Aceesen Signal Signal ID NO: Top Hit Aceesen Signal ID NO: Top Hit Aceesen Signal ID NO: Top Hit Aceesen Signal ID NO: Top Hit Aceesen Signal ID NO: Top Hit Aceesen Signal ID NO: Top Hit Aceesen Signal ID NO: Top Hit Aceesen ID NO:	Exon NO:- 1562 ID ORF SEQ ID NO:- 16881 Expression Signal (Top) Hit LASTE Value Top Hit Aceasedn Value Top Hit Aceasedn Source Top Hit Aceasedn Aceast Aceasta Top Hit Aceasedn Aceast Aceasta Top Hit Aceasedn Aceast Aceasta Top Hit Aceasedn Aceast Aceasta Top Hit Aceasta Aceast Aceasta Top Hit Aceasedn Aceast Aceasta Top Hit Aceasta Aceast Aceasta Top Hit Aceasta Aceasta Top Hit Aceasta Aceasta Aceasta Top Hit Aceasta Aceasta Aceasta Aceasta Aceasta Ace	Exam ONFF SEQ Expression (Top) Hit Accession Signal Most Similar In Top Hit Accession Top Hit Accession Source Signal Top Hit Accession In No. Top Hit Accession Source Signal Top Hit Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Accession Acces	SEQ ID ID NO: Signed Clap Hit Accession C	SEQ ID ID NO: Signel BLASTE No. Delabase Source Value IGS A.OE-81 AB037768:1 NT Delabase Source Value IGS A.OE-81 AB037768:1 NT IGS A.OE-81 A.	SEQ ID ID NO: Signal I	FEAT SEGN CREEK SEC Expression Most State Most State Most State Top Hit Accessed Top Hit A	ECD NO. CREATION (CREATION AND CASE) HIS ADDRESS Top-HIS ADDRESS

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SEQ ID ID NO: Signal Most Similar Top Hit Acesskn Top Hi	ses Expressed in Brain	Top Hit Descriptor	33/3 Human ratina cDNA randomly primed sublibrow Liberto contract Chair	EST372729 MAGE resequences, MAGF Homo serviers CDNA	2k45h09.r1 Soares_pregnent_uterus_NbHPU Homo sepiers cDNA clone IMAGE:485825 5' similar to PIR:552437 S52437 CDP-discutationary seathers for the first first	124504.vf NCI CGAP Bin52 Home sentence child close 144.0E: 2004.vf NCI CGAP Bin52 Home sentence child close 144.0E: 2004.co cit	Human acontrate hydratase (ACO2) gene even 3	Homo sapiens polymerase (DNA directed) gamma (POLG) mRNA	Homo septens polymerase (DNA directed), gamma (POLG), mRNA	285406.11 Sourse, NHHMPu_S1 Homo septens cDNA done IMAGE:882475 5' similar to SW:PRI2_HUMAN P49643 DNA PRIMASE 58 KD SI IRI INIT:	Homo saplens arm-repeat protein NPRAP/narmilingin (CTNNDs) mBNA	Homo sapients arm-repeat number NDRAB/host requirems (CTINID) — DAM	602137864F1 NIH MGC 83 Home series ANNA Ama NA ACC 477462 E	Homo sablens phosphodiesterase 10, calmort illn Janaphant (2000) (DDE 40)	Homo sapiens phosphodiesterase 1C. calmodulin-denember (70kD) (DE1C), months	Homo saplens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)	Homo sepiens polymenase (DNA directed) gomme (DNI O)DNA	201645051F1 NIH MGC 58 Home continue (1 CLG), III UNA	301645051F1 NIH MGC 58 Homo serviere CDNA Actual MACE 2830228 5	301343180F1 NIH MGC 53 Homo serdens cDNA clans IMAGE: 3830226 0	901.4406.s1 Strategene HeLa cell s3 937216 Homo septems cDNA clone IMGE:856427 3' similar to SW:YB36 YEAST P38478 HYPOTHETICAL an EVE DOCTETAL IN PROCESSES	REGION.;	301577339F1 NIH_MGC_9 Hamo septens cDNA done IMAGE:38382980 51	301577339F1 NIH MGC 9 Homo saplers cDNA clone IMAGE-383898 E	2M3-NN0069-140400-147-412 NN0069 Homo sepiens cDNA	John septens goldin-ilke protein (GLP), mRNA	MR0-CT0008-250599-019 CT0008 Homo sapiens cDNA	4R0-CT0006-250569-019 CT0006 Homo saciens cDNA	:ST372729 MAGE resequences, MAGF Hamo sepiens cDNA	101867714F1 NIH _MGC_17 Homo saplens aDNA clone IMAGE:4110459 5	formo sapiens phorbolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2) mRNA	Jomo saplens HSPC288 mRNA, partial cds
Exon NO: CRF SEQ ID NO: Expression Signal (Top) Hit Palsa Top Hit Acess No. 1 14149 26829 1.13 1.0E-81 W.28638.1 1 15397 26937 1.07 1.0E-81 W.28638.1 1 17335 29984 6.89 1.0E-81 AA040370.1 1 17335 29984 6.89 1.0E-81 AA040370.1 1 18075 30704 4.1 1.0E-81 AA040370.1 1 18075 30704 4.1 1.0E-81 BE047986.1 1 18075 30704 4.1 1.0E-81 BE047986.1 1 1824 30705 4.1 1.0E-81 BE047986.1 1 18274 30705 4.1 1.0E-81 H1420 1 18274 30705 4.1 1.0E-81 H2404 1 1927 32218 0.59 1.0E-81 H2404 1 9221 32218 0.59 1.0E-81 H24056.1 22328 3524 0.05 1.0E-81 AA030784.1 22328 3524<	gle Exon Pro		EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Ę	F	Ę	EST HUMAN	E	¥		Ί.	¥			T HIMAN	HUMAN	HUMAN				HUMAN	HUMAN		Г	Г	Γ	T_HUMAN		
Exon NO: ORF SEQ Expression (No: 10 No:		Top Hit Acession No.	W26539.1	AW960658.1	AA040370.1	BE047996.1	U87928.1	11432966	11432966	AA255569.1	J52351.1	J52351.1	3F674841.1	11420965	11420965		32966									8923636			_		18138	
Exon ORF SEQ Express No:		Most Similar (Top) Hit BLASTE Value	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81	1.0E-81		1.0E-81	1.0E-81 B	1.0E-81 B	1.0E-81	1.0E-81	1.0E-81 A	1.0E-81 A	1.0E-81 A	1.0E-81 B	1.0E-81	8.0E-82 A
Exen ORI NO: 10 ID NO: 14149 17214 17214 17214 17214 17214 17214 17214 1836 1836 1836 1836 1836 1836 1836 1826 1826 1826 1826 1826 1827 1826 1927 1927 1927 1927 1937 2236 233 236 2350 332 236 332 2370 332 24108 3270 3270 3270 3270 3270 3270 3270 3270		Expression Signal	1.13	1.07	3.56	68.9	4.69	4.1	4.1	0.85	3.47	3.47	1.81	0.59	0.59	0.87	8.45	5.09	5.09	5.06		65.	3.27	3.27	1.59	2.9	1.97	1.97	1.72	86.	4.13	3.0
		ORF SEQ ID NO:	26829	28037	29839	29964			30705	30922	31273	31274	31796	32218	32219	32416	33444	35523	35524	35715		35863	35865	35886	38289	36787	36966	36967	28037	37421	31093	25452
Probe SEQ ID NO: 1402 3844 4473 3844 4600 5269 5269 5269 5269 6639 10005 11029 11029 11029 11029 11029 11240 11507 12132			L.]					ł	-	18214	18365	18385	18834	19221	19221	19401	20333	22328	22328	22519		22661	22053	22653	23061	23540	23700	23,700	16397	24108	24822	12839
		Probe SEQ ID NO:	1402	3644	4479	4600	5157	5269	6289	5415	929	5568	6054	6453	853	6639	7669	9676	9676	6986 6		10003	2002	10005	10405	10860	11029	11029	11240	11507	12132	121

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Table 4
Single Exon Probes Expressed in Brain

		\neg		Т	Т		_	_	_	_		_				 _			_					_			- 4	iali
Top Hit Descriptor	Homo serviene HSDC298 mDNA Anticl als	Human CREBA cars, narrial cde	Human CR-FB4 cene hartist cyte	Human CRFB4 cane partial cds	Homo sepiens mRNA for KIAA1327 protein partial cots	Homo sepiens glutathione percoddase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA	from series headhalted FI 199464 /FI issued /FI issued	MACAGASTE NIH MOC 68 U. C. C. C. C. C. C. C. C. C. C. C. C. C.	ALTAMOSTI FINIT MINO OF THE SECOND SINITED SECOND SINITED SECOND SINITED AND SECOND SINITED AND SECOND SINITED AND SECOND SINITED AND SECOND SINITED AND SECOND SINITED AND SECOND SECOND SINITED AND SECOND	8888904 s1 Statemene exhim brain 244 Lorens Collection Collections	m69e11.51 NCI CGAP Cos Homespries CNA close MACE costos of	Homo septems with the third in section 1 months of the septems with the septems with the septems of the septembs of the septemb	OV2-HT0540-120000-382-098 HT0540 Long and Land All A	QV2-HT0540-120900-362-008 HT0540 Home series CNA	Human von Willebrand factor dene even o	wp75e09.x1 NC]_CGAP_Brn25 Home sepiens cDNA clone IMAGE:2467624 3' similar to TR:075276 075276 PtD1 :	Homo secients mesenilin-1 degle errors 1 and 2	forms sentional basis (AA) resources	RC2-RN0120-01040-013-00-00-00-00-00-00-00-00-00-00-00-00-00	Homo seplens transforming norwith factor being artifucted, through Lindia.	Avec see 1 (1 AB 1), INCNA	100 in Saprens anymou bear (A4) precursor protein (proteinse nextrali, Alzheimer disease) (APP), mRNA	PLOS DITAGES, SESUE MAY I DATE SEPTEMBER CLIVIA CONE 1343648 3'	However I out of 1 and 1	PCH and septents of the septent HSZI (ABS)	NO. 1-DINGUES-250/100-018-504 ENGOOD Homo septems cDNA	Homo septens adenyate cyclese activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA Homo septens neumboratio transfer to	The companies included the Cyricalite Annas as receptor, type 2 (N I RK2) mRNA
Top Hit Deterbase Source	LN TN	Į.	Ę	Į.	NT LN	5	5	FST HIMAN	ST HIMAN	EST HUMAN	EST HUMAN	NT.	EST HUMAN	EST HUMAN	Į.	EST HUMAN	IN		HIMAN			T	Т	T	FINAN	NOMOLI		
Top Hit Acessian No.	8.0E-82 AF161406.1			8.0E-82 U08988.1	8.0E-82 AB037748.1	EV15601 NT	8923432 NT					4.0E-82 AF081484.1				4.0E-82 AI937300.1	2	2168		74702	45021AR NT	3.0E-82 AA725848 1		T		5	5453811 NT	
Most Similar (Top) Hit BLAST E Value	8.0E-82	8.0E-82	8.0E-82	8.0E-82	8.0E-82	8.0E-82	8.0E-82	7.0E-82	7.0E-82	7.0E-82	5.0E-82	4.0E-82	4.0E-82	4.0E-82	4.0E-82 M25833.1	4.0E-82	4.0E-82	3.05-82			3.0F82	3.0F-82	3.0E-82.A	3.0E-82	3.0E-82.R	3 05 80	3.05-82	
Expression Signal	245	1.1	283	0.84	1.42	1.43	0.9	1.7	1.2	1.71	0.71	49.82	0.8	0.8	0.65	11.61	5.05	21.65	3.11	5.7	10.65	18.58	125	3.44	191	2	2.52	
ORF SEQ ID NO:		25704			26907	27089	29585		28218	37682	29473	27103	30915	30916	31381	37633		25721	26110	26203	26290	-	26758	26881	27341	27459		
SEQ ID NO:	12839	13065			14221	14400	16960	14180	15474	24350	16847	14412	18208	18208	18466	24310	24773	13079	13462	13542	13620	13799	14082	14197	14631	14735	16028	
Probe SEQ ID NO:	104	257	795	867	1474	1654	4210	1433	2769	11759	4194	1666	2400	5409	5671	11718	12374	271	687	770	820	1039	1333	1460	1894	2000	3266	

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			7	T	T	T	7	7		7	7		٦	\neg	1			П	7	7	Т	T	T	Т	T	T	T	T	Ť	7	- " .	'' '
Single Exon Probes Expressed in Brain	Top Hit Descriptor	2n93b04.r1 Stratagene lung cardinoma 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to SW-PAGT ROVIN Onzest bot vocative at a contract of the contract	Homo seciens and circuits with transmembrane domains 4 (ANICTALIA).	Home sections contactin 8 (CNTNS) mRNA	Horro saciers contectin 6 (CNTN6) mRNA	Homo septens mRNA for KIAA1077 protein partial cds	Homo series mRNA for KIAA1077 protein water and	Homo seciens mRNA for KIAA0990 protein partie Ale	Homo sapiers mRNA for KIAA0000 protein pertial cus	DKFZ0434M117 rt 434 (swooner: https://htms.endine.com/	Homo septeme DNA for smiled amount of the control o	Homo seniers although receipt brown, complete cos	Home sentence mDNA for KIAAAMS ——————————————————————————————————	Homo society mRNA for KIAA1008 protein period	Homo sepiens wheat (WBSCR1) and wheats (WBSCR5) genes, complete ods, alternatively spiroed and	Industrial industrial Caudinates (REC2) gene, complete cds	Home sevices times to the control of	Homo septents united to the KIA & 0.727 models and A.A.	Homo septens FAM4A1 solice variant a (FAM4A1) mbNA	th/21g05x1 Sogres NFL T GBC S1 Homo senions con a characteristics	Homo saplens hypothetical protein FLI20128 (FLI20128) mRNA	Homo sepiens sit (Drosophile) homolog 3 (SLIT3), mRNA	Homo saplens microrchidia (mouse) homolog (MORC), mRNA	Homo sapiens microrchidia (mouse) homolog (MORC) mRNA	Human endogenous retrovirus-K, LTR U5 and gen gene	Human endogenous retrovirus-K. LTR U5 and oan oans	Homo saplens leucy/cystiny aminopentidese (1 NDED) mRNA	Homo saplens feucy/cystiny aminopedidese (I NPED) mRNA	Homo saplens CAGF9 mRNA, partial cds	Homo saplens CAGF9 mRNA, partial cds	Homo sapiens EGF-like repeats and discoidin Filles domains 3 (EDII 3) mRNA	#34.440 = 4 C
gie Exon Pro	Top Hit Detabase Source	EST HUMAN	Z	Z	Z	ΝŢ	N	¥	Z.	EST HUMAN	LV.	<u> </u>	Į	Ž	5	5	15	Į.	F	EST HUMAN	1	5	5	=	Į	Z Z			Z	F		TANKE TO LOU
Sin	Top Hit Acession No.	3.0E-82 AA135979.1	25206	11432889 NT	11432889 NT	3.0E-82 AB029000.1	Γ		2.0E-82 AB023216.1			4504116	2.0E-82 AB029019.1			7580	4507580 NT	2.0E-82 AB018270.1			8923130 NT	11321570 NT	7657340 NT	7657340 N			11417191 NT	11417191 NT			5031660	
	Most Similar (Top) Hit BLAST E Value	3.0E-82	3.0€-82	3.0€-82	3.0E-82	3.0E-82,	3.0E-82	2.0€-82	2.0E-82)	2.0€-82,	2.0E-82 D87675.1	2.0€-82	2.0E-82/	2.0E-82/	2.05-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82	2.0E-82 Y08032.1	2.0E-82 Y08032.1	2.0E-82	2.0E-82	2.0E-82 U80736.1	2.0E-82 U80736.1	2.0E-82	2 OF ROINDADED 4
	Expression Signal	96.0	3.14	0.88	0.88	3.23	3.23	2.55	2.55	1.21	1.25	1.17	1.01	1.01	2.85	1.46	1.46	5.85	4.73	0.91	0.85	2.16	0.45	0.45	1.84	187	1.27	1.27	4.45	4.45	1.91	1.58
	ORF SEQ ID NO:	30216	33878	34287				25990			29210	29575	29890	29891	30172	30352	30353	30874	31827		33482	34035	34397	34398	35870	35871	37187	37188	37233	37234	37670	
	Exan SEQ ID NO:			\Box				13363	13363	14425	16578	16949	17256	17256	17547	17742	17742	18184	18861	25426	20369	20898	21260	21200	22657	22657	23900	23000	23940	23940	24341	24508
	Probe SEQ ID NO:	4964	8052	8454	8454	9724	9724	88	283	1681	3827	4208	4521	4521	4816	5021	5021	5384	6082	7581	7705	8204	8 8	8008	10000	900	11237	11237	11279	11279	11750	1857

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		Γ	Γ	Τ	Τ	Γ	Γ	Τ		Τ	Γ	Τ	Τ	Τ	Τ	T	Τ	_	ø		Γ	Γ				7		Γ	Γ	٦	_	Γ	Τ	Τ	\Box
Ongle Lyon Flores Lypessed III Dialli	Top Hit Descriptor	201g09.r1 Source_fetal_liver_spleen_1NRLS_S1 Home septens dDNA clone IMAGE:429568 5	Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA	Homo eaplens melanoma differentiation associated protein-5 (MDA5), mRNA	601510859F1 NIH_MGC_71 Hamo sapiens cDNA clane IMAGE:3912207 5'	RC4-BT0310-110300-015-f10 BT0310 Hamo sepiens cDNA	Homo eaplens mRNA for KIAA0538 protein, partial cds	Homo sapiens mRNA for KIAA1417 protein, partial cds	Homo septens mRNA for KIAA0662 protein, partial cds	UI-H-BW 1-ace f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'	Homo sepiens chromosome 21 segment HS210009	602150403F1 NIH_MGC_81 Hamo septens dDNA done IMAGE:4291561 5'	601117160F1 NIH_MGC_16 Hamo sepiens cDNA clane IMAGE:3357734 5	601273346F1 NIH MGC_20 Homo septens cDNA clone IMAGE:3614362 5'	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'	QV4LT0016-271299-068-h11 LT0016 Hamo sapiens cDNA	not 2h01.s1 NCI_CGAP_Phet Homo sepiens a DNA done IMAGE:1100497 3' similar to contains Alu	repetitive element;	7p37a07.x1-NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:3647893 3' similar to TR:09Y316 09Y316	D/207H1.1;	Homo sepiens KIAA0100 gene product (KIAA0100), mRNA	Homo sepiens transcription factor CA150 (CA150) mRNA	Homo espiens transcription factor CA150 (CA150) mRNA	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29	hi31h03.xf Sogree_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE:2833525 3' similar to	SWITBER TAEN P4441 HTPOINEICAL PROTEIN HIGGS.:	QV4-ST0234-181199-037-f05 ST0234 Homo septens cONA	Homo septens chromosome 21 unknown mRNA	Homo septens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA,	and varieties products	Homo septiens hyperion gene, econs 1-50	Homo sepiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA	Homo septens myomesin (M-protein) 2 (166kD) (MYOM2), mRNA	Homo septems pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
פופ בייטוו רוטג	Top Hit Database Source	EST_HUMAN	IN	N	EST_HUMAN	EST_HUMAN		IN	LN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN		EST_HUMAN	NT	NT	LN	NT		ESI HOMAN	EST_HUMAN	NT	<u> </u>	Z	NI	NT	NT	TN	L
	Top Hit Acession No.	2.0E-82 AA011278.1	11418097 NT	11545921 NT	1.0E-82 BE885106.1	1.0E-82 BE064386.1	1.0E-82 AB011110.2	1.0E-82 AB037838.1	1.0E-82 AB014562.1	1.0E-82 BF515938.1	1.0E-82 AL 163209.2	9.0E-83 BF672220.1	9.0E-83 BE253347.1	8.0E-83 BE383973.1	V66951.1	7.0E-83 AW385529.1		7.0E-83 AA584655.1		7.0E-83 BF221813.1	11426657 NT	5720753 NT	6729763 NT					6.0E-83 AF231919.1		88	AJ0107/0.1	11422024 NT	4505314 NT	11430647 NT	11430647 NT
	Most Similar (Top) Hit BLAST E Value	2.0E-82	2.0E-82	1.0E-82	1.0E-82	1.0€-82	1.0E-82	1.0E-82	1.0E-82	1.0E-82	1.0E-82	9.0E-83	9.0E-83	8.0E-83	8.0E-83 N66951.1	7.0E-83		7.0E-83 /		7.0E-83	7.0E-83	7.0E-83	7.0E-83	6.0E-83 M33320.1	100	0.0E-83 /	6.0E-83 /	6.0E-83 /	100	9.05		6.0E-83	6.0E-83	6.0E-83	8.0E-83
	Expression Signal	3.47	1.95	1.14	0.77	3.1	1.26	1.13	0.59	1.17	2.34	4.51	0.53	3.33	5.63	0.97		1.88		6.68	0.58	1.4	1.4	1.98		0.	0.71	1.08	0	2.02	1.52	2.27	2.85	2.34	2.34
	ORF SEQ ID NO:			25985		26879	26880	34578	35390		36576	34449	38039	28816	27115	26759					31702	37634	37635	25826	7000	47717	28432		77900	1400	316/4	33160	35413	35517	35518
	Exen SEQ ID NO:	24844	25029	13358						22793	23337	21307	22822	14139	15523	14084		15635		17497	18742	24311	24311	13179	44630	14041	15783	15812	200	3	18/19	20079	22228	22321	22321
	Probe SEQ ID NO:	12485	12775	678	1186	1263	1284	8841	9553	10145	10646	8615	10174	1392	1678	1335		2868		4765	2960	11717	11717	394	ļ	8//	3017	3048	2	1170	2833	7401	9675	6996	886

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		810 3' similar to contains	nsferase theta 1 (GSTT1)			ú						rijugating enzyme E2D 3		Mirus ERV9			similar to TR:Q92814	similar to TR:Q92614		295823 3'		SHEET	· saved	NA, perties cds		P tool	A1 and B1	4	- J1 - 4)	radi Tand
Single Exon Probes Expressed in Brain	Top Hit Descriptor	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cONA clone IMAGE:840810 3' similar to contains THR.tz THR receifting element	Homo sepiers glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	Human suscipale deby throughout	Homo septens 26S prohesome recultables cultumit (SLICA) — Data	Novel human gene manning to chompens V	Homo seciens decomponiches (ICNASE) "DNA	Homo seciens catalase (CAT) mena	Homo sepiens catalana (CAT) minut	Homo seniore FOE III - III III III III	Home serions ECF that repeats and discolor life domains 3 (EDIL3), mRNA	Horno septems mannosidese, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(CDE.LLJ.) genes, complete ode	np87c07.st NCI_CGAP_Thyr Hamo sepiens cDNA clone IMAGE:1133292 similar to compine THR 12 THR	repetitive element;	off 3e06 xt Scares_testis_NHT Homo septens cDNA clone IMAGE:17556823*	oro4g03.81 Sogree_testis_NHT Hamo septens cDNA clone IMAGE:1621592.3' similar to TR:092814 092814 MYELOBLAST KIAA0218	ot64g05.s1 Sources, teads, NHT Homo saplens aDNA dane IMAGE:1621592.3' similar to TR:092614	TOURS OF SOME SALE	ROSETIONA 280800 049 L42 ETAGAS 1.	Homo septens sel (Drescobile III.s 1/04) 147 - Date	Homo especial chicago interpretation (CALLI), MINA	Homo espision benefit and the segment HSZ1C002	Homo saniens entrein second (CD34) mRNA, pertial cds	Homo sabians enturing recording protein ASB-2 (LOCS1676), mRNA	Himen cercinombrania	Homo seniers manufactured and gene terminy member 18 (CGM18) gene, exons A1 and B1	AN 4507482E4 MILL MOC 74 L	Homo sapiens F-hor provide ENDI (ED 20) - DAIA	Homo septens F-box protein Fb3b (FBL3B) mRNA, partial cds
gie Exon Pro	Top Hit Detabase Source	EST HUMAN	L	LN	N	N	F	Z	Z	Ę	5		EST HIMAN		EST HUMAN	EST HOMAN	EST_HUMAN	Ι	Т	Т								T HI MAN	NUMO: 1	
200	Top Hit Acession No.	6.0E-83 AA486105.1	6.0E-83 AF240786.1	5.0E-83 U17883.1		5.0E-83 AL133207.2	4885190 NT	4557013 NT	4557013 NT	5031660 NT	5031680 NT	4.0E-83 AF224A80 1	T			3.0E-50 AIZ1/223.1	2.0E-83 AA993492.1	2.0E-83 AA993492 1		2	20834	2.0E-83 AL 163202 2		8398	7706398 NT		428081	2.0E-83 BE885401.1		П
	Most Similar (Top) Hit BLAST E Value	6.0E-83	6.0E-83	5.0E-83	5.0E-83	5.0E-83	5.0E-83	5.0€-83	5.0E-83	6.0E-83	5.0E-83	4.05-83	3.0E-83	8	3.0E-80	9.0E-90.	2.0E-83	2.0E-83	2.0E-83 N 0 6951 1	2.0E-83	2.0E-83	2.0E-83	2.0E-83 A	2.0E-83	2.0E-83	2.0E-83 U06679.1	2.0E-83	2.0E-83 B	2.0E-83A	2.0E-83 AF129533.1
	Expression Signal	2.53	4.27	2.03	1.55	1.18	0.77	11.53	11.53	1.07	1.07	1.72	4.9	2,	2	70.0	1.88	87	4.07	1.1	1.89	0.7	4.11	6.14	6.14	6.0	0.85	1.31	1.12	6.38
	ORF SEQ ID NO:					28022	20275	30350	30351	30428	30429	26039				-	27240	27241	27365	28288			29668	29968	29969	30620	31468	31603	32423	33005
	SEQ ID NO:	24117				16382	18636	17741	17741	17812	17812	13404	13742	15485	19250		.14532	14532	14655	15624	16025	16508	17041	17330	17330	17997	18547	18662	19408	20017
	Probe SEQ ID NO:	11517	11908	925	2843	3629	3886	2020	2020	5083	50 50 50 50 50	625	226	2780	6483		1792	1702	1918	2856	3383	3756	4302	284	468	5189	5755	6875	0047	7335

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Homo seplens hydrocystcyl-Coenzyme A dehydrogenese/3-ketoecyl-Coenzyme A thiolese/encyl-Coenzyme A Homo sepiens hydrocyacyl-Coenzyme A dehydrogenase/3-ketoecyl-Coenzyme A thiolass/enoyl-Coenzyme A 049908.X1 Soeres_testis_NHT Homo sepiens cDNA done IMAGE:1646431 3' similar to gb:IM84241 QM Homo sapiens amyold beta (A4) precursor protein (protease nextr-il, Alzheimer disease) (APP), mRNA AU117669 HEMBA1 Hamo septens cDNA clone HEMBA1001910 5 UI-HF-BNO-amd-h-07-0-UI:r1 NIH_MGC_50 Homo septens cDNA clone IMAGE:3081852 6 DKFZp434H0322_r1 434 (synonym: htes3) Homo saptens cDNA clone DKFZp434H0322 5 DKFZp547J135_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547J135 5: DKFZp547J135_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547J135 5: se88s03.s.1 Stratagene schizo brain S11 Homo saplens cDNA clone IMAGE:971020 3 Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end 601822080F1 NIH_MGC_75 Homo sepiens cDNA clone IMAGE:4042318 6 Homo sepiens lipopolyseccharide-binding protein (LBP) mRNA, complete cds Homo sepiens lipopolyseccharide-binding protein (LBP) mRNA, complete cds 601976023F1 NIH_MGC_21 Homo septems cDNA done IMAGE:3958853 5 Homo septens phosphorylese kinase, gamma 1 (muscle) (PHKG1) mRNA Homo septens phosphoryese knese, gamma 1 (muscle) (PHKG1) mRNA H.saplens gene for mitochondrial dodecency/ CoA delta-Isomerase, exon 3 Homo sepiens provein kinase CK2 catalytic subunit alpha gene, excn 1 Homo sapiens protein kinase CK2 catalytic subunit alpha gone, exon 1 Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA Homo sepiens mRNA for brain ryanodine receptor, complete ods Homo sapiens mRNA for brain ryanodine raceptor, complete ods Top Hit Descriptor hydretase (trifunctional protein), beta subunit (HADHB) mRNA hydrafase (trifunctional protein), beta subunit (HADHB) mRNA RC2-FN0119-200600-011-g05 FN0119 Homo septens cDNA RC2-FN0119-200600-011-g05 FN0119 Homo septens cDNA Homo sepiens KIAA0985 protein (KIAA0985), mRNA Rattus norvegicus densin-180 mRNA, complete cds Homo expiens gene for AF-6, complete ods Single Exon Probes Expressed in Brain PROTEIN (HUMAN); EST_HUMAN Top ⊞ Database EST_HUMAN EST_HUMAN EST_HUMAN Source EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN 눋 5453881 NT 4504328 NT 4504326 NT z 4502166/NT Top Hit Acession 5453881 11436448 7662349 2.0E-83 AB001025.1 2.0E-83 BF105097 4 2.0E-83 AB001025,1 2.0E-83 AF011920.1 2.0E-83 AU117659.1 2.0E-83 AW 505600.1 AF011920.1 AL1344521 2.0E-83 AB011399.1 2.0E-83 U68707.1 2.0E-83 AL 134452.1 1.0E-83 AF105067.1 1.0E-83 AF053768.1 1.0E-83 AF105067.1 2.0E-83 M22094.1 6.0E-84 BE838884.1 6.0E-84 AL042863.2 6.0E-84 BE838864.1 6.0E-84 AA778574.1 M22094.1 1.0E-83 Al027614.1 7.0E-84 BE901209.1 1.0E-83 Z25822.1 2.0E-83 2.0E-83 Most Similar 2.0E-83 2.0E-83 BLASTE 100元 1.0E-83 1.0E-83 1.0E-83 Value 1.0E-83 1.79 0.48 0.48 4.01 1.39 Expression 4.01 0.77 6.64 2.18 2.19 2.18 0.98 1.18 0.98 3.83 1.99 3.36 99. Signal 3.8 8.28 3.33 ORF SEQ 34042 35329 35328 35780 35781 35881 36682 36770 ÖΖΩ 35952 26813 26814 26874 28593 29237 29586 30184 32373 29167 26688 26687 27854 20438 SEQ ID 20438 20581 20907 20907 22147 22147 22582 22582 22664 14137 22737 14137 14189 15942 14189 16600 19359 17562 16961 16528 14021 14021 15117 17892 SEG ID 7886 8213 8213 9494 9494 9934 9834 10018 10089 10845 10753 10845 12522 1390 1380 1442 1442 3179 3850 4220 **6331** 6596 1272 2396 5160 1272

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		8	ł		1	ŀ									1		-	I	r		=		I]	L.	r	P		6	E.F
	Top Hit Descriptor	al47g03.s1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA done IMAGE:1460500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA	Homo saplens acetyl LDL receptor, SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA	PM0-LT0019-190600-004-F02 LT0019 Homo sepiens cDNA	Homo sapiens pre-mRNA splicing fector (PRP16) mRNA, complete cds	PM4-FT0054-180800-004-e10 FT0054 Hamo saplens cDNA	EST96094 Teetis I Homo sapiens aDNA 5' end	Homo sepiens chromosome 3 subtelomeric region	2439e07.r1 Stratagene INT neuron (#637233) Homo sapiens cDNA clone IMAGE:632100 5' similar to TR:0483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 10	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA	Homo sapiens mRNA for KIAA1131 protein, partial cds	Homo sepiens mRNA for KIAA1131 protein, partial cds	Homo sepiens tropomodulin 2 (neuronal) (TMOD2), mRNA	wa78c04.x1 Soares, NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN 043847 NARDILYSIN PRECURSOR;	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA	Homo sapiens protein tyrosine phosphetase, receptor type, G (PTPRG), mRNA	Homo sapiens histone descetylase 3 (HDAC3) gene, complete cds	Homo saplens KIAA0783 gene product (KIAA0783), mRNA	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo sapiens discs, large (Droecaphila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo saplens mRNA for KIAA1130 protein, partial ods	Homo saplens Bach1 protein homolog mRNA, partial cds	Homo saplens pericentriolar material 1 (PCM1) mRNA	Novel human mRNA containing Zinc finger C2H2 type domains	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo saplens X-linked Juvenile retinoschisis precursor protein (ALRS1) mRNA, complete cds	
8	Top Hit Database Source	EST_HUMAN	Ę	Ę	EST HUMAN		EST_HUMAN		TN	EST_HUMAN	NT	Z.	F	TN	EST_HUMAN	FN	FX	NT	TN	NT	NT	NT	TN	LN	Ę.	N.		LN	N	ı
	Top Hit Acession No.	6.0E-84 AA897339.1	11426718 NT	11426718 NT	6.0E-84 BE810371.1	6.0E-84 AF038391.1	6.0E-84 BE770199.1	5.0E-84 AA382811.1	5.0E-84 AF109718.1	5.0E-84 AA167678.1	11428740 NT	5.0E-84 AB032957.1	5.0E-84 AB032957.1	11433550 NT	4.0E-84 AI685321.1	4.0E-84 AP069601.2	11386168 NT	11386168 NT	4.0E-84 AF059650.1	11421326 NT	4557526 NT	4557526 NT	4.0E-84 AB032956.1	3.0E-84 AF026200.1	5453855 NT	3.0E-84 AL096880.1			3.0E-84 AF014459.1	
	Most Similar (Top) Hit BLASTE Value	6.0E-84	6.0E-84	6.0E-84	6.0E-84	6.0E-84	6.0E-84	€.0E-84	5.0E-84	5.0E-84	5.0E-84	5.0E-84	5.0E-84	5.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	3.0E-84	3.0E-84	3.0E-84		3.0E-84/	3.0E-84	
	Expression Signal	1.87	1.04	1.04	2.94	78.0	2.37	0.71	1.82	68.0	3.17	1.77	1.71	44.1	2.19	1.79	1.38	1.36	1.88	14.38	121	121	4.51	1.24	1.15	2.41		1.07	5.2	
	ORF SEQ ID NO:	30943	31282	31283	33134	33367	33789	26121		31758	37438	37570	37571-	37738	26812	30242	31168	31169	31925	33319	34647	34648	36759	26752	27401	27460		28977	29121	
	Exen SEQ ID NO:	18230	18371	18371	20053	20259	20687	13472	15779	18796	24133	24240	24249	24401	14138		18274	li	18952	20217	21601	21501	23517	13112	14688	14736		16333		
	Probe SEQ ID NO:	5431	5574	5574	7373	7591	7972	269	3013	6015	11533	11652	11652	11813	1389	4897	6475	5475	6175	7547	8808	8809	10835	308	1953	2001		3578	3731	

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Single Exton Floores Expressed in prain	Top Hit Descriptor	wu20d05x1 Source Diedkgradfe, odon, NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05083 60S RIBOSOMAL PROTEIN L18A (HUMAN);	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA	CM1-BT0795-190600-272-b08 BT0795 Homo saplens cDNA	Homo sepiens myelin transcription factor 1-like (MYT1-I) mRNA, complete cds	H. sepiens DNA for endogenous retroviral like element	ULH-BI4-ed-e-02-0-UI.s1 NCI_CGAP_Sub8 Homo septens oDNA clone IMAGE:3084963 31	UHH-BI4-ed-e-02-0-UI.s1 NCI_CGAP_Sub8 Hamo sapiens cDNA clone IMAGE:3084963 3'	y55e11.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:2093243'	qm87c09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896728 3'	Homo sepiens chromosome 21 segment HS21 0004	Homo saplens chromosome 21 segment HS21C004	AU120280 HEMBB1 Homo septems cDNA clone HEMBB1000339 5'	ym49e11.r1 Soeres infant brain 1NIB Homo sapiens cDNA clone IMAGE:51383 5 similer to SP:APOH_RAT P28644 BETA-2-GLYCOPROTEIN I	nee30a02.x1 Lupski_sympathetic_trunk Homo saptens cDNA clone IMAGE:4090251 3' similar to TR:09UGS3 Q9UGS3 DJ766G23.1;	nee30a02.x1 Lupski, sympathetic_trunk Homo saplens cDNA clone IMAGE:4090251 3' similar to TR:09UGS3 Q9UGS3 DJ756G23.1;	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	Homo septens tyrosine 3-monooxygenase/Tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA	Homo saplens complement component 5 (CS), mRNA	em85b11.s1 Strategene achizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'	601308006F1 NIH_MGC_44 Homo septems CDNA clone IMAGE:3626257 5	Homo sepiens pericentrioler material 1 (PCM1), mRNA	mv12e06.s1 NCI_CGAP_SS1 Homo seplens cDNA clone IMAGE:1239108 3'	Homo seplens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	DKFZp434N0323_r1 434 (synonym: hise3) Homo sapiens cDNA clone DKFZp434N0323 5	DKFZp434N0323_r1 434 (synonym: hise3) Homo sepiens oDNA clone DKFZp434N0323 5'	Homo saplens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3	Homo sepiens ceterrin (cacherin-essociated protein), alpha 2 (CTNNA2), mRNA	Homo saplens specide-type POZ protein (SPOP), mRNA	
gie caon Pio	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	ᅜ	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	F	F	Ę	EST_HUMAN	EST_HUMAN	TN	EST HUMAN	NT	EST_HUMAN	EST HUMAN	NT	Nī	Ι	
10 1	Top Hit Acession No.	3.0E-84 AI983801.1	2.0E-84 BE695397.1	2.0E-84 BE696397.1	2.0E-84 AF036943.1	2.0E-84 X89211.1	2.0E-84 BF511575.1	2.0E-84 BF511575.1	2.0E-84 H63370.1	2.0E-84 AI298674.1	2.0E-84 AL163204.2	2.0E-84 AL163204.2	2.0E-84 AU120280.1	2.0E-84 H22841.1	2.0E-84 BF448000.1	2.0E-84 BF448000.1	1.0E-84 AF114488.1	4507952 NT	11427631 NT		1.0E-84 BE392137.1	27197	1.0E-84 AA720851.1	1.0E-84 AJ229041.1	1.0E-84 AL043314.2	1.0E-84 ALD43314.2	1.0E-84 AJ229041.1	7656998 NT	11434422 NT	
	Most Similar (Top) Hit BLAST E Vatue			2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	2.0E-84	1.0E-84	1.0E-84	1.0E-84	1.05-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	
	Expression Signal	3.55	6.94	6.94	9.31	0.77	0.82	0.92	0.75	1.35	0.49	0.49	0.81	0.61	3	8	1.89	20.64	-	3.17	1.92	1.13	2.46	5.01	3.53	3.53	2.67	1.15	0.98	
	ORF SEQ ID NO:				28362	28378	30962	30853	32310		34118	34119	35004	35476	31100	31101	25748	25953		20685	27508	27686	29123	29752	30017	30018	29752	30483	31651	
	Exan SEQ ID NO:	23473	14829	14829	15710	15728	18238	18238	18305	20651	20978	20978	21924	22283	24643	24643	13108	13319	13478	14019	14781	14948	16486	17120	17385	17385	17128	17870	18619	
	Probe SEQ ID NO:	10790	2098	2088	2944	2962	6439	5439	6540	7956	9284	8284	9245	9631	12169	12159	304	536	703	1270	2048	222	3733	4383	1661	4651	4855	5153	6830	

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	,	1340																		4	֓֞֟֞֟֟֟֟֟֟ ֓֞֞֓֞֓֞֓֞֞֞֓֓֞֞֞֓֓֞֞֞֓֓֞֞֓֓֓֞֞֓֓֓֓֡	-			L	1	11.0	1	70		7667
Single Exon Probes Expressed in Brain	Top Hit Descriptor	uterine water channel=28 kda erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340]	Novel human gane mapping to chambers 42	Novel human dana manohing to chomosome 43	Novel human gene manoping to chomosome 13	Homo sapiens polymerase (DNA directed) slohe (PO) A) mRN/A	Homo sepiens NGFLA binding proper 1 (FR24 Hinding profess A) Alabata	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA	Homo sapiens Ce2+-binding protein CABP3 (CABP3) gene, exon 8 and partial cds	Homo sapiens ubiquitin specific protease 13 (Isopeptidase T-3) (USP13) mRNA	Homo septions ubiquitin specific professe 13 (isopeptidase T-3) (USP13) mRNA	Home services with the receptor, longrophic, AMPA 4 (GRIA4), mRNA	Homo september a mitro-handrist (ACCA) mental most (P2RXL1), mRNA Homo september 8 mitro-handrist (ACCA), mental	Homo servers chromosome 24 source 1000 0000	Homo september profesh Side mBNA complete and	Homo septems nuclear protein Skin mBNA ameniate at	Homo septiens leuparin (LDP) mena	Human plasmingen gene. econ 7	Human plasmincren nene ann 7	Hamo saciens DKF70434P211 profiein (DKF7D444D214) DNA	Homo sapiens chromosome 21 comment LC2/Chan	Homo saplens heat shock transcription factor 2 hindian protein (USE300)	Homo sapiens chromosome 21 segment HS21Chas	Homo sapiens ribosomal protein (27 mRNA complete colo	Homo sapiens MSTP030 mRNA complete cds	Homo serviene DEADUL (Ass. Cl., Als. Ass. 8 11.)	Charles Control (Aspertitus and Paypeptide 10 (RNA helicase) (DDX10), mRNA	Inomo saptens DEAD/H (Asp-Cliu-Ata-AspArlis) box polypeptide 10 (RNA helicase) (DDX10), mRNA zi62b01.r1 Soaras, tastis, NHT Hymn, septem, ANNA Alexandra, 1888 CF 20000	G1335769 GAG-POL POLYPROTEIN;	Homo sapiens chromosome 21 segment HS210084	
gle Exon Pro	Top Hit Detabase	Ę	N.	Z	LN TA	L	LN FN	LN.	LZ!	L L	2 2	1	Ż	Į.	Z	Z	Z	Z	Z	Ę	Ε	5	Ε	Z	. FZ				EST_HUMAN	뉟	
Sin	Top Hit Acession No.	1.0E-84 S73482.1	1.0E-84 AL049784.1	1.0E-84 AL049784.1	1.0E-84 AL049784.1	8393994 NT	11430846 NT	31984	1.0E-84 AF:Z24511.1	4607848 NT	11437356 NT	11417812INT	11418185 NT	9.0E-85 AL163209.2			1758669			57020	9.0E-85 AL163280.2	5901979 NT	3.2		7.0E-85 AF113210.1	11438573 NT	11400570				
	Most Similar (Top) Hit BLAST E Value	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.01-84	100.0	105.84	1.0E-84	1.0E-84	9.0E-85	9.0E-85 U51432.1	9.0E-85 U51432.1	9.0E-85	9.0E-85 M33282.1	9.0E-85 M33282.1	9.0E-85	9.0E-85	9.0E-85	9.0E-85	7.0E-85 L05094.1	7.0E-85 A	6.0E-85	28. AC		6.0E-85 AA403053.1	5.0E-85 AL163284.2	
	Expression Signal	1.41	1.66	1.66	2.32	1.26	2.42	3.05	9.05	305	1.08	234	3.2	1.06	239	2.39	0.95	1.23	1.23	3.6	96.0	96.0	1.12	1.45	4.32	3.35	3.35		1.28	1.49	
	ORF SEQ ID NO:						33229	25E40			36368		31096		26469	28470	26783	27004	27005	27108	29591	30177	30208	28530		37300	37301		37690	78/17	
	SEQ ID NO:	18875	19525	19625	19699	20049	20137	2213	17007	17900	23142	24586	24638	13712	13810	13810	14108	14319	14319	14415	16966	17565	1/385	13871	24239	23998	23998		24357	0000	
	Probe SEQ ID NO:	6097	6781	6781	7007	7369	7501	9435	0896	0696	10496	12046	12151	88	1051	1051	1380	1572	15/2	1870	4225	4824	828	1114	1042	11392	11392		11788	7707	

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Lower and the state of the stat	Roughseases 1 111 100 cardum channel alpha 1 subunit Alpha 1 Ha isoform (CACNA11) mRNA, complete cds	601458646F1 NIH MGC AR Home appliens CUNA clone IMAGE:3862402 5	Homo septens mannosidase, beta A, Iysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds.		inomo sapiens 1-type carcium channel alpha1 subunit Alpha11-a isoform (CACNA11) mRNA, complete cds	BOOGSTROET MILL MACC. 83 Hamp septens CDNA clane IMAGE:4249087 5	RC1-RThesa 13020 At 127 Press - 127 Press	Home series and a feet of the	vestande d'Access statilles au la comma subunit gene, excu 6	AND 1807AE2 NILL 1700 7 LL	Home seriese Flore series 2.7 (FROSE)	Homo septems F-box only protein 24 (FBXO24), mRNA	Homo sepiena legimal bulba substantia (1000)	Home services and seeks of the process (L. 14.7), mich	Homo earliese KIA A0772	Homo earlies (1/4 4072)	Homo septems mBNA for chosen beautiful (DNA), mRNA	Homo seplens GTP ase regulator associated with the focal adhesion kinese 2010/EALV: VIA Account	(KIAAD821), mRNA	Homo septens DENN mRNA, complete cds	Homo sepiens CGI-81 protein (LOC51108), mRNA	Homo seplens phospholipese C. ensilin (P) CE1 mBMA	Homo sapiens small nuclear ribonucle contrain polymentals Bill Cations and	Homo septens small niclear ribonic accompanies objective and properties of control of the contro	Homo saplens phospholinia exemplice month	ROI-HT0288-031/30-012-mo HT0288 U	TOTAL Services BIGE IN PRODuction and All Control Services CONA	HOTO SECIETS MINA for KIA A 1107 TO THE COMBINS 3 (EDIL3), MRNA	Homo septens mRNA for KIAA1107 protein partial cut	Homo sepiens Ran GTP asse activating protein 1 (RANGAP1), mRNA
gle Exon Pro	Top Hit Database Source	F	EST HIMAN	EST HUMAN	LN	Ę	EST HIMAN	EST LIMAN	EST HIMAN	L	EST HUMAN	EST HIMAN	L	Z	- -		: 5	5										EST HUMAN				
Sir	Top Hit Acession No.	5.0E-85.AF211.89.1	BF035674 1	5.0E-86 BF035674.1	AF224669.1	5.0E-85 AF211189 1	BF677910 1	4.0E-85 BF877910 1	4.0E-85 BE079283.1	Γ		9.1	4695	11024695 NT	11436001 NT	11422024 NT	7682309 NT	7882309 NT	-		1416870			11430889 NT	11421422 NT	11421422 NT	3.0E-86 AF098642.1		1660		4	11418177 NT
	Most Skniler (Top) Hit BLAST E Value	5.0E-85	5.0E-85 BF03567	5.0E-85	5.0E-85 AF22466	5.0F-85	4.0E-85 BF67794	4.0E-85	4.0E-85	3.0E-85/	3.0E-85 T97495.1	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85	3.0E-85 AJ404468		3.0E-85	3.0E-85 U44953.1	3.05-85	3.0E-85	3.0E-85	3.0E-85	3.0E-86/A	3.0E-85 BI	3.0E-85	3.0E-85 AB029030.1	3.0E-85 AB029030	3.0E-85
	Expression Signal	0.8	4.1	4.1	2	5.28	1.51	1.51	1.3	2.98	3.51	6.53	1.45	1.45	1.07	0.63	5.71	6.71	7.79	3	16.0	80.	0.74	3.8	0.96	0.98	0.56	1.88	2.25	1.79	1.79	1.98
	ORF SEQ ID NO:		30851	30852	37005		31797	31798		28694	27215	29646	30194	30195	30777	31737	31783	31784		23006	33504	34325	24740	34/12	35257	35258	36242	30659	37403	37742	37743	
	Exan SEQ ID NO:	17138		18166	23733	17136	18836	18836	23118	14026	14515	17019	17571	17571	3 3 3 3 3 3 3	18775	18823	18823	19553	10078	20467	200	34560	8 2 3	22085	C8077	23027	23418	24091	24408	24408	24937
	Probe SEQ ID NO:	4398	5364	5364	11063	12743	9020	8056	10472	1276	=	4280	4841	4841	23.18	2685	8043	6943	0853	7295	144	8408	244	300	9028	200	10381	10730	11490		_	12040

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Single Exon Probes Expressed in Brain Page 390 of 536 Table 4

wi67h08.x1 NCI_CGAP_Kit12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element 245703.s1 Source_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:453245 3' 801897003F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4128440 5' 801897003F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4128440 5' 245f03.s1 Soeres_fetal_fiver_spieen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3 aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3' aj88f08.s1 Scenes_penathyrold_tumor_NbHPA Homo sepiens cDNA clone IMAGE:1403559 3' Homo sapiens Taxt (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA Homo sapiens similar to rat Integral membrane glycoprotein POM121 (POM121L1), mRNA wd49d03.x1 Soeres_NFL_T_GBC_S1 Homo sepiens cDNA done IMAGE:2331461 3' Homo saplens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA qi56807.x1 NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:1860468 3' wm94d12x1 NCI_CGAP_UZ Homo septens cDNA clone IMAGE:2443607 3 801482817F1 NIH_MGC_67 Hamo septens oDNA clane IMAGE:3888021 5 801462817F1 NIH_MGC_67 Hamo sapiens cDNA clone IMAGE:3898021 5 801109738F1 NIH_MGC_16 Hamo sepiens aDNA clane IMAGE:3350553 5 801120778F1 NIH_MGC_20 Hano sapiens cDNA done IMAGE-2967690 5 801591416F1 NIH_MGC_7 Hamo sapiens cDNA clone IMAGE:3945818 5 Homo sapiene fumor endothetial marker 7 precursor (TEM7), mRNA Homo septens tumor endothettel marker 7 precursor (TEM7), mRNA Homo sepiens celcineurin binding protein 1 (KIAA0330), mRNA Top Hit Descriptor Homo explans celoineurin binding protein 1 (KIAA0330), mRNA Homo sepiens intersectin 2 (SH3D1B) mRNA, complete cds Homo sepiens galactocerebrosidase (GALC) gene, expn 15 Homo saplens epolipoprotein C-II (APOC2) mRNA Humen DNA polymerase beta gene, exons 12 and 13 Homo sepiens CGI-201 protein (LOC51340), mRNA Homo sepiens chromosome 21 segment HS21C084 Human Ku (p70/p80) subunit mRNA, complete cds Homo sepiens epolipoprotein C-II (APOC2) mRNA Homo sapiens plasminogen (PLG) mRNA Homo sapiens reelin (RELN) mRNA Human mRNA for T-oall cyclophilin MSR1 repetitive element EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN **EST HUMAN** EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST HUMAN **EST HUMAN** EST_HUMAN **EST HUMAN** Detabase EST HUMAN 五岛工 Source 눋 7706205/NT 5174776 NT Z 눌 4505880 NT z 5174775 NT 4826977 NT TN|8889998 11417862NJ Top Hit Acession 7657468 11417862 4503224 11421737 989996 2.0E-85 AL 163284.2 2.0E-85 AF248540.1 1.0E-85 BE794306.1 1.0E-85 BE6183021 1.0E-85 BE6183921 1.0E-85|AA778785.1 7.0E-86 AA860801.1 2.0E-85 AI760820.1 2.0E-85 AID14450.1 1.0E-85 BE257917.1 1.0E-85 AA778785.1 1.0E-85 BF311552.1 .0E-85 AI198420.1 9.0E-86 BE274217.1 8.0E-86 45 7.0E-86 AA880801.1 .0E-85 BF311552.1 ģ 2.0E-85 AIBB6384.1 M30938.1 I.0E-85 Y00052.1 7.0E-86 L38557.1 20E-85 2.0E-85 20E-85) 20E-85 .0E-85 20E-85 1.0E-85 2.0E-85 7.0E-86 7.0E-86 7.0E-86 2.0E-85 Most Similar 世(金儿 BLASTE Value 8.28 1.53 5.28 4.51 0.97 1.08 2.86 8.42 8.42 4.38 1.28 8.28 2.7 241 4.74 2.34 234 3.06 0.97 4.4 1.57 Expression Signal 26438 29896 35385 26824 26825 27692 29068 32008 36029 36786 36848 28346 28435 30207 27851 35528 30847 37096 31053 28346 31848 ORF SEQ 36767 36927 31053 37818 ÖZ SEQ ID 14130 14148 14146 16788 17262 15113 23599 13777 14954 17039 21843 15113 22333 23524 23524 23500 23670 24722 14158 24293 13683 **1**4063 15010 24364 24722 13683 17584 18881 18881 21335 1383 1399 2285 2392 10842 10919 10910 1399 2228 2828 3022 800 9173 10162 2392 9681 10842 2295 408 918 8843 4527 4854 10997 12050 11698 918 **6**103 6103 9880 ġ

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Homo septems similar to ectorucieotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), yz19908.r1 Sogres_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE-283478 5 Homo sapiens lysophosphatidic acid acytransferase-delta (LPAAT-delta) mRNA, complete cds Homo sapiens lysophosphatidic acid acytransferase-delta (LPAAT-detta) mRNA, complete cds Homo saplens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA Homo septems similar to transcription factor CA150 (H. septems) (LOC63170), mRNA Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete ods Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds x282112x1 NCI_CGAP_Lu24 Homo sepiens cDNA done IMAGE:2871719 3 AV722329 HTB Homo sepiens cDNA done HTBBSD04 5 hd87g08.x1 NCI_CGAP_GC8 Homo sepiens aDNA dane IMAGE_29165423" 601072594F1 NIH_MGC_12 Homo sepiens cDNA clone IMAGE:3458830 5' 601176865F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:3531953 5' 601509696F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3911303 5' 801509696F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3911303 5' tu18b02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:22513713 601072594F1 NIH_MGC_12 Homo sepiens cDNA clone IMAGE:3458830 5 Homo sepiens DiGeorge synchrome critical region gene 6 (DGCR6), mRNA Homo sepiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA Homo sepiens 24 kDe Intrinsic membrans protein (PMP24), mRNA **Top Hit Descriptor** EST378215 MAGE resequences, MAGI Homo sepiens cDNA EST177232 Jurkat T-cells VI Homo saplens cDNA 5' end Homo seplens RAN binding protein 7 (RANBP7), mRNA Homo saplens mRNA for KIAA1277 protein, partial cds Homo sapiens enteropeptidase gene, excris 20 and 21 Homo sepiens chromosome 21 segment HS21C003 Homo sapions chromosome 21 segment HS21C027 Human endogenous retrovirus, complete genome H.sapiens mRNA encoding phospholipase c H.saplens mRNA encoding phospholipase c Homo sapiens neureain III (NRXN3) mRNA Homo sepiens neuredin III (NRXN3) mRNA Homo saplens myosin X (MYO10), mRNA Single Exon Probes Expressed in Brain ARNA ANA Top Hit Database EST HUMAN **EST HUMAN** EST HUMAN EST HUMAN EST HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN **EST HUMAN EST HUMAN** EST_HUMAN EST HUMAN Source 11417012 NT 4505492|NT 5453997 NT 11526307 N 11417012 N 호 支 4758827 NT 눋 Þ 11419429NT 눋 È 6005833 Top Hit Acession 9635487 11037058 3.0E-86 AW340946.1 4.0E-86 BE295843.1 4.0E-86 BE547173.1 2.0E-86 AW998142.1 4.0E-86 BE547173.1 2.0E-86 AA306264.1 AL 163203.2 3.0E-86 AV722329.1 3.0E-86 BE886479.1 2.0E-86|AW515742.1 3.0E-86 AI659240.1 2.0E-86|AF156776.1 3.0E-86 BE896479.1 2.0E-86 AL163227.2 2.0E-86 AB033103.1 2.0E-86 AF055490.1 2.0E-86 AF156776.1 2.0E-86 N58977.1 2.0E-86 Z16411.1 2.0E-86 U84744.1 2.0E-86|Z16411.1 7.0E-86 7.0E-86 6.0E-88 2.0E-86 7.01-86 6.0E-86 6.0E-86 2.0E-86 2.0E-86 Most Simila (Top) HR BLASTE 3.0E-88 2.0E-86 2.0E-86 Value 4.98 5.14 202 1.07 3.37 259 8 1.83 121 . 8 5.09 1.55 3.54 2.64 0.00 0.47 Expression Signal 30442 30440 31208 ORF SEQ 36810 20686 31684 25660 33985 35980 36408 25660 35981 37628 26910 28911 27651 28817 30106 32478 33733 31502 ÖΝΩ SEQ ID 22310 23562 22252 23562 14020 17825 18726 22768 17823 13018 20854 22768 23180 13068 14225 13018 14225 14002 18307 24303 13190 13922 16168 20603 14917 16481 16765 17469 25098 21107 16481 18573 6696 9658 SEQ ID 10882 10882 5105 206 5944 11205 5509 8160 10120 11413 1478 1271 10120 11708 1478 2188 3410 5107 55 168 2266 3729 4737 7908 8414 Ö 280 5782 6974

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Top Hit Descriptor	Homo sepiens butyrobetaine (gamma), 2-cxxglutarate dicxygenase (gamma-butyrobetaine hydroxylasse) (BBOX), mRNA	Homo sepiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA	Homo sepiens phospholipid scramblase 1 (PLSCR1), mRNA	Homo saplens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA	Horno sepiens besic-helix-toop-helix-PAS protein (NPAS3), mRNA	Homo sepiens besic-helix-loop-helix-PAS protein (NPAS3), mRNA	Homo sepiens mRNA for KIAA1411 protein, pertial cds	Homo sepiens ribosome protein S8 kinase, 90kD, polypoptide 5 (RPS6KA5) mRNA	Homo sepiens thyrold autoentigen 70kD (Ku antigen) (G22P1), mRNA	Homo sapiens gene for AF-6, complete cds	Homo seplens NADH dehydrogensee (ublquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA	Homo sepiens fibrulin 5 (FBLN5) mRNA	Human gamma-glutamy transpeptidase mRNA, complete cds	Homo sepiens chromosome 21 segment HS21C009	Homo seplens diramosome 21 segment HS210009	Homo saplens hypothetical protein (LOC51318), mRNA	Homo septens hypothetical protein (LOC51318), mRNA	Homo saplens dramosome 21 segment HS21C100	Homo sepiens synaplojemin 1 (SYNJ1), mRNA	Homo seplens chromosome 21 segment HS210084	Homo saplens chromosome 21 segment HS21C084	qb77c09.xt Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1708128 3' similer to SW:K1CJ_MOUSE P02636 KERATIN, TYPE I CYTOSKELETAL 10;	Homo sepiens a distriberin and metalloproteinase domain 22 (ADAM22), mRNA	Homo sepiens a distritegrin and metalloproteinase domain 22 (ADAM22), mRNA	O.cuniculus mRNA for elongetion factor 1 alpha	7h85f02.x1 NCI_CGAP_Co16 Hamp septions aDNA dane IMAGE:3322779 3'	7h85f02.x1 NCI_CGAP_Co16 Homo septems cDNA done IMAGE:3322779 3'	MR0-NT0039-020500-004-e11 NT0039 Homo sepiens cDNA	L3-HT0619-060700-198-D10 HT0619 Homo septens cDNA	IL5-HT0702-160600-103-d06 HT0702 Homo saplens cDNA
Top Hit Database Source	۲	Į.	N	۲	۲	TN	Z.	TN	¥	Z	¥	¥	Ę	NT	Į,	Ę	Ę	NT	בא	L	Ŋ	EST_HUMAN	7	F	F	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	11437135 NT	11437135 NT	10863876 NT	11422084 NT	11545848 NT	11545846 NT	AB037832.1	4759051 NT	11418189 NT	2.0E-86 AB011399.1	4826855 NT	5453649 NT		1.0E-86 AL163209.2	1.0E-86 AL163209.2	7706161 NT	7706161 NT	1.0E-86 AL163300.2	4507334 NT	2	1.0E-86 AL163284.2	A1150703.1	4757721 NT	4757721 NT		1		7.0E-87 AW890336.1	7.0E-87 BF352776.1	1
Most Símilar (Top) Hit BLAST E Value	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	2.0E-86	1.0E-86	1.0E-86	1.0E-86 L20492.1	1.0E-86	1.0E-86	1.0E-88	1.0E-96	1.0E-86	1.0E-86	1.0E-86/	1.0E-86 /		9.0E-87	9.0E-87	8.0E-87 X62245.1	7.0E-87 BF063211	7.0E-87 BF063211.	7.0E-87	7.0E-87	7.0E-87 BE712961.
Expression Signal	231	2.31	0.65	1.95	2.91	291	1.15	2.64	3.07	4.28	2.28	1.5	27	1.32	1.32	0.88	0.88	5.2	1.23	2	1.37	1.81	1.7	1.7	15.93	1.79	1.79	0.57	3.4	1.15
ORF SEQ ID NO:	34307	34308	34640	35067	36210	38211	36262	36742	31027		27027	28569	28645	28689	28700	20318	29319	29589	29941	31155	31155		33105	33106	25893	27755	27756	32064	33913	33544
Exen SEQ ID NO:	21164	21164			22882	22882	23046	23503	24827	24926	14338	15923	15992	16051	16051	16878	16676	16974	17313	18264	18264	18078	20029	20029	13252	15019	15019	19079	20783	20425
Probe SEQ ID NO:	8472	8472	8801	9218	10346	10345	10400	10820	12458	12821	1592	3160	3220	3290	3290	3926	3926	4233	4578	25 25 25	11606	5272	388	7348	467	2294	\$	6307	8089	8354

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		1								mRNA								atled to, 4	1	Suppose	L _	1		4	5		C)	1	1				5	s,
	Top Hit Descriptor	DKFZp434N0323_r1 434 (synarrym: htes3) Hamo sapiens aDNA clane DKFZp434N0323 5	DKFZp434N0323_r1 434 (synonym: Mas3) Hamo sapiens cDNA clane DKFZp434NU323 b	ax59h01.s1 Soeres_NHHMPu_S1 Hamo sepiens cDNA clane IMAGE:1660657 37	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A	Homo sepiens hormonally upregulated neu tumor-essociated kinase (HUNK), mRNA	Homo sapiens hormonally upregulated neu tumor-essociated kinase (HUNK), mKNA	Homo sapiens mRNA for KIAA1081 protein, partial cds	Homo sapiens similar to SET translocation (myeloid leukemia-essociated) (H. sepiens) (LOC63102), mRNA	EST86094 Testis I Hamo sepiens cDNA 5' end	EST96094 Testis I Homo saplens cDNA 5' and	Hamo sapiens chromosome 21 segment HS21C010	Homo saplens mRNA for KIAA1414 protein, partial cds	Home sepients mRNA for KIAA0456 protein, pertial cds	Home sepiens CGI-60 protein (LOC51626), mtNA	Homo sapiens CGI-80 protein (LOC51626), mRNA	Homo sapiens myeloid/lymphold or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4	(MILLIA) MINNA FER DEL ATER BOOTEIN 24 (ETS TRANSI OCATION VARIANT 2)	ELGARENTED TROLLING TO THE CONTROL OF THE CONTROL O	CBAPTEAU31 Pediginic pre-b cer acute lyriphromesus rounding caylor 1 CCC process to a DNA done TCBAP4051	Homo sapiens tuborin (TSC2) gene, excn 10	Human von Willebrand factor pseudogene corresponding to exons 23 through 34	Homo saplens calcineum binding probein 1 (KIAA0330), mRNA	Homo sepiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2PXL1), mKNA	Homo sepiens high-mobility group (nonhistone chromosomal) protein 4 (HMC4) mixny	AU116035 HEMBA1 Homo saplens cDNA clone HEMBA1000307 5	CMO-TN0038-150800-552-h08 TN0038 Homo sepiens CUNA	RC5-HT0560-200300-031-004 HT0580 Hamo septens aDNA	601560041F1 NIH_MGC_21 Hamp septems aDNA clane IMAGE:3843730 5	601569041F1 NIH_MGC_21 Hamo sepiens cDNA clane IMAGE:3843730 5	601341383F1 NIH_MGC_53 Hamo sapiens cDNA clone IMAGE:3683348 5	
יייי ווייים פול	Top Hit Defebase Source	EST_HUMAN	EST HUMAN	EST_HUMAN	TN	F	F	NT	LN-	NT	EST HUMAN	EST HUMAN	TN	LN	NT	NT	H		IN IN	SWISSPROI	EST_HUMAN	TN	LN TN	LN.	Z	INT	. 1	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	
S. S.	Top Hit Acession No.	7.0E-87 AL043314.2	7.0E-87 AL043314.2	7.0E-87 AI081585.1	(03002.1	(03002.1	7857213 NT	7857213 NT	6.0E-87 AB029004.1	11432444 NT	AA382811.1	5.0E-87 AA382811.1	4.0E-87 AL163210.2	4.0E-87 AB037835.1	4.0E-87 AB007925.1	TN 66239 NT	TN 6029077		5174574 NT	000321	4.0E-87 BE247284.1	4.0E-87 L48524.1	4.0E-87 M80678.1	11417862 NT	11417862 NT	11417812 NT	4885420 NT	2.0E-87 AU116935.1	2.0E-87 BF378311.1	20E-87 BE175478.1	2.0E-87 BE734190.1	2.0E-87 BE734190.1	2.0E-87 BE567183.1	
	Most Similar (Top) Hit BLAST E Vatue	7.0E-87	7.0E-87	7.0E-87	7.0E-87 K03002.1	7.0E-87 K03002.1	6.0E-87	6.0E-87	6.0E-87	6.0E-87	5.0E-87	5.0E-87	4.0E-87	4.0E-87	4.0E-87	4.0E-87	4.0E-87			4.0E-87 000321	4.0E-87			4.0E-87		4.0E-87	2.0E-87							
	Expression Signal	3.85	3.85	0.61	6.65	6.65	80	0.68	2.02	4.13	1.42	1.56	1.51	13.58	1.53	1.03	1.03		1.8	2.77	£.8	0.72	3.44	1.5	1.5	2.25	277	0.83	1.28	1.47	10.34			
	ORF SEQ ID NO:	35822	Ĺ		36724				32085		26551	26551	26376			27874				30846	31695						28223	l		L				
	Exan SEQ ID NO:	22619	22810	25120	23489	23489	16273	17846	19097	23318	13891	1380	13711	13904	14750	15142	45142		16213	18162	18736	20334	23788	25268	25266	24881	15484	1_	L	17834	1	1	1	1
,	Probe SEQ ID NO:	1200	9074	10368	10806	10806	3517	5128	6327	10625	1135	12287	8	41.	2024	2421	2424		3457	5360	5054	07.07	41118	12398	12396	12541	2779	3784	4857	4007	5575	5575	6234	

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W21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE.243396 5 W21607.rl Sceres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE.243396 5 y/21e07.rl Soeres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5 Homo septens treicheal epithelium enriched protein (PLUNC) gene, complete cds Homo sepiens IQ mofff containing GTPase activeting protein 1 (IQGAP1) mRNA of50404.s1 Soares_testis_NHT Homo septens cDNA clone IMAGE:1620199.3 601176032F1 NIH_MGC_17 Hamo sapiens cDNA clane IMAGE:3531511 5 Homo septens growth factor receptor-bound protein 10 (GRB10) gene, excn 8 Homo septens growth factor receptor-bound protein 10 (GRB10) gene, exon 8 601278315F1 NIH_MGC_39 Homo sepiens cDNA clone IMAGE:3810539 6 Homo saplens EGF-like repeats and discoldin I-like domains 3 (EDIL3), mRNA Homo saptens EGF-like repeats and discoldin Like domains 3 (EDIL3), mRNA Homo septens mRNA for alpha2,3-statyftransferase ST3Gal VI, complete ods Homo seplens mRNA for alphe2,3-sialyftransferase ST3Gal VI, complete cds Homo suptens carticotropin-releasing factor type 1 receptor gene, excn 8 Homo sapiens controproprintelessing factor type 1 receptor gene, excn 8 Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds Homo seplens intersectin long isoform (ITSN) mRNA, complete cds Top Hit Descriptor Homo saplens sulfotransferase-related protein (SULTX3), mRNA Homo sapiens sulfotransferase-related protein (SULTX3), mRNA PM2-C10265-141089-001-g04 C10265 Homo sapiens cDNA PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA RC8-BN0276-050700-012-E02 BN0276 Homo septens cDNA RC8-BN0276-050700-012-E02 BN0276 Homo septiens cDNA AV654143 GLC Hamo sapiens aDNA done GLCDSG043 Homo sapiens hect domain and RLD 2 (HERC2), mRNA Homo sepiens protein kinase C, beta 1 (PRKCB1), mRNA Homo sapiens hect domain and RLD 2 (HERC2), mRNA Human cyclophilin gene for cyclophilin (EC 5.2.1.8) Homo sapiens RGH1 gene, retrovirus-like element Homo sepiens neuredn III (NRXN3) mRNA Human mRNA for T-cell cyclophilin Human L-plastin mRNA, 5' end Single Exon Probes Expressed in Brain EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** Database 平安里 **EST_HUMAN** EST HUMAN EST_HUMAN Source 11433046|NT 互定 F 눋 11431690 NT Y Ę 눋 z 눋 5031660 NT 5031690 NT 7657632 NT 7657632 NT Top Hit Acession 4506786 4758827 6729867 1.0E-87 AW381977.1 1.0E-87 AW361977.1 AV654143.1 2.0E-87 BE294432.1 2.0E-87 BE531136.1 AF114487.1 ģ 1.0E-87 AF039517.1. AF073371.1 1.0E-87 AF039617.1 1.0E-87 AB022918.1 1.0E-87 AF114487.1 1.0E-87 AF073371.1 AI004091.1 1.0E-87 AF214582.1 1.0E-87 AB022918.1 BE818183.1 1.0E-87 BE818183.1 2.0E-87 N48128.1 2.0E-87 N48128.1 N48128.1 1.0E-87 Y00052.1 20E-87 X52851.1 .0E-87 M34428.1 20E-87 20E-87 1.0E-87 1.0E-87 1.0E-87 BLASTE ± (&) 1.0E-87 .0E-87 1.0E-87 .0E-87 .0E-87 .0E-87 Value 1.0E-87 1.0E-87 35.45 2.09 2.43 39.61 5.72 0.69 0.68 Expression 6.23 0.62 1.18 12,83 9. 19. 1.23 2 0.97 2.85 2.85 0.67 35. 1.08 Signal ORF SEQ 32882 33362 32828 33112 34127 28090 26841 30431 30432 25570 31878 31879 32832 32833 ÖZ 32838 33057 33840 34644 34645 35371 35372 36131 36893 36894 19362 19600 SEQ ID 19814 19764 14158 14158 17814 2003 20988 16451 16470 12833 18910 18910 19768 20710 1552 17814 21499 19768 19773 18881 21489 22186 22188 23325 23641 23601 23641 25404 25240 7073 SEQ ID 8883 7126 7363 8234 9685 1159 7587 141 1411 5095 6132 6132 3697 3717 5096 7077 7083 7298 8015 9533 Š 10272 707 8807 8807 9633 10633 10965 12809 10921 10965 12383

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	Top Hit Descriptor	Homo sepiens double stranded RNA activated protein kinase (PKR) gene, excn 12	Homo septens mRNA for KIAA1399 protein, pertiel ods	Homo servers mRNA for KIAA1399 protein, partial ods	Learning DK EZDERAD1 K22 randah (DK EZD58871522) mRNA	TOTIO SACRETO DAY LA COMPANIA HIS ACTIONS		H. septems ECE-1 gene (exam 9)	H. septens ECE-1 gene (each 9)	Homo sapiens DNA, DLEC1 to ORCILL4 gene region, section 1/2 (ULEC1, GNOTES, CRUTES, Society) complete cds)	Homo sapiens X-linked enhidrotito ectodermal dysplasia protein gene (EDA), exon 2 and tranking repeat	regions	Homo sapiens KiAA0063 gene product (KIAA0063), mktiva	K9719F Human fetal heart, Lambda ZAP Express Homo sepiens cONA clone K97195 smiller to zilvo. FINGER PROTEIN HZF1	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds	washon of NCI CCAP Lu24 Homo septems cDNA clone IMAGE:2336799 3: similar to contains Alu	repetitive element/contains element MER22 MER22 repetitive element;	Homo sapiens intersectin short teorom (115N) mikina, comprete cus	VMOGDIO, TI SOBRES International living requires con concernations.	Homo sepiens chromosome 21 segment nozilovon	602154968FT NIM MCC_65 Trails equials Cut of Calculations and Calculation process on the Tailong Laws earling colons	PMI-INUACO-JOSECO-COLT IS TROUBLE FORMS CONTACT TRANSPORTED TO TRANSPORTED CONTACT TRANSPORTED TO TRANSPORTED CONTACT TRANSPORTED TO TRANSPORTED CONTACT TRANSPORTED TO TRANSPORTED CONTACT TRANSPORTED TO TRANSPORTED T	PMT-INUUZG-CSUB-UC-CV-T IV INVEZG I CAID OFFICIA CON C.	Horizon de La la la la la la la la la la la la la la			HOME BECAUSE NICHOLD SE USE FROM (INC. 127), INC. 3	Homo sapiens hypothetical protein richal total (richary), illington	Homo septens zind miger protein 20e (ZNF 209) illinum Andro 4 6	2845012.81 Source 1988 and special III to I to I to September 23 (ADAM23) mRNA		Indian seguens a usa keguni an indianah manan 10020 (FI 12020) mRNA	Home separation containing making (VCP), mRNA	
	Top Hit Database Source	٤	5						Z	Þ				T HUMAN	NT		EST HUMAN		EST HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	Z	5	5	Ę	Z	!	EST HUMAN	Z	2	<u> </u>	Z
	Top Hit Acession No.	9 0F-88 AF167465.1			9.0E-88 AB037820.1	5	12			0 OF -88 AB026898.1		6.0E-88 AF003528.1	7661887 NT	180300 1	2.4		5.0E-88 AI693217.1	5.0E-88 AF114488.1	5.0E-89 H10932.1	5.0E-88 AL163284.2	5.0E-88 BF680206.1	4.0E-88 BF091229.1	4.0E-88 BF091229.1	11416585	4502694 NT	7061947 NT	7861947	11545800 NT	4508020 NT	3.0E-88 N66951.1				11429567 IN I
-	Most Similar (Top) Hit BLAST E	9 OF-88	0 0 0	S.UE-00	9.0E-88	9.0E-88	9.0E-88	9,0E-88 X91929.1	9.0E-88 X91929.1	A 88-70 a		8.0E-88	5.0E-88	P GONORIN SO TO A	5.0E-88/		5.0E-88	6.0E-88	5.0E-89	5.0E-88				4.0E-88				3.0E-88						3.0E-88
	Expression Signal	10.24	97.0	2.70	2.76	1.57	1.35	2.73	2.73			3.82	1 02	35.0			228		3.19		0.45	1.42	1.42	1.43	1.8		1.89	1.85	1.98	4.11	1.24		4.08	2.85
	ORF SEQ ID NO:	28500				27575	29012					34754	l		W182			30056	32825		L	26729	26730	32899	36749	37380	37381			28367		7 29580		4 30648
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	Probe SEQ ID NO:	139	1001	1327	1327	2115	3617	4236	4238		24	90	8 6	1920	24.5	3000	3394	4687	6672	7830	9211	1308	1306	7143	10827	11471	11471	715	1805	2948	4218	4218	4444	5216

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Table 4
Single Exon Probes Expressed in Brain

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									4	D Fig									I	1	-		7	J	5	1]	1	7	D C	5	67
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA	Homo sepiens v-ral simian leukernia viral oncogene homolog A (ras related) (RALA), mRNA	Homo septens interfeukin 13 (IL.13), mRNA	Homo septens activator of S phase kinase (ASK), mRNA	Homo septems activator of S phase kinase (ASK), mRNA	Homo sepiens putative anion transporter 1 mRNA, complete cds	Homo seplens retinoblastome-binding protein 2 (RBBP2), mRNA	Homo sapians growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA	Homo saplens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds	Homo sapiens wets avian erythroblastosis virus E26 cncogene related (ERG), mRNA	Homo sepiens mRNA for RALDH2-T, complete cds	Homo sepiens mRNA for RALDH2-T, complete cds	Homo sepiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA	Homo sepiens transcobelerran II; mecrocytic enemia (TCN2), mRNA	Homo sepiens Calsenilin, presentiin-binding protein, EF hand transcription factor (CSEN), mRNA	Homo sepiens SNARE probein Idnese SNAK mRNA, complete cds	Homo sapiens SNARE protein kinase SNAK mRNA, complete ods	Homo sepiens SNARE protein tinase SNAK mRNA, complete cds	Homo sapiens dynein, excremel, light polypeptide 4 (DNAL4), mRNA	UHH-BI1-eest-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo espiens cDNA done IMAGE:2718750 3'	UFH-BI1-ece-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone IMAGE:2718750 3'	Homo saplens KIAA0417 mRNA, complete cds	Homo sapiens KIAA0417 mRNA, complete cds	wq70s12x1 NCI_CGAP_GO8 Hamo sapiens cDNA done IMAGE:2476806 3'	ae54a11.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:824732.3' similar to WP:80272.2 CE00851;	zp87c02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627170 5' similar to	SW.POL1_HUMAN P10288 RETROVIRUS-RELATED POL POLYPROTEIN;	DKFZp434N0323_11 434 (synonym: hies3) Homo sapiens cDNA done DKFZp434N0323 51	os01g03.s1 NCI_CGAP_GC3 Homo sapiens dDNA cione IMAGE:1612766 3' similer to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN):	Homo sapiens chromosome 21 segment HS21C046	
gle Exon Pro	Top Hit Database Source	Ę	뉟	Þ	Ę	Þ	Z	칟	攴	۶	Ę	Ę	۲	M	NT	TN	NT	TN	IN	LN	EST_HUMAN	EST_HUMAN	IN	L	EST HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	TN	
	Top Hit Acession No.	TN 8888886	11420697 NT	11417370 NT	11419210 NT	11419210 NT	AF279265.1	11436400 NT	11421726 NT	3.0E-88 AF034374.1	11526262 NT	3.0E-88 AB015228.1	3.0E-88 AB015228.1	11439065 NT	11417974 NT	7305198 NT	2.0E-88 AF246219.1	2.0E-88 AF246219.1	2.0E-88 AF246219.1	5031686 NT		1.0E-88 AW 139565.1	1.0E-88 AB007877.1	1.0E-88 AB007877.1	1.0E-88 Al969034.1	1.0E-88 AA488981.1		1.0E-88 AA190368.1	1.0E-88 AL043314.2	1.0E-88 AA991479.1		
	Most Similar (Top) Hit BLAST E Value	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	2.0E-88	2.0E-88/	2.0E-88	2.0E-88 /	2.0E-88	1.0E-88	1.0E-88 /	1.0E-88	1.0E-88 A	1.0E-88 A	1.0E-88		1.0E-88	1.0E-88	1.0E-88	1.0E-88 A	
	Expression Signal	4.13	3.58	0.61	1.18	1.18	14.59	6.15	9.68	1.35	8.	0.58	0.58	1.28	5.97	3.32	1.38	3.13	1.52	2.13	5.63	5.63	23.81	23.81	1.4	4.42		9.0	2.97	2.39	3	
	ORF SEQ ID NO:	31194	31327	31812				33206	33642	33921	33521	35680	35681	35705		26432	27056	27185	28867	29760	31539	31540	32317	32318	32771	32839		35037	35311	36420		
	Exan SEQ ID NO:	18296	18414	18848	25088	25088	19447	20117	20516	20790	20405	22479	22479	22507	24628	13773	14367	14486	16214	17128	18610	18610	19313	19313	19714	19774		21872	22131	23189	24760	
	Probe SEQ ID NO:	5498	5818	6909	6319	6319	6965	7440	7821	8096	9334	9828	9828	9857	12139	1013	1620	1744	3458	4391	5821	5821	6548	6548	7022	7084		9141	9478	11422	12356	

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Table 4
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Top Hit Descriptor		601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'	Homo saplens similar to seme domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorn) 3A (H. sanians) (I OCA3232), DAIA	Hono saniers homonally interestient from the	Homo sapiens homonally intragulated near trace considered rings (HUNK), mRNA	Homo seriens complement component 8 has not accorded (not), many	DKF26434F346 of 434 (smoother: the 3) Home and the second of the second	H. Saplens CLN3 cene, complete CDS	Regions CIN3 cene complete CIN3	Homo septens blastin 3 (T textrom) (PI S3) mPNA	Homo sepiens plastin 3 (Tisoform) (PIS3) mRNA	Homo saciens actin related protein 2/3 complex such wit 16 (41 LO) (ADDC/44)	Homo sepiens KIAA0433 protein (KIAA0433) mRNA	Homo sepiens KIAA0433 protein (KIAA0433) mRNA	Homo seriens mRNA for KIAA0561 mortain partial calc	H. sepiens Weet hu gene	H.sapiens Weef hu gene	Homo saplens mRNVA for KIAA0823 profesin partial cds	Homo sapiens mRNA for KIAA0823 protein, pertial cds	Human aldose reductase (AR) gene, segment 2	Human accritate hydratase (ACO2) gene, excn 2	Homo saplens Inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA	Homo saciens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA	Homo saplens ublquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA	Homo saplens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA	Homo saplens HSPC159 problin (HSPC159), mRNA	Hamo sepiens mRNA for KIAA0406 protein, partial cols	Homo sapiens mRNA for KIAA0408 protein, partial cots	Homo septens low density incorrotein-related protein 2 (I RD2), mDNA	Homo septems low density incorrobein-related protein 2 (1 RP2) mRNA	TCBAPZE0383 Pediatrio pre-B cell acute fymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens	pre-B cell acute fymphoblastic leukemia Baykα-HGSC project≃TCBA Homo sapi
Top Hit Database Source		ESI HUMAN	Þ	L.	L	1	EST HUMAN	L	Į.	5	5	7	7	<u></u>	NT	NT	LN	ĽΣ	۲	E											EST HUMAN	
Top Hit Acession No.	DE044557 4	QUE-08 DE311337.1	11421514 NT		7857213 NT	4557390 NT	7.0E-89 AL045748.1			7549808	7549808 NT	11420754 NT	11417118 NT	11417118 NT	7.0E-89 AB011133.1				1.1		J87927.1	5803114 N	4506124 NT	4507788 N	4507788 NT	7861817 NT		6.0E-89 AB007886.2 N	5806918 NT	5806918 NT	5.0E-89 BE244323.1 E	5.0E-80 BE244323.1 E
Most Similar (Top) Hit BLAST E	200	0.0E-08	8.0E-80	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89	7.0E-89 X62048.1	7.0E-89 X62048.1	7.0E-89/	7.0E-89 /	7.0E-89 M59783.1	7.0E-89 U87927.1	6.0E-89	6.0E-89	6.05-89	6.0E-89	6.0E-89	6.0E-89	6.0E-80 A	6.0E-89	6.0E-89	5.0E-89 B	5.0E-89 B
Expression Signal	1 23	333	1.2	1.72	1.72	2.86	3.35	1.34	1.34	0.57	0.57	2.06	0.67	0.57	9.0	1.11	1.11	2.33	2.33	1.45	1.7	0.73	1.27	1.08	1.06	0.88	3.02	3.02	0.81	0.81	274	274
ORF SEQ ID NO:	28484		32519	25856		30181	30228			31997	31998	33156	33598	33599	35421	36296	36297	36320	36321	37154		20423	27676	27,000	27,889	CZ802	29954	20055	30436	30437	30346	30346
Exon SEQ ID NO:	15445	L		13210							19024	20078	20474	20474	22237	23075	23075	23094	23004) (2005/3	87057	29/27	14938	10.00	12122	10201	1/328	1/3/28	17819	17819	17737	17737
Probe SEQ ID NO:	2739		6833	424	424	4828	4878	345	5345	6250	822	88	2	2	884	10420	10 10 10 10 10 10 10 10 10 10 10 10 10 1	5 5	10445	3	4//2	3 2			100	200	3	200	9100	2100	5016	5016

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Single Exolt Floros Expresses	Top Hit Descriptor	QV3-NT0022-080600-219-g03 NT0022 Homo saplens cDNA	we01c03.xf Soares_NFL_T_GBC_S1 Hamo sapiens cUNA dane IMA/GE:2346452.5	EST388290 MAGE resequences, MAGN Homo seplens cDNA	AHATANS A SAGING NEL T GBC 51 Homo septens cDNA clone IMAGE:1844915 3'	United and the KIAA ROOM mans heritie Eds	TURBLITION IN TOTAL SECTION FOR THE SECTION OF THE	yw86e11.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259148 5 similar to SW:PIAK_HUMAN P42356 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA;	Homo sapiens PXR2b protein (PXR2b), mRNA	Home sepiens PXR2b proben (PXR2b), mrNA	Homo eaplens PXR2b protein (PXR2b), mRNA	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sapiens mRNA for KIAA1342 protein, partial cds	gg86c08.x1 Soares_NRT_GBC_S1 Homo sepiens cDNA done IMAGE:1843022 3' similar to gb:J04131 GAMMA-C3 LITAMM_TRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;	Communication of Sciences testils. NHT Homo explores cDNA clone 1320988 3'	1270 of Section Section 1970 Acres (2008) 3	all/box.si coares (see a funition professor (IRF4-2) mRNA, partial cds	Indiana Holf name for hunshe kinese (PTK), excess 10-11	Lisephane HCK name for homeine idnesse (PTK), exons 10-11	Homo seniens chromosome 21 segment HS21C003	Home caniene GGT refine extri 5	601065996F1 NIH MGC 10 Homo sapiens cDNA done IMAGE:3452423 5	Home septemble for LECT2, complete eds	Human N-ethylmatetmide-sensitive factor mRNA, partial cds	Homo saplers chromosome 21 segment HS21 0085	License Office O	The state of the s	Homo sepiens solute carrier family 24 (sodium/potessium/calcium exchanger), member 2 (SLC24A2), mRNA	Homo sapiens pertial mRNA for PEX5 related protein	Homo saplens mRNA for KIAA1333 protein, pertial cds	Homo sapiens CaBP5 (CABP5) gene, exon 5	Homo sapiens CeBP5 (CABP5) gene, exon 5	
III LAUIT FION	Top Hit Detabese Source	EST_HUMAN	EST HUMAN		1	LICENTA	Į.	EST HUMAN	IN	F	F	L	Z	HOL	TOT TOTAL	ESI HOMAN	EST HUMAN	Į.	N.	z	Z !	TOT LIMAN	10101	2 5	E L	N.	Z	Z	N.	Z	L _Z	LN	
Julio I	Top Hit Acession No.	4.0E-89 BE762749.1	4 OF 90 AITORR72 4	7.05 ON AMO78184 4	Werdion.	3.0E-89 AI217359.1	3.0E-89 AB002297.1	127357.1	TN06870 NT	7706870	TN06670 NT	7706870 INT	2 0F-89 AB037763.1		2.0E-89 AIZZZ085.1	2.0E-89 AA759149.1	2.0E-89 AA759149.1	2.0E-89 AF089897.1	2.0E-89 X58742.1	2.0E-80 X58742.1	2.0E-89 ALT63203.2	2.0E-89 AJ007378.1	DE041/44.1	2.0E-89 AB007349.1	2.0E-89 UU3963.1	2.0E-89 AL163285.2	2.0E-89 U81004.1	11428801 NT	2 0E-89 A J245503.1	2 DE-89 AB037754 1	AF170814.1	2 OF 80 AE470814 1	110011
	Most Similar (Top) Hit BLAST E	4.0E-89 B	1 05 80 4	A 00 TO 0	S.UL-OB	3.0E-89	3.0E-89 /	3.0E-89 N57357.1	2.0E-89	2.0E-89	20E-89	2 OF -RG	205-89/		2.0E-890	2.0E-89	2.0E-80	2.0E-89	2.0E-89	2.0E-89	Z.0E-88	2.0E-89	2.0E-89	2.0E-89	2.0E-89	2.0E-89	2.0€-89	2 OF-89	2 OF-89				
	Expression Signal	1 85	100	8 2	LC.L	1.26	0.48	78.6	0.87	0.87	155	1 85	2 4 2		1.53	1.01	1.01	1.28	5.16	5.16	0.75	1.1			1.61	0.63	5.33	202					0.08
	ORF SEQ ID NO:	93254	1077	37034			36374	Cesser					20007			28946	28947	29494	29504			29826				31861	33341	73067			30002		35558
	SEQ ID NO:	204 60	20103	23758	15648	19731	١.	i .	12184	12464	\perp	1	13184	ļ		16296	16296	16867	16875								20237	1	1	1		10077	-
	Probe SEQ ID NO:	7107		1088	2879	7040	10502	0.00	10/02	3 8	3 5	860	399	<u> </u>	2883	3540	3540	4125	4133	4133	4315	4463	5259	5393	5702	6116	7567		200	3	9152	DL/R	9710

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	Top Hit Descriptor	Homo sapiens integrin, eighe 3 (entigen CD49C, eighe 3 subunit of VLA-3 receptor) (ITGA3), mRNA	Homo sapiens hect domain and KLU 2 (MENCZ), hinner	Homo sapiens cell adheston materale with homotogy to L1CAM (close homotogue of L1) (CHL1), mRNA	Human MAGE-7 anigen (MAGE/) pseudogne, cuiped con MAGE:3134897 3' similar to TR:054778 054778	SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN; Leadon - VICI CARR Kidi 1 Homo sepiens cDNA clone IMAGE:3134897 3' similar to TR:054778 054778	SOLUTE CARRIER FAMILY 22 - LIKE 2 PROTEIN;	Homo septera di luci loscolo di 1 degino di 1 de 1 de 1 de 1 de 1 de 1 de 1 de 1	nomo separa su inclinación est acquient HS210046	Ponto sapario an unicontra programment HS21C046	Home septions of unitable 21 comments of A done IMAGE:3284583 3'	7 BS0105X1 NO. COAD 1 1/24 Homo seriens CDNA clone IMAGE:3284583 3	/ GSONGSXT NOT CONTINUE CONTINUE CONTINUE CONA	1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1	qg96c08.xt Soeres_NRL_T_GBC_S1 Homo septens cDNA clane IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;		qg96c08.x1 Sceres_NFL_T_GBC_S1 Home saplens cDNA clone IMAGE:1843022.31 stimser to go. 10-11-12 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);conheins Alu repetitive element;	282010.51 SOBIES 1943 INT SHOWN INTO SALLAMO SALLAW CON INA GOT INA GET 401442.3	282010.81 Source Texturing Spread Link Inc. (CACNATE) gene, excens 7-49, and pertial ods, alternative (CACNATE)		s.1 Sogres testis NHT Homo saplens cDNA done 1375503.3'	Annesses 7R1 NIH MGC 96 Home septems aDNA done IMAGE:3855824 3	POLICES STATE NIH MGC 66 Homo explens cDNA clone IMAGE:3855824 3'	E:212190 3' similar to			
Col I love pignio	Top Hit Detabase Source					EST HUMAN	r HUMAN	Ę.	L _N	L _N	L	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	EST HUMAN	5	TOT LIMAN	NAME TO THE	MAN II TOT	ES I DOMAN	EST HUMAN	EST_HUMAN	
2	Top Hit Acession No.	11434411	6729867 NT	11433673 NT	2.0E-89 U10892.1	1.0E-89 BF196052.1	1.0E-89 BF196052.1	9.0E-90 AL163246.2	9.0E-90 AL163246.2	8.0E-90 AL163248.2	8.0E-90 AL163248.2	8.0E-90 BE670561.1	8.0E-90 BE670561.1	8.0E-90 BE177830.1	8.0E-90 A 222095.1		8.0E-90 AI222095.1	8.0E-90 AA705222.1	8.0E-90 AA705222.1	7 OF 00 A E 2 2 2 2 4 4		7.0E-90 AA/828//.1	7.0E-90 BE962525.2	BE962525.2	7.0E-90 H68849.1	7.0E-00 H68849.1	
	Most Similar (Top) Hit BLAST E Value	2.0E-80	2.0E-89	2.0E-89	2.0E-89	1.0E-89	1.0E-89	9.0E- 8 0	9.0E-90	8.0E-90	8.0E-90	8.0E-90															
•	Expression Signal	2.83	2.3	5.03	2.11	5.97	5.97	1.67	1.57	2.23	2.0	3.78	3.78	0.55	3.	3	1.52	1.32	1.32		4.12	2.08		1.62	1.9	1.9	
	ORF SEQ ID NO:	37330	1	37472		37483	37484	33956		28459					2000		36532					3		8 34702	35901		
	Exan SEQ ID NO:	24038	23215	24160	24312	24169	24169	20820	١.	L	1_	1_	15565	\mathbf{I}_{-}	1	23233	23.293	Ι.	L	_		21016	21556	21556	22684	1	1
	Probe SEO ID NO:	24.0	448	445.82	11718	11570	11570	8128	8128	1041	1042	1307	1307	8458		10599	70500	10063	10963		816	8323	8865	8865	10036	10038	

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										1	131	131						1	_	۱ ٔ			٦			' –		٣	L,	Œ	את נבר!
	Top Hit Descriptor	602071208F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214257 5'	Homo saplens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo sepiens HsGCN1 mRNA, pertial cds	Homo septems HsGCN1 mRNA, pertial ods	Homo sepiens inosital 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo sepiens incettal 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo saplens TCL6 gene, expn 1-10b	Human gamma-aminobutyric acid transaminase mRNA, partial cds	qg99c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAAMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element	qq96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb.J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element	Hamo sapiens intersectin long Isafarm (ITSN) mRNA, complete ads	Homo sapiens pregnancy-zone protein (PZP) mRNA	DKFZp762P1616_r1 762 (synonym: hmel2) Homo sepiens cDNA clone DKFZp762P1616 5'	H.saplens mRNA encoding phospholipase c	Hamo sapiens ELKS mRNA, complete ads	H.sapiens mRNA encoding phospholipase c	Homo sepiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA	Homo sapiens angiopoiedin 4 (ANG4) mRNA, partial cds	Homo sapiens anglopoletin 4 (ANG4) mRNA, partiel cds	Homo sapiens adenylate cyclese 9 (ADCY9) mRNA	Homo sapiens ryanodine receptor 3 (RYR3) mRNA	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA	Homo sapiens cadherin 18 (CDH18) mRNA	Homo sepiens similar to ectorucleotide pyrophosphatase/phosphodiesterase 3 (H. sepiens) (LOC63214), mRNA	Homo saplens calcium-binding transporter mRNA, partial cds	Homo sepiens KIAA0433 protein (KIAA0433), mRNA	Homo sapiens KiAA0433 protein (KiAA0433), mRNA	
	Top Hit Database Source	EST HUMAN	FN	FN	NT	TN	L	L	TN	LN	EST_HUMAN	EST_HUMAN	Ł	Į,	EST_HUMAN	NT	NT	NT	NT	NT	NT	FN	NT	NT	TN	NT	5	Į.	K	NT.	
,	Top Hit Acession No.	BF526089.1	8922398 NT	8922398			4504794 NT	4504794 NT	1.1	J80226.1	5.0E-80 At222095.1		5.0E-90 AF114487.1	4506354 NT	5.0E-80 AL135549.1		7.1	216411.1	9910365 NT	9910365 NT	5.0E-90 AF113708.1	5.0E-80 AF113708.1	4557258 NT	4506758 NT	11345483 NT	4826670 NT	TN 902901711	AF123303.1	17118	11417118 NT	
	Most Similar (Top) Hit BLAST E Value	7.0E-90	6.0E-90	6.0E-90	6.0E-90 U77700.1	6.0E-90 U77700.1	6.0E-90	8.0E-90	5.0E-90	5.0E-80 U80226.1	5.0E-90	5.0E-80	5.0E-90	5.0E-90	5.0E-90	5.0E-90 Z16411.1	5.0E-90	5.0E-90 Z16411.1	5.0E-90	5.0E-90	6.0E-90	5.0E-80	5.0E-90	6.0E-90	5.0E- 0 0	5.0E-⊕0	70 Y		5.0E-90	5.0E-90	
.	Expression Signal	1.17	9.12	9.12	3.27	3.27	275	2.75	19.84	3.08	1.47	1.47	2.79	2.05	0.98	2.94	1.31	2.36	0.74	0.74	2.04	2.04	10.6	0.44	5.08	0.58	*	0.50	0.6	0.5	
-	ORF SEQ ID NO:	36216	29568		31625	31626		34057		28586	727Z	27.268	28011	29871	29892	31203	31316	31203		32408		32867	33228	33909	34025	34950	25,418		l		
	Exx SEQ ID NO:	22899	L		18679	18679	20919	20919		13924	14563	14583	15274	17238	17357	18302	18402	18302	19393	19393		19802	20138	20485	20886	21784		╄-	22959	<u>L</u>	
	Probe SEQ ID NO:	10352	4201	4201	5894	5804	8226	8225	151	1170	1813	1813	2680	4503	4622	5604	5606	5679	6831	6631	7114	7114	7463	7790	8192	9606	02.90	10181	10312	10312	

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U	1/57275	_	-		-																	_				P	CT/U	S01/0	0066	7
יינים ביינים ביי	Top Hit Descriptor	Homo sapiens ATPase, aminophospholipid transporter-like, Class I. type 8A, member 2 (ATP8A2), mRNA	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA	Homo sepiens KIAA0317 gene product (KIAA0317), mRNA	Homo sepiens KIAA0305 gene product (KIAA0305), mRNA	Homo sepiens gene for AF-6, complete cds	ar78h05.x1 Barstsad acrta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'	Homo septens chromosome 21 unknown mRNA	Homo saplens chromosome 21 unknown mRNA	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA	H.sapiens gene encoding discoidin receptor tyrosine kinase, exon 16	Homa sapiens prostate-specific membrane antigen (PSM) gene, complete cds	Homo sapiens low density lipoprolein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprolein-related protein 2 (LRP2), mRNA	Homo saplens DNA for emykold precursor protein, complete ods	Homo sapiens mRNA for KIAA1244 protein, partial cds	Human prohomone converting enzyme (NEC2) gene, exon 8	UI-H-BW1-any-b-04-0-UI:s1 NCI_CGAP_Sub7 Homo saptens cDNA clone IMAGE:3083839 3'	UI-H-BW1-4my-b-04-0-UI.81 NCI_CGAP_Sub7 Hamo septems cDNA done IMAGE:3083839 3"	601335244F1 NIH_MGC_39 Homo saplens cDNA clone IMAGE:3689147 5'	601067378F1 NIH_MGC_10 Hamo septens aDNA clans IMAGE:3453834 5'	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA	qc54c02.x1 Soares_plecenta_8b09weeks_2NbHP8b09W Homo sapiens cDNA clone IMAGE:1713410 3' ``\ similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.;	Homo sapiens mRNA for KIAA0289 gene, partial cds	Home seplens GRB2-related adeptor protein (GRAP) mRNA	be49d05.y3 NIH_MGC_10 Homo septens cDNA clone IMAGE:2899881 6' similar to TR:O75208 O75208 PPPOTHETICAL 35.5 KD PROTEIN;	Homo septens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. septens) (LOC63484), mRNA	Homo septiens similer to leminin receptor 1 (67/D), ribosomal protein SA) (H. septiens) (LOC63484), mRNA.	AU118985 HEMBA1 Hamo septens cDNA clone HEMBA1004795 5'
ale Laboratoria	Top Hit Database Source	Ę	Ę	Ę	F	۲	EST_HUMAN	IN	LΝ	L	LN	LN.	ĽN	Z	LN.	LN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT	EST HUMAN	N	F	EST_HUMAN	Ę	. FA	T HUMAN
5	Top Hit Acession No.	11433721	7662051	7662051	7882047	5.0E-90 AB011399.1	5.0E-90 AI523368.1	4.0E-90 AF231920.1	4.0E-90 AF231920.1	4505316	X99033.1	4.0E-90 AF007544.1	6806918	6806918	4.0E-80 D87875.1	4.0E-00 AB033070.1	4.0E-90 M95967.1	3.0E-90 BF516168.1	3.0E-90 BF516168.1	3.0E-90 BE563833.1	2.0E-90 BE537913.1	5031748	5031748	2.0E-90 Al138213.1	2.0E-90 AB006627.1	5729855	2.0E-90 AW672686.1	11427320	11427320	2.0E-90 AU118985.1
	Most Similar (Top) Hit BLAST E Value	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	5.0E-90	4.0E-90	4.0E-90	4.0E-90	4.0E-90 X99033.1	4.0E-90	4.0E-90	4.0E-90	4.0E-80	4.0E-90	4.0E-90	3.0E-90	3.0E-90	3.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90
	Expression Signal	9.16	0.54	0.54	2.41	2.08	4.43	1.93	1.93	3.28	B.09	96.0	1.07	1.07	7.65	2.17	2.33	1.08	1.08	17.81	4.71	2.67	2.67	1.7	1.05	7.31	4.86	4.78	4.78	1.37
	ORF SEQ ID NO:	36209	36264	36265	37648			25742	25743	26482	27125	28405	ĺ	28437	28975	30109	30123	33570	33571	37551	25862	26567	26568	29209	30008	30206	31410	35534	35535	35706
	Exan SEQ ID NO:	22991	23048	23048	24324	24948	24938	13101	13101	13822	14428	15758	15789	15789	17343	17475	17500	20447	20447	24227	13020	13905	13905	16577	17374	17583	18489	22341	22341	22510
	Probe SEQ ID NO:	10344	10402	10402	11731	12591	12641	295	295	1064	1684	2962	3023	3023	4608	4743	4788	7751	12//	11630	208	1150	1150	3826	4840	4853	5695	6896	6896	0986

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Γ			П		П										П			٦		F	7		Ī.	/ []	<u> </u>			4		- 1	11		5 :
	Top Hit Descriptor	AU118985 HEMBA1 Homo septens cDNA clone HEMBA1004795 5'	Homo saplens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	Homo sapiens emykold beta (A4) precursor protein (protease nextn-li, Alzhelmer disoase) (APP), mRNA	Homo sepiens chromosome 21 unknown mRNA	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens ALR-like protein mRNA, partial cds	Homo sapiens Kruppel-like factor 7 (ubiquitious) (KLF7), mRNA	Homo sepiens protein phosphatase 2A BR gamma subunit gene, exon 3	Homo sepiens protein phosphatase 2A BR gamma subunit gene, exon 3	601158563F2 NIH_MGC_53 Hamo sepiens cDNA clane IMAGE:3511118 5	Homo eapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA	Homo sapiens chromosome 8 open reading frame 2 (CBORF2), mRNA	Homo sapiens soluble interfeuklin 1 receptor accessory profein (IL1RAP) gene, exon 8, alternative exons 9	and complete cds, afternatively spliced	Hamo sepiens mRNA for KIAA0833 protein, pertial cds	Homo saplens KIAA0623 gene product (KIAA0623), mRNA	Homo sepiens cytochrome P450, 51 (lanosterol 14-alpha-demethylase) (CYP51), mRNA	Human retina-derived POU-domain factor-1 mRNA, complete cds	Homo sapiens giutamate receptor, fonotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamete transporter), member 6 (SLC1A6),	mRNA	Homo sapiens brefeldin A-Inhibited guanine nucleotide exchange protein 2 (BIG2), mRNA	Homo sapiens SNCA isoform (SNCA) gene, complete cds, atternatively spliced	Homo saplens CGI-15 protein (LOC51006), mRNA	Homo sepiens CGI-15 protein (LOC51006), mRNA	yg44d11.r2 Soares Infant brain 1NIB Homo saplens cDNA clone IMAGE:354775'	Human branched chain alpha-keto acid dehydrogenase mRNA, 3' end	Homo septens DNA for Human P2XM, complete cds		HUM000S381 Liver HepG2 cell line. Homo sapiens cDNA done s381 3'
	Top Hit Detabase Source	EST_HUMAN	NT	Į.	F	¥	Z	Į.	NT	N	Į,	LN	NT	EST HUMAN	¥	N		L	TN	N	F	NT	F		NT	NT.	TN	F	F	EST_HUMAN	Z	Ę	Ŋ	EST HUMAN
6	Top Hit Acession No.	2.0E-90 AU118985.1	11024711 NT	4502168 NT	1.0E-90 AF231920.1		1.0E-90 AJ237589.1	1.0E-90 AJ237589.1	1.0E-90 AF284750.1	1.0E-90 AF264750.1	37828	1.0E-90 AF096154.1	÷	3E379884.1	11420514 NT	6005720 NT			1.0E-90 AB014533.1	11428910 NT	11419408 NT		3008002		11426758 NT	11422086 NT	1.0E-90 AF163864.1	11422109 NT	11422109 NT			9.1	.1	12234.1
	Most Similar (Top) Hit BLAST E Vatue	2.0E-90 /	2.0E-90	1.0E-90	1.0E-90/	1.0E-90/	1.0E-90/	1.0E-90 /	1.0E-90/	1.0E-90/	1.0E-90	1.0E-90/	1.0E-90/	1.0E-90 BE379884	1.0E-90	1.0E-90		1.0E-90/	1.0E-90/	1.0E-90	1.0E-90	1.0E-90 U91934.1	1.0E-90		1.0E-90	1.0E-90	1.0E-90	1.0E-90	1.0E-90	1.0E-90 R25686.1	1.0E-90 J04474.1	1.0E-90 /	1.0E-90[/	8.0E-91 D12234.1
	Expression Signal	1.37	2.8	4.55	1.36	1.43	2.32	232	13.22	13.22	247	5.58	5.56	123	3.33	8.46		1.29	2.58	0.96	0.57	99.0	9.0		277	3.73	96.0	1.63	1.83	1.5	1.78	1.40	1.49	80
	ORF SEQ ID NO:	35707	36446	25720			20098		28137	28138		26703			27342	28271		29758	31295	31460	32240		32965		33345	34555		35062	35063		36896	31001		28642
	Exen SEQ ID NO:	22510	!	13078	15518	15516	13454	13454	13487	13487	13846	14033	14033	14408	L	15626		17128	18385	18538	19240	L	19889		20240	21412	21863	21894	Í _		23643	24904	24904	16912
	Probe SEQ ID NO:	0986	11447	270	385	388	678	679	713	713	1088	1283	1283	1662	1895	2858		4389	5589	6746	8473	6973	720		7571	8720	9183	9215	9215	10657	10987	12580	12680	4172

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40667 qe70f11xf Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1744366 3' similar to contains SW:ASPG_FLAME Q47898 N4(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR EST01579 Hippocampus, Stratagene (cat. #936205) Homo saplens cDNA clone HHCMC80 similar to EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC90 similar to Homo sepiens genma-eminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript varient 2, mRNA au49f09x1 Schneider fetal brain 00004 Homo sapiana cONA clone IMAGE:2518121 3' similar to z190604.s1 Socrets feltal liver splean INFLS_S1 Homo supiens cDNA clone IMAGE:448015.37 Homo sapiens lysophosphatidic acid acytransferase-delta (LPAAT-delta) mRNA, complete cds Homo septens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds Homo saplens solute cerrier family 4, anion exchanger, member 3 (SLC4A3), mRNA Homo sepiens solute carrier femily 4, anion exchanger, member 3 (SLC4A3), mRNA 801901624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130833 5 Homo sepiens chromosome 22 open reading frame 5 (C22ORF5), mRNA Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds AU143539 Y79AA1 Homo sepiens cDNA clone Y79AA1002087 5 AU143539 Y79AA1 Homo sepiens oDNA olone Y79AA1002087 5 Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA Top Hit Descriptor Homo saplens makorin, ring finger protein, 1 (MKRN1), mRNA AV649878 GLC Homo septens oDNA clone GLCBYF08 3' AV649878 GLC Homo septens cDNA clone GLCBYF08 3' Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA Homo sapiens mRNA for KIAA1278 protein, partial ods Homo saplens mRNA for KIAA1278 protein, partial cds CM-BT043-090299-075 BT043 Homo sapiens cDNA Homo seplens chromosome 21 segment HS21C084 Homo sapiens chromosome 21 segment HS210083 Humen Ku (p70/p80) subunit mRNA, complete cds MIR.b2 MIR MIR repetitive element; Retrovirus-related gag polyprotein Retrovirus-related gag polyprotein Single Exon Probes Expressed in Brain EST_HUMAN EST_HUMAN EST HUMAN Top Hit Database HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** Source EST 7110634 NT F 7110634 NT 11419234 NT Ę F ĹΝ E F 눋 눋 ż Ξ 11434964[NT 11497611 NT Top Hit Acession 11430183 11430193 4502740 5.0E-01 AU143539.1 5.0E-91 AV649878.1 5.0E-01 AA702794.1 4.0E-01 AL 163284.2 AL163283.2 5.0E-01 AU143539.1 5.0E-91 AV649878.1 AB033104.1 7.0E-81 AF053769.1 7.0E-01 AIGO4151.1 5.0E-91 BF314682.1 4.0E-91 AF156776.1 4.0E-91 AF156776.1 3.0E-91 AB033104.1 3.0E-91 AF084530.1 5.0E-91 AI879995.1 5.0E-01 AI193568.1 4.0E-91 M77994.1 4.0E-01 M77994.1 3.0E-01 M30938.1 3.0E-91 7.0E-91 5.0E-91 5.0E-01 3.0€-91 3.0E-91 **Most Similar** (Top) Hit 3.0E-91 3.0E-91 3.0E-91 BLASTE 3.0E-91 0.68 1.83 11.73 1.08 11.73 1.25 1.52 89. 1.69 1.96 1.52 1.74 1.88 1.62 3.07 3.39 3.39 1.45 5.82 0.97 0.97 3.07 2.48 127 Expression Signal 34036 36062 28840 30116 ORF SEQ 28877 29841 32289 30117 28612 36775 33931 34405 34498 31082 27049 27050 28746 29159 32256 28611 28863 20015 28864 31305 ÖNÖ 14174 20899 22846 16223 17215 17215 17489 19285 SEQ ID 17489 24596 20799 21350 21350 24919 15960 14360 5000 23530 14380 16094 16520 18395 19255 17286 16211 16211 18987 Š 8 8519 SEQ ID 1427 8205 10198 3467 480 4757 4757 8105 8658 1613 6488 8658 10848 12094 1613 3334 3456 3768 12812 3197 3455 4551 5600 12004 3197 6212 Š

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Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) Homo sapiens gamme-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA UI-H-Bi3-aks-d-01-0-UI.st NCI_CGAP_Sub5 Homo saplens cDNA clone IMAGE: 2735280 3' Homo sepiens brefeldin A-Inhibited guenine nuoleotide-exchenge protein 2 (BIG2), mRNA Human L-type celclum channel beta-1 subunit (CACNLB1) gene, exons 10 and 11 Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11 Homo sepiens hypothetical protein PRO1855 (PRO1855), mRNA 802022088F1 NCI_CGAP_Bm67 Homo sepiens cDNA clone IMAGE:4157804 5 ym30e03.r1 Soeres Infant brain 1NIB Homo sepiens cDNA clone IMAGE.49587 5' 602022088F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4157804 5 801273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614687 5 2013 Human retiria cDNA randomly primed sublibrary Homo sapiens cDNA Human mRNA for very low density lipoprotein receptor, complete cds Homo septens partial TM4SF2 gene for betraspanin protein, exon 5 Homo sepiens pertiel TM4SF2 gene for tetraspenin protein, exon 5 Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA Top Hit Descriptor Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6 Homo sapiens beta-ureldoproplonase (BUP1) gene, exon 6 Human Na+,K+ ATPase alpha-subunit mRNA, partial ods Homo sepiens mRNA for KIAA0694 protein, pertiel cds Homo saplens mRNA for KIAA 1080 protein, partial cds Homo seplens mRNA for KIAA1080 protein, pertiel cds Homo seplens mRNA for KIAA0833 protein, partial ods Homo sapiens mRNA for KIAA1512 protein, partial cds Homo saplens mRNA for KIAA1512 protein, partial cds Homo sapiens chromosome 21 segment HS21C084 Homo sepiens EHM2 mRNA, complete ods Homo sepiens NALP1 mRNA, complete cds Homo sapiens NKG2D gene, expn 10 Homo sapiens NKG2D gene, expn 10 Homo sepiens RNB6 (RNB6), mRNA Single Exon Probes Expressed in Brain genes, complete cds Top Hit Database EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN **EST HUMAN** Source 11497611 NT Ż Ę Ę z Z Ę 호 Ę F 11427149 NT z z LΝ Top Hit Acession 11434402 11422086 7706686 3.0E-91 AB032179.2 1.0E-91 AW449748.1 3.0E-01 AB011108.1 3.0E-01 AB029003.1 3.0E-91 AF240786.1 3.0E-01 AF189555.1 AL163284.2 BF348182.1 ģ 3.0E-01 AB029005. 9.0E-92 AJ001689.1 9.0E-92 AF310105.1 3.0E-01 AF169555.1 9.0E-02 AJ001689.1 9.0E-92 AB020640.1 9.0E-02 AJ250568.1 9.0E-92|AB040945.1 9.0E-92 AB040945.1 1.0E-91 BF348182.1 8.0E-02 BE386363.1 9.0E-92 AJZ50588.1 186959.1 3.0E-81 D16494.1 3.0E-01 U86069.1 .0E-91 H15212.1 9.0E-92 J03007.1 8.0E-82 W 26367.1 3.0E-91 1.0E-01 1.0E-01 3.0E-91 (195) 拓展 BLASTE 1.0E-01 9.0E-92 Value 4.97 283 1.68 5.06 Expression 2,28 1,28 90.6 4.86 2.83 1.35 6.31 0.97 90.6 6.0 0.92 0.92 Signer 35023 33307 34508 ORF SEO 36723 37105 30489 28645 37106 31057 30490 30790 32810 28640 30454 32811 31217 33576 30867 32127 35010 25554 ÖΝΩ 25728 33577 SEQ ID 19255 20208 21858 20208 23486 21361 23827 24749 13973 13970 17838 17898 18131 19577 18178 18316 12876 1957 25340 13970 Ö 20452 19132 20452 20966 21844 12917 13086 20000 6488 7538 SEGIO 7538 88 9188 11160 12335 10803 11100 1233 1219 6743 6743 12245 1219 ö 12667 12667 5328 5120 5378 5518 6362 7758 7756 8272 9174 8272 279 11191

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N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2940) กใ N-CAM≖145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960] Homo saplens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete Hamo sepiens dihydralipoemide S-succinyltransferase (E2 companent of 2-axo-glutarate complex) (DLST) Hamo sapiens nuclear mitagen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds eu83h08.x1 Schneider fetal brain 00004 Home sepiens cDNA clone IMAGE:27829113' similer to Homo sepiens DNA polymenase zeta catalytic subunit verlent 1 (REV3L) mRNA, complete ods Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds TR:060302 060302 KIAA0555 PROTEIN ; contains element MER22 repetitive element; Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA Human von Willebrand factor pseudogene corresponding to exons 23 through 34 Homo seplens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA Homo seplens mRNA for KIAA0758 protein, pertiel cds Homo seplens cytoplesmic Seprese truncated teaform mRNA, complete cds Homo sepiens T-cell lymphome invesion and metastasis 1 (TIAM1) mRNA Homo sepiens T-cell lymphome invesion and metastasis 1 (TIAM1) mRNA Homo sepiens DNA, MHC cless I region, 7.1 ancestral habiotype Homo sepiens DNA, MHC class I region, 7.1 ancestral haplotype Top Hit Descriptor Homo sapiens B-cell CLL flymphoma 7b (BCL7B) mRNA Homo sapiens mRNA for KIAA0758 protein, partial cds Homo septens NRAS-related gene (D1S155E), mRNA Homo septens mRNA for KIAA0611 protein, partial cds Homo sapiens mRNA for KIAA1600 protein, pertial cds Human lens membrane protein (mp19) gene, exon 11 Human lens membrane protein (mp19) gene, excn 11 Homo saplens AIM-1 protein (LOC51151), mRNA Homo sepiens mRNA for MBNL protein Single Exon Probes Expressed in Brain Homo sepiens MCP-4 gene **A**NSE 쁑 EST_HUMAN Top Hit Database Source Z 뉟 5031570 NT 占 4507500 NT Ż Z 눋 6005738 NT z 4507500 NT 支支 4503340 NT F 눌 5031570 NT Ę 4502384NT ¥ 눋 11416961 NT 둗 눋 11426569 NT Top Hit Acession 7.0E-92 AB031007.1 7.0E-92 AB018301.1 7.0E-82 AF187706.1 8.0E-02 AF074393.1 8.0E-92|AW157571.1 8.0E-92 AB014511.1 7.0E-92|AF007822.1 7.0E-92 AB018301.1 7.0E-02 AB031007.1 8.0E-02 AF264717.1 8.0E-92 AF179428.1 8.0E-92 AB046820.1 8.0E-02 AJ000979.1 7.0E-92|S71824.1 7.0E-02|S71824.1 7.0E-92 M80676.1 8.0E-92 L04193.1 L04193.1 8.0E-92 Y13829.1 7.0E-92 7.0E-92 7.0E-92 8.0E-92 8.0E-92 7.0E-92 8.0E-92 7.0E-92 8.0E-92 Most Similar (Top) Hit BLASTE 2.69 2.30 1.34 2.27 1.46 0.92 2.82 3.2 1.02 0.87 66'1 ğ 1.08 0.58 1.01 0.87 2.27 0.55 3.91 1.18 86.0 0.65 0.07 3.91 1.31 Expression Signal 29913 27646 28205 29912 26875 27645 28020 28750 25525 25680 25681 38636 37320 25466 34253 34801 30374 30918 34152 34153 32222 35771 ORF SEQ 30771 3221 Ö N Ö 12892 15538 14006 14913 15282 15435 15462 17282 17282 15538 21115 24024 13357 14913 17871 17871 18210 23397 18113 19219 21017 21017 22573 12851 10223 20685 1700 21651 SEQ ID ğ ö 4547 2184 3340 2184 2728 4647 8960 10707 1333 2 230 230 57 1257 2568 2757 5411 6455 7990 8324 8324 8422 5041 5308 6451 SEQ ID Š

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									Z Z	¥.		-	· -		Ē ·) y		•	1	1	٦,			4	4	1	4		.# [567
Top Hit Descriptor	Homo sapiens zinc finger protein 198 (ZNF198), mRNA	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA	Homo sapiens mRNA for KIAA1093 protein, partial cds	Homo sapiens calcineum binding protein 1 (KIAA0330), mRNA	y80e08.r1 Scares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'	y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 6'	Homo sapiens ribosomai protein, large, P1 (RPLP1) mRNA	HTM1-288F HTM1 Homo sepiens cDNA	Igotb02x1 NCI_CGAP_CtL1 Homo sepiens cDNA clone INAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element,contains element IMER17 repetitive element;	tgotb02.x1 NCI_CGAP_CL1 Homo septens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN	IQ18823 PROTEIN-1 TROSINE PROSPRATASED I COMMISS AND EXPOSITE COMMISS COMMISS AND EXPOSITION COMMISS C	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'	EST188414 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal	properties and the second seco	Home sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, attentatively ispliced	1601281867F1 NIH MGC 44 Homo saplens cDNA clone IMAGE:3603832 5/	Homo saplens ribosomal proben L10a (RPL10A), mRNA	UI-H-BIO eart-h-06-0-UI s1 NCI_CGAP_Sub1 Homo septens cDNA clone IMAGE:2709371 3'	UI-H-BIO-eah-h-06-0-UI.s1 NCI_CGAP_Sub1 Homo saplens cDNA done IMAGE:2708371 3'	601460521F1 NIH_MGC_68 Homo sepiens cDNA clane IMAGE:3863908 5	Homo sapiens chromosome 21 unknown mRNA	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA	Homo sapiens mRNA for KIAA1287 protein, pertial cds	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds	Homo sapiens mRNA for KIAA0611 protein, pertial cds	wc09c08.x1 NCI_CGAP_Pr28 Homo saplens cDNA clone IMAGE:2314670 3'	wc08c08.x1 NCI_CGAP_Pr28 Homo supjens cDNA clone IMAGE:2314670 3'	Human skaletal muscle 1.3 kb mRNA for tropomyosin	Human somatic cytochrome c (HC1) processed pseudogene, complete cds	
Top Hit Detrabase Source	NT	IN	¥	F	EST_HUMAN	EST HUMAN	6668 NT	EST_HUMAN	EST HUMAN		EST_HUMAN	EST HUMAN	1444	ESI HUMAN	Ę	FOT HIMAN	8526 NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	IN	IN	Į.	TN	N	EST_HUMAN	EST_HUMAN	NT	NT	
Top Hit Acession No.	11434759 NT	5803103 NT	2.0E-92 AB028016.1	6912457 NT			हि		1.0E-62 Al380356.1		1.0E-92 Al380356.1	9.0E-83 AU121681.1		9.0E-03 AA316723.1	O NE.03 A F223391 1		1~	8.0E-83 AW014042.1	8.0E-03 AW014042.1	8.0E-93 BF036364.1	7.0E-93 AF231919.1	11526176 NT	6.0E-93 AB033093.1	6.0E-93 AF095771.1	5.0E-83 AB014511.1	5.0E-63 AI674184.1	5.0E-83 AI674184.1	5.0E-93 X04201.1	6.0E-83 M22878.1	
Most Similar (Top) Hit BLAST E Value	2.0E-92	2.0E-92	2.0E-92	2.0E-92	1.0E-92 R78078.1	1.0E-92 R78078.1	1.0E-92	1.0€-92 E	1.0E-92 /		1.0E-92/	9.0E-83/		9.0E- 0 3/	0 05-03	200	9.05-83	8.0E-93	8.0E-03	8.0E-93	7.0E-93	6.0E-93	6.0E-93	6.0E-93	5.0E-83	5.0E-93	5.0E-93	5.0E-93	5.0E-83	
Expression Signal	1.48	2.54	2.69	2.51	1.13	1.13	8.83	1.29	3.82		3.82	8		5.48	1.45	777	9.71	0.58	99.0	2.51	8.82	0.94	1.02	1.12	3.51	7.28	7.28	2.98	1.01	
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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens wascr1 (WBSCR1) and wascr5 (WBSCR5) genes, complete cds, atternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds.	Homo saplens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, econ 11, complete cds and afternatively spliced product	Homo sepiens discs. James Describilia homelog 2 (chansus, 440) (DLCs)	Homo septens discs, large (Drosophila) homolog 2 (chapsyr-110) (Dt.G2) mRNA	Fomo saciens secretory pathway commonent Se-24B.4 mBNA Alemania.	Hano seriens TAR (HIV) RNA-binding nation of (TARBA) while	Homo seciens WSB1 profein (WSB1) mRNA complete and	Homo seplens nucleobindin 2 (NUCB2), mRNA	Homo sapiens camma olukamytransfarase 1 (GCT1) mRNA	Homo sepiens gamma-dlutamytransferase 1 (GGT1) mRNA	250e09.81 Source_bests_NHT Hamo sapiens CDNA clone IMAGE:795688 3' similar to SW:CLPA_RATE P37397 CAL PONIN A CIDIC ISCEDENT.	Home contract to the contract	Homo sanians interferon names receptor 1 (IFNGKT) MIKNA	Home explains the state of the	Homo eaplens peacedillo (zeoranish) nomolog 1, containing BRCT domain (PES1), mRNA	Home serious broodbalked south El 2022 (El 2022)	Homo sections destrooking (DMO) seems destrooking 4.3 to 1.5 to 1	Homo saplens DNA polymenses zwis catalytic suly mit (REV/3) mBNA Complete Catalytic Suly mit (REV/3) mBNA Complete Catalytic Suly mit (REV/3) mBNA Catalytic	Homo septens chromosome 21 segment HS24C404	Homo saplens tumor articlen SIP-8e (HCC8) mRNA	Homo sapiens Interleukin 18 receptor 1 (IL 18R1) mRNA	yb94c12.r1 Stratagene liver (#837224) Homo sapiens cDNA done IMAGE:78838 5' similar to similar to SP-A44391 A44391 84439 BASE SERVINGE ET ELIZENT DINIDIA OF DESTRUIT DE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF T	AVGRANET CACHEN SENSON AND AND CACHENDED FOR THE STATE OF THE MAN .	602246664F1 NIH MGC 62 Home servine and Albertan MA Action MA Acti	802246554F1 NIH MGC 62 Homo seriens CDNA close INA CE 4222005	Homo saciens tensin mRNA complete ods	tr29g03.x1 NCI CGAP Brt26 Home senions cIDNA close 11/4 CE-21/2017 8 21	tri29g03.x1 NCI_CGAP_Bm25 Homo saplens cDNA clone IMAGE 218so78.3	
igle Exon Pro	Top Hit Database Source	IN TN	۲	N	NT	Þ	LN.	Į.	F	7 NT	Z L	HAMINAN	LV O	L	L'A	LZ	LN	L	Į.	LN	LN	H	EST HUMAN	EST HIMAN	Т	Τ	Т	EST HUMAN	Γ	
Sir	Top Hit Acession No.	5.0E-63 AF045555.1	5.0E-63 AF067136.1	4557528 NT	4557526 NT	5.0E- 8 3 AF274863.1	5032156 NT	5.0E-03 AF060313.2	36588	11417877	11417877 NT	4.0E-83 AA459833 1	18	4657879INT	7057454	7867454 NT	8923658	4.0E-83 AF047677.1		4.0E-03 AL163301.2	7705396	4504654 NT		-		Γ				
	Most Similar (Top) Hit BLAST E Value	5.0E-83	5.05-03	5.0E-83	5.0E-83	5.0E-83	5.0E-83	5.0E-03	5.0E-03	5.0E-83	5.0E-63	4.0E-83/	4.0E-03	4.0E-93	4.0E-83	4.0E-93	4.0E-03	4.0E-83	4.0E-93	4.0E-03	4.0E-83	4.0E-93	4.0E-63 T48864.1	4.0E-03 A	3.0E-03 B	3.0E-93 BF690630.1	3.0E-63 AF225898.1	3.0E-63 AI553853.1	3.0E-83 A1553853.1	
	Expression Signal	1.02	3.8	-	1	2.16	1.25	1.9	2.25	2.15	1.44	6.52	1,39	1.30	1.67	1.67	1.53	4.3	96.0	1.65	0.73	1.67	6.4	6.17	7.35	7.35	1.31	0.79	0.79	
	ORF SEQ ID NO:		33388	34338	34339	35360	35554	35821	38866	30929	30829		25863	25864	26186	26187	26577	27424	27707	27855	28958	29403	31264	37023	29035	29036		31412	31413	
	Exen SEQ ID NO:	18799	20280		21195						25052	12912	13218	13218	13527	l	13914	14708	14969	15118	16308	16771	18354	23748	16396	16396	16951	18401	18491	
	Probe SEQ ID NO:	8018	7814	8503	8503	9623	9707	02650	10727	1283 1283	12805	8	432	432	755	755	1160	1970	2241	2397	3653	4026	5557	11078	3843	3843	4210	2692	5697	

Page 409 of 536 Table 4 Single Exon Probes Expressed in Brain

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sapiens GCN5 (general control of amiho-acid synthesis waset homoton Lilius 2 (2004)	W602405.X1 NCI CGAP GC6 Homo sapiens CINA clone IMAGE: 2304480 2	Ohldroogbus aedhioos mRNA for ribosomal modeln SAV	Chlancebus aethloss mRNA for thosewal protein SAV complete cas	Homo seriens chromosome 24 serment LICOACNOE	Homo sepiens chromosome 21 segment HS210085	Homo septems female commission and c	Human CK-associated RS curponlin CABS Company	60117588F1 NIH MGC 48 Home and the Child Alexanders Constitution of Constituti	EST376458 MAGE resembnose MACH Lights actions 1011	Homo saniens deafress autocome dominant E/DDIAE	QV3-HT0613-290300-128-bot HT0643 Home - 1111-1201	Homo seciens hypothetical protein (1 OCE 1928) - DNA	HSU74313 Human chromosome 14 Homo senies chair ales a se	ULHE-BND-aks-d-00-0-11 d NIH MOC 60 L	AV721846 HTR Homo services CDNA Almo Little All 1804 8:	AV721846 HTB Home services and Average 1 into a little at 150 ft.	229c10 c1 States premont idea; NILLD 11	Homo earliere CVD47 Anna E and	601458531F1 NIH MGC 68 Home septem obara data in the or appeared	Homo sapiens CTR1 pseudonena	Homo sepiens CTR1 new idonera	Homo sapiens hypothetical protein (D. 13/28-19 Cr. 1), mRNA	oy84b08.x1 NCI_CGAP_CL11 Homo saplens cDNA clone IMAGE:1672503 3' similar to TR:062384 Q62364	Homo sanlens DNA for emitted	Homo sarions cilitamete december december (1975)	Home selection and a selection of the se	Homo expension by the second protein PLU20291 (PLU20291), mRNA	Home september 1990 to the common of the com	LIGHTS SERVET BITTEN TO FLAAT 363 protein, partial cds	Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds	Homo saplens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA	
gle Exon Pro	Top Hit Database Source	82 NT	EST_HUMAN	LN LN	N	NT	TN	N	۱	EST HUMAN	EST HUMAN	LN LN	EST HUMAN	Į.	EST HUMAN	EST HUMAN	EST HUMAN	EST HIMAN	EST HUMAN	Į.	EST HUMAN	NT.	LN LN		EST HUMAN	Т							TN	
Si	Top Hit Accession No.	25	3.0E-93 AI824829.1	2.0E-93 AB015610.1	2.0E-03 AB015610.1	2.0E-93 AL163285.2	2.0E-93 AL163285.2	20E-98 AF225896.1	2.0E-93 U40763.1	20E-03 BE252982.1	2.0E-93 AW964385.1	4758153 NT	2.0E-03 BF351459.1	11430039 NT	ľ	=		2.0E-83 AV721846.1	2.0E-83 AA126735.1	41825.1	2.0E-93 BF035327.1	1.0E-93 AF238997.1		7657016	1.0E- 0 3 A1146755.1		1503872			_	T		1.0E-93 AF231981.1	
	Most Similar (Top) Hit BLAST E Value							2.0E-98	2.0E-93	20E-03	2.0E-93	2.0E-83	2.0E-03	2.0E-93	2.05-93	2.0E-03	2.0E-93	2.0E-93	2.0E-93	2.0E-93 L41825.1	2.0E-93	1.0E-93 /	1.0E-93 /	1.0E-93	1.0E-93	1.0E-93 D87675.1	1.0E-93	1.0E-93	1.0E-93	1.0E-93	1 0F-02 A		1.0E-93 A	
	Expression Signal	121	4.27	7.61	7.51	9.36	9.48	1.33	1.33	1.66	5.42	0.66	1.04	1.13	0.65	1.1	1.27	127	2.64	217	10.79	2.29	2.29	4.25	4.57	8.91	2.9	7.65	7.65	£.	000		1.33	
	ORF SEQ ID NO:								27587			30824		31256	31270		36946	36947				25564	25565	25923	25994	26292	26560	26632	26833	28744	26746		27798	
	SEQ ID NO:		_	\perp									$oldsymbol{\perp}$		_	19347	23686	23686	24686	24736	24899	12927	12927	13289	13366	13622	13899	13965	13965	14071	14073		15061	
	Probe SEQ ID NO:	6468	70/03	185	185	315	316	1610	2128	2490	5332	5342	5455	5550	5565	88	11014	11014	12233	12314	12571	ē	ģ	505	586	862	14	1215	1215	1322	1324		2337	

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	Т	1	Т	7	Т		T	Т	Т	٦		٦	Т	Т	٦	٦	Τ	F	T,		7	4.	Ţ	31		IJ,	1	7	П	1	I	7E	
Top Hit Descriptor	Homo sapiens MHC class 1 region	Novel human gene mapping to chamosame 1	601177686F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:3532365 5	601177686F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:3532365 5	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens long chein polyunsaturated faitty acid elongation enzyme (HELO1) mRNA, complete cds	Hamo sepiens chromosome 21 segment HS21C084	Homo sapiens glucocarticald receptor (GRL) gene, intron D, exon 5, and Intran E	Homo sapiens glucoccriticald receptor (GRL) gene, intron D, exon 5, and intron E	Homo sepiens candidate taste receptor T2R14 gene, complete cds	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA	Homo sapiens KiAA0672 gene product (KIAA0672), mRNA	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA	Human mRNA for NF1 N-isoform-excn11, complete cds	Homo sapiens mRNA for KIAA1411 protein, partial cds	H.sapiens mRNA for MEMD protein	Homo sapiens protein khase inhibitor gamma (PKIG) mRNA, complete cds	Homo sapiens mRNA for KIAA1485 protein, pertial cds	Homo sapiens Trio Isoform mRNA, complete cds	Human PreA4 gene for Al zheimer's dissass A4 emyloid protein precursor (excn 9)	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (excn 9)	Novel human gene mapping to chamosome 13, similar to rat RhoGAP	Homo sapiens ryanodine receptor 3 (RYR3), mRNA	Homo saplens GGT1 gene, excn 1	- 1	ions S-transferase theta 2 (GSTT2) and glutathions S-transferase theta 1 (GST11)	genes, complete cds	Homo seplens chromosome 21 segment HS210009	complete cds			zg87g06.s1 Soares_fetal_heart_NbHH19W Homo septens cDNA clone IMAGE:409594 3'	
Top Hit Database Source	N.	IN	HUMAN	EST_HUMAN	۶	Ę	Z	NT	TN	NT	Ę	Ŀ	TN	IN	Z	F	FN	TN	L	NT	L	TN	NT .	NT	LN TA		Ę	ᅜ	MT	ᅜ	TN	EST HUMAN	
Top Hit Acession No.	1.0E-93 AF055066.1		1.0E-93 BE297369.1	1.0E-93 BE297369.1		1.0E-93 AF231981.1				1.0E-93 AF227138.1	4567792	7062241 NT	11431590	42072.1	17		7.	1.0E-63 AB040918.1				1.0E-93 AL049801.1	11433646 NT		11417856 NT		1.0E-63 AF240786.1		8.0E-94 AF142482.1	5.0E-94 AB014512.1	5.0E-94 AB014512.1	5.0E-94 AA722434.1	
Most Similar (Top) Hit BLAST E	1.0E-93 A	1.0E-93 A	1.0E-93 B	1.0E-93 B	1.0E-93 D87675.1	1.0E-93 A	1.0E-93 A	1.0E-93 U78509.1	1.0E-93 U78509.1	1.0E-93 A	1.05-93	1.0E- 0 3	1.0E-03	1.0E-83 D42072.1	1.0E-83	1.0E-83 Y10183.1	1.0E-83	1.0E-83	1.0E-63	1.0E-83 X13474.1	1.0E-93 X13474.1	1.0E-93	1.0E-83	1.0E-93 A	1.0E-93		1.0E-83 A	8.0E-94	8.0E-94	5.0E-94	5.0E-94	5.0E-94	
Expression	1.7	96.0	1.47	1.47	7.48	1.27	28	2.38	2.38	98.0	10.32	1.4	2.01	3.49	2.54	1.2	1.38	1.79	1.28	8.29	8.29	0.70	0.62	1.84	2.64		1.49	1.03	1.63	4.23	4.23	4.22	
ORF SEQ ID NO:	27924		26689	26690	28349		29763	31173	31174	31389	31546	31850	32650	32807	33984	34269	34382	33542	33546	35319	35320	35467	35910						29333				
Eten SEQ ID NO:	15184	15228	Ì	l		15973	17132	18278	18278	18472	<u> </u>	1_	L	19837	20862	21133	L	L _	1			L	22693	24846	L	L	25391	23138		<u>L</u>		L	
Probe SEQ ID NO:	2486	2511	2825	2825	2834	3210	4395	5470	5479	5678	5825	9	98	7150	8458	8441	8547	8352	9356	9488	9488	9625	10045	12487	12568		12739	10492	3944	5283	5283	5957	

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Homo sepiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3' xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2201679 3' tw11f10.x1 NCL_GGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE; Homo septens solute cernier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA Homo sapiens solute carrier family 22 (organic cation transporter), member 1-life (SLC22A1L), mRNA Homo seplens cleavege and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA ot83d05.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3' zw63g08.r1 Sogres_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5 Homo septens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds Homo saplens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds yd98b04.s1 Scares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:116239 3' 602042163F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180023 5 Homo sepiens protocadherin alpha 13 (PODH-elpha13) mRNA, complete cds Homo sapiens chromosome 21 open reading frame 18 (C210RF18), mRNA Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA Hamo sapiens ASHZL gene, complete cds, similar to Drosophila ash2 gene Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete ods Homo sapiens exonal transport of synaptic vesicles (ATSV) mRNA Homo saplens hypothetical protein FLJ12455 (FLJ12455), mRNA Top Hit Descriptor Homo sepiens ribosomel protein L27 mRNA, complete cds Homo septens E1A binding protein p300 (EP300) mRNA Homo sapiens zinc finger protein 277 (ZNF277), mRNA Homo sapiens mRNA for MEGF2, partial cds Homo sepiens mRNA for KIAA0679 protein, pertial cds Homo sepiens mRNA for KIAA0027 protein, pertial cds Homo sapiens complement component 5 (C5) mRNA Homo sapiens hepatic leukernia factor (HLF), mRNA Homo sapiens hepatic leukemia factor (HLF), mRNA Homo sepiens glycogenin-1L mRNA, complete cds Homo sapiens huntingtin (HD) gene, exon 37 EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** EST HUMAN **EST HUMAN** Database Top I Source 11440670 NT Z 뇐 ż 4757821 NT ż 11440670 NT z 둗 눋 눋 11427779 NT 11545792|N 4502508|NT 4557558 NT 4826863 11427779 11496268 11526228 9558724 4506008 Top Hit Acession 4.0E-94 AW 197851.1 3.0E-94 AF152309.1 3.0E-94 AB011536.1 4.0E-94 AW 197851.1 3.0E-04 AA464805.1 3.0E-04 AF087942.1 AB022785.1 3.0E-94 AF167706.1 3.0E-94 AF167706.1 3.0E-94 AB014579.1 BF529115.1 4.0E-94 AI591312.1 5.0E-84 AI015800.1 5.0E-84 T89398.1 5.0E-84 D25217.2 3.0E-94 U26711.1 4.0E-84 L05094.1 3.0E-04 3.0E-94 3.0E-94 4.0E-04 5.0E-04 4.0E.94 3.0E-04 3.0E-94 3.DE-94 3.0F.94 4.0E-94 3.0E-04 5.0E-94 4.0E-94 Most Simila (Top) Hit BLASTE Value 1.18 4. 1.19 0.83 1.94 204 2.87 1.82 0.88 2.61 1.27 1.27 3.41 4.35 866 <u>.</u> 1.38 ধ্ব 1.86 0.92 Expression Signal 36083 30038 27208 27536 35326 3214 36420 32693 32143 2005 27173 27534 31800 32125 33923 34371 30619 28053 29054 31301 28111 ORF SEQ ÖΝQ 19130 20792 23713 19145 19145 23198 13375 13479 1476 14475 14805 14805 16906 24274 19648 16372 19473 18839 SEQ ID 2123 25394 26017 25021 14573 16414 17403 14507 18390 1841 ö 7696 8488 1834 1733 2073 5595 9059 6360 8088 11679 8537 12209 2662 4669 6376 6376 6812 11431 597 ğ 1733 1785 2073 4108 9492 11043 6910 12758 12761 3661 SEQ ID

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	Top Hit Descriptor	AND COAB Cods Home seniers (2)NA clone (MAGE:2391813.3)	WASUNITATION OF COMPLETE SEPTEMBERS OF STATES	WISHTIAN INC. COLL COLOR TOWN OF THE WAY OF	601175/62FT NIT MGC_I/ Holina services con access MAGE:3352559 5	CONTINUES IN THE MACE OF HER SENTENCE CONTINUES CONTINUE	601111090FT Nin _MCC_ TO TION SQUARES COLOR COLO	Homo servers 1) yourselves to constitute the complete genome	Escriptions of the months of the construction	Lorzes de Comes Infant Ivain 1NIR Home septems CDNA cigne IMAGE: 45053 5	NOTIVET COMES REPORTED TO THE CONTRACT OF THE PROPERTY OF THE	AVICOSEL III O I INI III ospanoma 21 seemaat HS21C004	Homo separas critationals 21 separati HS21C00	Hono separate carculation of a comment of the separate activator protein (PAXS), mRNA	Hame sapiens paired box gene 3 (b-cer lineage spound above process)	6014687481-1 NFT MGC 07 Hailo septens contraction in the contraction of the contraction o	Homo sapiens IL-1 receptor entegonist IL-1Ra (IL-1RN) gene, atternatively spliced forms, complete cds	angual of Schiller olicodendrogloma Homo sepiene cDNA clone IMAGE:1956122 3' similar to TR:U62845	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ;	HOME SERVICE NATION AT LINES SERVICE THAT HAVE FOR IMAGE 3531038 5'	6011/3/62F1 NIT MGC 17 TOUR SEPTEMBER CONTROLL STATES FOR THE WAS TAKEN THE WORLD AND AND AND AND AND AND AND AND AND AN	6011/3/62F1 NIT MGC 17 1 WILD CAPACITY COMPLETE CAS	Library September KIA A0255 gene product (KIA 40255), mRNA	Linux series KIAA0255 sere product (KIAA0255), mRNA	M. my lang alv T game (excris 10 and 2)	M. murezaldus olv/1 cerne (excrns 1c and 2)	Lines services grant and services and services like protein (ANK) mRNA, complete cds	Months Septemble From Septembles CDNA clone IMAGE:2340606 3' similar to gb: K00558	TUBULIN ALPHA-1 CHAIN (HUMAN);	wedsect.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:2340808 3 SIMIER to go:Nucoso TUBULIN ALPHA-1 CHAIN (HUMAN);		Homo seriens professorine (prosonie, mecropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA		
	Top Hit Database Source		EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	5	Į.	EST HUMAN	EST HUMAN	EST HUMAN	Į.	LN	F	EST HUMAN	¥		EST HUMAN	Ł	EST HOMAN	EST HUMAN				į t	į.	Z	EST_HUMAN	EST HUMAN			12	
	Top Hit Acession No.		1910393.1	1910393.1	1.0E-04 BE205714.1	1.0E-94 BE253433.1	1.0E-94 BE253433.1	9506692	1.0E-94 AE000289.1	1.0E-94 AL040518.1	108270.1	1.0E-94 AV725992.1	1.0E-94 AL163204.2	1.0E-04 AL163204.2	11428710	1.0E-94 BE780478.1	IRSSON 1	, cooper	1.0E-84 AI272244.1	11418871	1.0E-84 BE295714.1	1.0E-94 BE295714.1	9.0E-95 AF027302.1	7662027	/ BOZUZI	9.0E-95 X82509.1	9.0E-95 X8Z569.1	9.0E-95 AF274753.1	8.0E-96 A 700908.1	O OF OR A PROPOSE 4	A1700850.1	1141937	1142052	714203
	2 * U	Value V	2.0E-94 AI910393.	2.0E-94 AI910393.1	1.0E-04 B	1.0E-94 B	1.0E-94 B	1.0E-04	1.0E-94.4	1.0E-94 /	1.0E-94 H08270.1	1.0E-94 /	1.0E-94 /	1.0E-04/	1.0E-94	1.0E-94	4 05,04 1 185590 1	1	1.0E-04	1.0E-94	1.0E-94	1.0E-94	9.0E-95	9.0E-95	9.0E-95	9.05-65	8.0E-85	9.0E-95						8.05-95
	Expression Signal		0.7	0.7	1.94	2.07	2.07	1.7	0.64	0.73	0.72	0.58	0.63	0.63	2.76	2.04	000	3.00	2.82	1.72	1.45	1.51						1.77	3.18					1.76
	ORF SEQ ID NO:		35501	35502	25601	28492	28493	76962	34727	31922	31933	32190	33836	33837				308.02	37245	37675	25601	25601	26892					33974	200866	1_				32898
	SEQ ID		22305	22305	12959	15851	15851	17065	18763	18950	18959	19194	20707	20707	21888	22339		23673	23949	L	1_	12959	14206	15916			18123	20844					Ц	19828
	Probe SEQ ID		9853	9653	4	3086	3088	4328	5982	6173	6182	8428	8012	8012	9455	2884		11000	11288	11754	12330	12608	1459	3163	3153	5320	6320	8150		8	4489	6840	7141	7141

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Tigle Exon Flobes Expressed III brain	Top Hit Descriptor	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo sepiens proline dehydrogenese (proline oxidase) (PRODH) mRNA	Homo sapiens mRNA for KIAA1395 protein, partial cds	Homo sepiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA	Homo seplens developmental arteries and neural crest EGF-like protein mRNA, complete cds	Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA	zu84b01.st Soeres_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.t1 L1 repetitive element;	Homo sapiens DNA for emylaid precursor protein, complete cds	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sepiens Ly-6-like protein (CD59) mRNA, complete cds	Homo saplens chromosome 21 segment HS21C046	HTM1-288F HTM1 Hano sapiens cDNA	602071146F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214147 5'	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA	EST370191 MAGE resequences, MAGE Homo sepiens cDNA	EST370191 MAGE resequences, MAGE Homo sepiens cDNA	au93b08.x1 Sohneider fetal brain 00004 Homo sepiens cDNA clone IMAGE:2783799 3' similer to TR:060463 060463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];	aus3b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone INAGE:2783799 3' similar to	Homo sardens KidA0783 news product (KidA0783) mBNA	Homo sepiens K/AA0783 cene product (K/AA0763) mRNA	801845212F1 NIH MGC 55 Homo eaplens cDNA clone IMAGE:4070451 6	DNA clone IMAGE:194468 5	Homo sepiens KIAA0255 gene product (KIAA0255), mRNA	Homo sepiens KIAA0255 gene product (KIAA0255), mRNA	Homo sepiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3)			Homo sepiens G protein-coupled receptor 19 (GPR19) mRNA	
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 | Human muscle-type phosphofnuctokinase (PFK-M) gene, exon 7
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 | Homo sapiens transcription factor 2, hepetic; LF-B3; varient hepetic nuclear factor (TCF2), mRNA | Homo saplens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds | Homo sapiens huntingtin (Huntington deease) (HD), mRNA | Homo sapiens ribophorin II (RPN2), mRNA
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Page 415 of 536 Table 4 Single Exon Probes Expressed in Brain

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19 EXON Probes Expressed in Drain	Top Hit Descriptor	RC6-FN0019-290600-011-G11 FN0019 Homo sepiens cDNA	RC6-FN0019-290600-011-G11 FN0019 Homo seplens cDNA	801437232F1 NIH MGC_72 Hamo septems cDNA dane IMAGE:3922423 5	PMA-1 T00/19-090300-002-409 LT00/19 Horno septems cDNA	Linear anima distriction 21 information mRNA	Horito september on originations are accommended to the commended of the c	בותושום מולסם מספום וליים ביות היות היות היות היות היות היות היות ה	Homo sepiers sielytrensferase 6 (N-acetyflacoseminide alpha 2,3-sielytrensferase) (SIAT6), mRNA	Homo seplens KIAA0763 gene product (KIAAU763), minuka	Homo septens KIAA0763 gene product (KIAAU/63), mrava	Homo sapiens myosin, heavy polypepade 2, sretous muscle, edunt (MTD2), till dan	Home septens KIAA0763 gene product (NAA0 765), mixtra	Hamo saplens KIAA0783 gene product (KIAA0703), minning	Homo saplens mRNA for KIAA11/2 protein, petrell ous	Homo eaplens mKINA for KIAA1172 protein, per last cus	Hamo septens mitthe for KIAAT112 property, par teal outs	Home septiens prospinational and the septient of the septient	H.saplens DNA for monoamine codease type A (7) (palled)	Homo septens NOUT protein (NULT) genes, exchib. 1, 2, 4 M. 5	Homo septens A kinese (PrivA) michol protein (Arkaba) michol	Home sapiens A kinase (Frith) end of process (Arithmetics)	Homo sabiets mixes in a sussession procession and	Home septens michal of 1450-spaning, companies one	Human type IV Cutagentage (VLC-IL) gains, man 5	Human type IV Canada nase (C.C.) gain, wall of	Trust a grant of the subset of the subset of the services CDNA done IMAGE:212327 5	YOUTHER DATE THE THE THE THE THE THE THE THE THE T	HOID SECTION S	Homo separas critariosadire z i seginari nozicono		QV4-GNOT20-208-00-42/012 GNOT20 India september CNNA	COVE-GNOT ZU-ZOUBOU-AZI-BIZ GNOT ZU TRATIO BEBIEFIS COT CO	AV059401 GNU TRAITO SEMANIS CONTA CARIS GNUS MODES IN A GE 2819351 5	
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| Homo sepiens neuronal cell adhesion molecule (NRCAM) mRNA | Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA | Human endogenous retrovirus type K (HERV-K), gag, pol and env genes | EST367124 MAGE resequences, MAGC Homo septems cDNA | EST367124 MAGE resequences, MAGC Homo septens cDNA | Fells catus superfact myosin heavy chain (sMMHC) mRNA, complets cds | Homo sapiens transfert receptor potential channel 5 (TRPC5), mRNA | Homo saplens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA | Homo saplens HSPC144 protein (HSPC144), mRNA | Homo eapiens HSPC144 protein (HSPC144), mRNA | Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214)
mRNA | Homo sepiens secretory pethway component Sec31B-1 mRNA, alternatively spliced, complete cds | Homo sapiens mRNA for KIAA1290 protein, partial cds | Homo saplens mRNA for KIAA1200 protein, partial cds | Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA | Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA | L5-HT0117-011099-004-D07 HT0117 Homo septens cDNA

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 | 601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5

 | EST22872 Adipose tissue, white II Homo sapiens cDNA 5' end | EST22872 Adipose tissue, white II Homo sepiens cONA 5' end

 | Human mRNA for alpha-actinin | DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5 | 2x97e12.s1 Sogres_NhHMPu_S1 Homo septens cDNA clone IMAGE:787758 3' similar to TR:01304125
01304125 PMS4 MRNA | RC0-BT0812-250900-032-a09 BT0812 Homo septens cDNA | MR0-HT0241-150500-010-b02 HT0241 Homo septems cDNA
 | MR0-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA | CMO-BN0106-170300-283-406 BN0106 Homo septems cDNA | Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete ods | Homo sepiens PAD-H19 mRNA for peptida/arginine delminase type II, complete cds | Homo saplens brefeldin A-Inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
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Page 417 of 536 Table 4 Single Exon Probes Expressed in Brain

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Top Hit Descriptor	Homo saplens apolipoprotein H (beta-2-ghycoprotein I) (APOH) mRNA	Human N-mothyl-D-esperiate receptor modulatory subunit 2A (hNR2A) mRNA; complete ods	Himman Numeriny D. espandate receptor modulatory eutounit 2A (INNR2A) mRNA, complete cds	11	Home separa minna id Calino aprilez, Carayina istano, i orgina.	HOMO SECTION IN TALK ATD ACCOUNTS TO SECTION OF THE	Homo saciens ligase III, UNA, A I P-dependent (Eldo), ususkript variant aprix, in var.	Homo sepiens cystic mousis radiation in conductance inguinary, (1) minus management (CFTR), minus minu	Homo septens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMAZ) mrava	Homo serviens were avian servicine (Schmidt-Kuppin A-2) viral oncogene normong (SNC), minutes	Homo septens cybodrome P-450, subtamity IV b, polypopude 1 (017-451), missing	Homo septions middly to Nivausy prount, per use cus	Homo sapiens mRNA for KiAA0384 protein, perdal cus	Homo septens AXL receptor tyrosire idnase (AAL), transcript varient I, moves	Hamo sepiens AXI, receptor tyrosine kinase (AXL.), transcript variant 1, micura	Home saplens mYNA, similar to rat myomegalin, complete cus	Hamo sepiens mRNA for KIAA1290 protein, perties ads	Home septems mYNA for KIAA1230 prosent, perser cus	Homo sapiens G-2 and G-phase expressed 1 (G OFF), michay	Homo sepiens mrthA for KIAA11/2 protein, perust cus	Homo sepiens amyold beta (A4) precursor protein (protesse neotn-ti, Alzheimer disease) (APP), mRNA	Homo sapiens amyold beta (A4) precursor protein (protesse nextr-II, Abrielmer disease) (APP), mRNA	Homo sapiens N-myc (and STAT) interactor (NMI), mKINA	Human beta-prime-adaptin (BAMZ2) gene, exch /	Homo eapiens pericentrin (PGN1) mRNA	Homo sepiens eukaryong translation elongation Laptical Laptical Laptical Laptical Laptical Laptical Laptical Laptical Labtical Lab	601339520F1 NIH MGC 63 Hamp eaplens author dans inwage: 3001021 0	RC0-H10258-211189-011-g05 H10256 H0m5 septens cDNA	KCCH10258-271198-011-gub nijezo namo saprans curion	CALC CIVIL IN CALL I AS I CALC		Homo especie newcore gala product (newcore), illing of
Top Hit Database Source	Z	117	E LA		الحال	Ž	Ę	ᅜ	NT	LN	Į.	<u></u>	¥	LN.	L	NT	N	NT		Z	ΓĀ	ΤN		F	Z	_	EST_HUMAN	EST HUMAN	EST_HUMAN			N
Top Hit Acession No.	4557326						7710125	11422155	4557708		3233		4.0E-97 AB011168.1	11863122	11863122	4.0E-97 AB042557.1	4.0E-97 AB033116.1	4.0E-07 AB033116.1	11418318	3.0E-97 AB032998.1	4502168	4502166	4768813	J36255.1	5174478	4503470	1.0E-07 BE508486.1	1.0E-97 AW379976.1	1.0E-07 AW379978.1	1.0E-97 R10887.1	11427757	11427751
Most Simiter (Top) Hit Teles SLAST E Value	4.0E-07	7 000001	4.05-07	4.0E-3/ CUSOUZ.1	4.0E-07 Y11339.2	4.0E-07 Y11339.2	4.0E-97	4.0E-07	4.0E-97	-4.0E-97	4.0E-07	4.0E-97	4.0E-97/	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-07	4.0E-97	3.0E-97	3.0E-97	3.0E-07	3.0E-97	3.0E-97 U36255.1	3.0E-07	1.0E-97	1.05-97	1.0E-07		1.0E-97	1.0E-97	1.0E-97
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ORF SEQ ID NO:	24470	7	31482	31483	32590	32591	32703	32468	33863	34087	34353	35043		37062		36407				25685	26294	26295						33534	33535	35513		36539
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Page 418 of 536 Table 4 Single Exon Probes Expressed in Brain

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Chigo Lyon Flores Expressed in Brain	Top Hit Descriptor	vol7009 r1 Soares soluit brain N2454HB55V Home concluse and a line of the solution of the solu	Homo sanions (inchementalized home marrier politics of inchementalized by Noo (billion)	A 1403124 3 4 (Augment dated to be simple of protein binase), mich	A language a (Agreement of the Language of the	601673696F1 NIH MGC 21 Home earliest chart A constant chart	Linear Control of the	Home series (New) mDNA Assessed (1.1) minuted to the encoding mitochondrial protein, complete cds	80128706551 NIH MGC 40 Home series ONIA - Learning Construction of the Construction of	Home senses Pan CIDes - Almin senses Control (Almin City)	801172658F1 NIH MGC 47 Home employed and the contraction of the contra	Homo saniens chrowcome 24 comment UC24/200	Homo services potassism chemial sub-mit (HEBO 3) DNA	Homo seriens fathered Commans & Brees loss shells 4 (25.2)	Homo saviens attractin preciment (A TDN) person 40	Homo servious attraction menurose (ATDN) was a man 46	Anno sedens under process (n. 1747) Burg. 2011 10	International Architecture Allega (FIRZB) III KINA	Homo seniens phosphetiduling these plans also also also also also also also als	Homo series hundielics make El 140409 (El 140409) - DAYA	Homo series broothed profile E. Janes (E. 1908) - DAIA	Homo saplens SH3-domain GRB2-like 2 (SH3/C) 2 mRNA	Homo saplens SH3-domain GRB2-like 2 (SH3/GP 2) mRNA	Homo septers NKA T45 mRNA complete ets	Homo septens N/KA T4b mRNA complete ede	H. sapiena archivasa com avm 3 (FC 3 K 3 4)	Homo serviens AIM-1 produit (1 OCS-1454) mBNA	Human cyhraktorna Para (Cybolata) casa complete ca	W380-07-07-07-07-07-07-07-07-07-07-07-07-07	PMO-BN0085-100300-001-008 BN0088 Livers and an arrived the control of the control	y 23/05.17 Soeres fetal liver spleen 1NFLS Homo eaplens dDNA clone IMAGE:243585 5' similer to	PIR:S64204 S54204 ribosomal protein L29 - human;
ואים באחוו רוטים	Top Hit Daterbese Source	EST HUMAN	NT	FST HIMAN	EST HIMAN	EST HUMAN	l L	L Z	EST HUMAN	Ί.	EST HIMAN	L	NT	L	L	LN	Į.	L	L	Z									HIMAN	Т	1	ESI MAMA
5	Top Hit Acession No.	3.0E-98 H46698.1	N 9822088	3.0E-98 AJ403124.1	3.0E-98 A.1403124 1	3.0E-98 BE900454.1	3 OF - DR [150309 4	3.0E-98 L26405.1	3.0E-98 BE382519.1	11418177 NT	2.0E-98 BE294281.1	2.0E-98 AL163202.2	2.0E-08 AF032897.1	4758331 NT	4F218902.1	2.0E-98 AF218902.1	4758975 NT	7706512INT	4505798 NT	11431271 NT	11431271 NT	11428813 NT	11428813 NT				7705868			-		
	Most Similiar (Top) Hit BLAST E Value	3.0E-98	3.05-88	3.0E-88	3.0E-98	3.0E-98	3.015.08	3.0E-98	3.0E-98	3.0E-98	2.0E-98	2.0E-98	2.0E-08	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-98	2.0E-08	2.0E-98	2.0€-98	2.0E-08	2.0E-98 L79986.1	2.0E-98 L78686.1	2.0E-08 X12884.1	2.0E-98	2.0E-98 U22028.1	1.0E-98	1.0Ε-98/4	4 OF OB M40040	I OF TOTAL
	Expression Signal	2.73	0.48	1.42	1.42	0.96	4.11	1.56	1.47	3.56	2.66	1.53	8.0	3.21	45.1	1.34	1.39	4.03	1.15	1.07	1.07	4.94	4.94	0.58	0.58	1.48	1.37	1.42	16.4	2.12	11.24	1.4
	ORF SEQ ID NO:	34485	35030	35639	35640	36233	36799				27531	27699	29637	29870	30129	30130	30466	30757	32329	33286	33287	34342	34343	34421	34422	35290		37103	25820	25871	72237	
	Exon SEQ ID NO:	21341	21886	22434	22434	23017	Z322Z	24447	25262	25013	14803	14959	17005	17045	17508	17508	17849	18097	19322	20194	20194	21198	21.08	21283	21283	22115	22980	23822	13181	13228	14520	
	Probe SEQ ID NO:	8640	9197	82/83	9783	10371	10872	11863	12868	12751	2071	2231	4264	4306	4778	4778	5131	5232	6557	7523	7523	828	8208	8691	<u>3</u>	9437	10313	11155	396	442	1789	

Page 420 of 536 Table 4 Single Exon Probes Expressed in Brain

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Top Hit Descriptor	과8809.11 Strategene muscle 837209 Homo sepiens cDNA clone IMAGE:628240 5' similar to TR:G806562 G806662 NEBULIN. ;	601284988F1 NIH MGC 44 Homo saplens cDNA clone IMACE:3606692 5'	601284036F1 NIH MGC 44 Homo septens cDNA clone IMAGE:3606692 5	Lance series testa in this mRNA complete cds		Homo sapiens beta-tubulin mktv4, complete cus	QV-BT073-191298-012 BT073 Homo sapiens cDNA	QV-8T073-191298-012 BT073 Homo septens cDNA	EST380711 MAGE resequences, MAGJ Homo septens cDNA	Im68h07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMACE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONST;	im69h07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN Ps5957 BH3 INTERACTING DOMAIN DEATH AGONIST;	3700002 r1 Stratagene lung carcingma 837218 Homo septens cDNA clone IMAGE:565443 5' similar to	TR:G8622904 G8622004 GPLANCHORED PROTEIN P137.;	Human endogenous retrovirus, complete genome	Homo sapiens oscillin (hl.n) gene, exon 5	Homo sapiens NK-raceptor (KIR-G2) gene, linker region exon	Human G2 protein mRNA, partial cds	EST388473 MAGE resequences, MAGN Homo sepients cDNA	Homo sapiens CD34 antigen (CD34) mRNA	Homo sapiens GAP-like protein (LOC51308), mRNA	Homo sepiens polycystic kidney disease (PKD1) gene, exons 27-30	Homo sepiens polycystic kidney disease (PKD1) gene, exona 27-30	H.sapiens mRNA for estrogen receptor	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA	Homo sepiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds	Homo sapiens lodestar protein mRNA, complete cds	Homo sepiens todestar protein mRNA, complete cds	Homo sapiens inostici 1.4,5-triphosphate receptor, type 1 (TPR1), mRNA	Homo sepiens inceital 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA			Homo sapiens UDP-glucose:glycoprotein glucosyfransferase 1 (HUGT1), mRNA
Top Hit Database Source	EST HUMAN	EST HUMAN	MAN ILL TOUR	TOWN TO LET	Z	N	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN		EST_HUMAN	N	Z	FZ	NT	EST HUMAN	TNO	E	F	LN	Z.	TN	TN	IN	L	LNT	LN	LN.	L	LN
Top Hit Acession No.	1.0E-98 AA195854.1					1			9.0E-00 AW988635.1	9.0E-99 Al479829.1			9.0E-09 AA134604.1	9635487	7.0E-99 AF035808.1			4	888	7708138 NT				158	6.0E-99 AB036429.1	6.0E-99 AF080255.1		3189	11431994 NT	11628299 NT	9910279 N	D910279 NT
Most Similar (Top) Hit BLAST E Value	1.0E-98.A	1 OF -08 B	200	1.05-901	1.0E-88 /	1.0E-98 A	9.0E-99	9.0€-99	9.0E-99	9.0E-99	9.0E-99		9.0E-99/	8.0E-99	7.0E-99/	7.0E-99/	6.0E-09 U10991.1			6.0E-99	6.0E-99 L43610.1	6.0E-99 L43610.1	6.0E-99 X99101.1	6-30.9	6.0E-99	6.0E-99	6.0E-99/	6.0E-99				8.0E-90
Expression Signal	3.4	-	1		2.7	2.7	0.88	0.88	4.21	2.75	275		2.13	188	1003	280	1 80	1.15	121	0.72	101	1.01	1.18	0.53	2.28	3.33	3.33	90	0.6	3.89	2.01	2.01
ORF SEQ ID NO:	30808	24478	0/110	311/9	34726	34727	31441	31442	31691	37009	37010		37298	34461	21458	37532	25886			32270	32354	32355			34502	34602						
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Single Exon Probes Expressed in Brain Page 421 of 536 Table 4

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	H.sapiens IMPA gene, exon 8	Homo saplens T cell receptor beta locus. TCRBV7S3A2 to TCRBV12S2 recton	801513157F1 NIH_MGC 71 Homo saplens cDNA clone IMAGE:3914391 5	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds	2008-063X1 NCI_CGAP_HN9 Homo septens cDNA clone IMAGE:2736874 3' stmiler to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MISCIE ISOFORM (HI IMAN).	Human Ku (p70/p80) subunit mRNA, complete cds	Homo sapiens short chain L-3-hydroxyacyf-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	246408.rf Scares_fetal_Jung_NbHL19W Homo septens d2NA come IMAGE:306635 5' similar to dbM15182 BETA-G; LICLIRONIDASE PRECEIRSOR /LILIMAN).	W81509.1 Scenes blacenta Nb2HP Home seniors of Na Consulty,	Homo sepiens myosin X (MYO10) mRNA, complete cds	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA	Homo sapiens intersectin long teoform (ITSN) mRNA, complete cds	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Human Ku (p70/p80) subunit mRNA, complete cds	Homo septens truncated Niemanin-Plok C3 protein (NPC3) mRNA, complete cds	Homo sepiens truncated Niemenn-Pick C3 protein (NPC3) mRNA, complete cds	Homo septens FK508-binding protein 6 (36kD) (FKBP6) mRNA, and translated products	Hamo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products	Human interferon-eipha receptor (HulfN-eipha-Rec) mRNA, complete cds		Homo septens fatty acid amide hydrolase (FAAH) gene, exon 14	Homo sepiens cell recognition molecule Caspr2 (KIAA0868), mRNA	Homo saplens glyche receptor, alpha 2 (GLRA2), mRNA	Homo septens glyche receptor, alpha 2 (GLRA2), mRNA	H. sepiens E6-AP gene exon 2	Homo septens ALEX1 protein (LOC51309), mRNA	hd02h02x1 Soures_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711FT 002711 PRO-POL-DUTPASE POLYPROTEIN	Homo septens hundingtin interacting protein 1 (HIP1), mRNA	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
gle Exon Pro	Top Hit Database Source	N FN	Ę	EST_HUMAN	LN	EST HUMAN	NT	LN ⊢N	L	EST HUMAN	EST HUMAN	LN	N	TN	TN	LN	IN	NT	L/N	LV.	N	ĽΝ	L	NT	Ŋ	卢	TN	F	EST HUMAN		TN1
Sin	Top Hit Acession No.	111365.1	5.0E-99 AF009660.1	5.0E-00 BE800177.1	A95586.1	2.0E-00 AW274792.1	A30938.1	2.0E-99 AF095703.1	2.0E-99 AF257737.1			2.7	109639601	1.0E-09 AF114487.1	1525150			1.0E-99 AF192523.1	4503730 NT	4503730			1.0E-99 AF098018.1	7882349 NT	11421007 NT	1421007	X98022.1	11419721 NT	1.0E-89 AW340174.1	7514	7427514
	Most Similer (Top) Hit BLAST E Value	5.0E-99 Y11365.1	5.0E-99/	5.0E-99	3.0E-99 M95586.1	2.0E-00	2.0E-99 M30938.1	2.0E-99	2.0E-99	2.0E-00 W23507.1	2.0E-99 R78254.1	2.0E-99 A	2.0E-00	1.0E-99 A	1.0E-89	1.0E-99 M30938.1	1.0E-99 A	1.0E-99 A	1.0E-99	1.05-99	1.0E-99 J03171.1	1.0E-09 A	1.0E-99.A	1.0E-99	1.0E-99	1.0E-00	_	1.0E-99	1.0E-89 A	1.0E-99	1.0E-99
	Expression Signal	1.38	1.56	2.81	4.88	6.88	1.29	1.04	0.58	9.55	0.76	3.39	1.48	1.63	1.02	2.09	2.64	2.64	1.41	1.41	1.38	2.82	2.82	0.68	1.28	1.28	0.78	1.49	1.71	2.01	2.01
	ORF SEQ ID NO:		29895				28666		33348	34444	34897	36990	37708	26751	25809	26826	26981	20062	27367	27368	28480	28715	20/16	31367	32005	32688	32789		35270	37029	37030
	Exen SEQ ID NO:				20914	13968	16015		20243	21300	21739	23719	24378	13111	13106	14147	14295			1466/	13848	980/-	980/-	2 2 2 3	19822	19822	25104	21787	22098	23754	23754
	Probe SEQ ID NO:	1957	4526	12208	823	1217	3253	4506	7574	8008	9050	11049	11788	307	370	1400	1540	1549	1920	200	3063	2 3	3	RCS RCS	6707	6/0/	88	88	9420	11084	11084

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Top Hit Descriptor	Homo sepiens heat shock trenscription factor 2 binding protein (HSFZBF), tilinary	Home services cliniathione Subarsferase theta 2 (GSTT2) and glubathione Subarsferase theta 1 (GSTT1)	genes, complete cds	Homo sepiens chromosome 21 segment nozi locari	Homo septens chromosome 21 septiment not inch.	Hamp separate 1 estimation 2017 control of the cont	SARATA NO. CGAP Britis Homo saciens CDNA clone IMAGE 2824605 3	Lynn series chromosome 21 segment HS21C006	House series chronosome 21 secment HS21C049	FESTOROSE Essal Prain Strategiane (cat#036206) Homo saplens cDNA done HFBCR32	ESTUZBOTOTOR Main, Other Company of the Company of	regions	G.gorilla DNA for ZNF80 gene homolog	RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cL/NA	Homo sapiens UKFZF boodwu 124 protein (Dru 21 common 22), mRNA	Homo september Living Cooking Living septembers CDNA character (A215039.5)	6020/2064F1 NCL COAR BIND FROM September CDNA clone IMAGE:2722164 3'	Accorded to the Second	qtoznes.xt soeres_trin i sans appress	Homo sepiens mRNA for KIAA1168 protein, partial cus	Rat mRNA for short type PB-caunatin, complete cus	H. septemb mRNA for II-N-gamma (pNC-2)	Homo sapiens KiAAUeo/ protein (ninchoso), illingen	Homo septens Korl 2 gens, redown denies a contract of the cont	HOMO saparts myourcurer in service property (FSHR) mRNA	Homo septients remove the formation of the factor 1-like (MYT1-1) mRNA, complete cits	The service amail confe labora (Droscobile) handog (SOLH) mRNA		2 6550	
Top Hit Database Source		- E	Ę	N.	L	١	٠ŀ	ESI HOMAN	Į,	I.V	EST_HUMAN	Į,	N	EST_HUMAN .	Z	.	EST HUMAN	EST HUMAN	EST_HUMAN	ŢŃ	ᅜ	N.	LN1	LZ.	L	LN C	Z !	N.	POT LINAN	LOI LICIMOIA
Top Hit Acession No.	1979	1.0E-99 AB023222.1	1.0E-99 AF240786.1	1.0E-100 AL163247.2	1.0E-100 AL163247.2	11418230 NT	8230		1.0E-100 AL163206.2	1.0E-100 AL163249.2	105087.1	1.0E-100 AF003528.1	(89631.1	1.0E-100 BE180809.1	7061085 NT	7681685 NT	1.0E-100 BF530735.1	1.0E-100 AW 207555.1	1 OE-100 AI200857.1	1.0E-100 AB032994.1	D83340.1	X62468.1	11418976 NT	D11078.1	1.0E-100 AF057354.1	4503792 NT	1.0E-100 AF036943.1	5032104 N	5032104 N	1.0E-100[BF-244Z18.1
Most Similar (Top) Hit BLAST E Value	1.0E-99	1.0E-99 A	1.0E-99	1.0E-100	1.0E-100 A	-1.0E-100	1.0E-100	1.0E-100	1.0E-100 /	1.0E-100 /	1.0E-100 T05087.1	1.0E-100]/	1.0E-100 X89631.1	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1 OE-100	1.0E-100	1.0E-100 D83349.1	1.0E-100 X62468.1	1.0E-100	1.0E-100 D11078.1	1.0E-100				1	
Expression Signal	1.8	2.77	89.9	0.95	1.53	1.54	1.54	0.69	1.24	0.83	3.06	8	7 19	133	328	322	3.14	1.14	1.81	1.41	1.39	1.33		5.5	1.52	2.14	1.03			1.62
ORF SEQ ID NO:	37088	37343		25443	25443	25528	25527	25550	25618	25753	25770			25015					2007			27894			29658		29785			5 30637
Exam SEQ ID NO:	23808	24040	24525	12830	L	l	12894	12911	12979	13113	13136		13213		1_	1_	1	1		14504	1	1	1_	1	1	1_	1	1		7 18015
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	Top Hit Descriptor	288201.37 NCL CGAP_CML1 Homo sepiens cDNA done INAGE 2573305 3' similar to gb:X12433 PROTEIN PHPS1-2 (HIMAN):	AU118182 HEMBA1 Homo septiens CDNA clone HEMBA1002018 F.	Homo sapiens NF-E2-related factor 3 name complete cite	Human miRNA for plasma inter-alpha-thosin inhibitor heavy chain 17/2)	Homo septens ER to nucleus signalling 1 (ERN1) mRNA	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA	Homo saplens hect domain and RLD 2 (HFRC2) mRNA	AU140214 PLACE2 Homo serviens cDNA clone PLACE2 homo clone PLACE2 Homo serviens cDNA clone PLACE2 homo clone PLACE2 homo clone PLACE2 homo clone PLACE3 FC	AU136800 PLACE1 Hamo sapiens cDNA clane PLACE1005080 F	V38c08.s1 Soares fetal fiver soleen 1NFI S Home sealens china Avan Land Course (1905)	Homo sablens Rho GTP assa articular models (ADEL/CARS) to the control of the cont	ee33b06.r1 Geesler Witne tumor Hono eaples CNA clone IMAGE:897587 5' similar to TR:G487418 G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN PROTEIN	8633b06.r1 Gessler Wilms tumor Homo sepiens cDNA clone IMAGE:897587 5' similar to TR:G487418	MR1-TWOME AND DATE TO THOUSE IT THE PROJECT TO THE	MR1-TN0048-060000-004-LN5 TN0048-Hmm september ADMA	Human mRNA for kidney entidermal armuth feather (ECE) present	801647357F1 NIH MGC 61 Homo serviews cDNA close MACE-2024240 F1	Homo saciens chromosome 21 segment HS21CAC3	AU110951 HEMBA1 Homo sepiens CDNA clone HEMBA1000343 5	AU116951 HEMBA1 Hamo sepiens aDNA dane HEMBA1000343 5	Homo sapiens mRNA for KIAA1485 protein, partial cds	ne IMAGE:2489020 3' similar to contains element	PMO-BN0065-100300-001-00-BN0085-Umms-services - CNIA	AU127720 NT2RP2 Home services cDNA chose NT2RP2201648 R	Homo septens mRNA for KIAA1626 profish partial cyle	Homo septens mRNA for KIAA 1628 protein, pertiel ods	MeSc11.y1 NCI CGAP QU1 Homo seriens cDNA clone MAGE posonos F	hh83c11.y1 NCI_CGAP_GU1 Homo septens cDNA clone IMAGE:2050206 5	AV732101 HTF Homo sepiens cDNA clone HTFBIG01 6'	802020554Ft NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE-4156165 51
	Top Hit Dafabase Source	EST HUMAN	EST HUMAN	Ŀ	Z	LN.	N	TN TN	EST HUMAN	EST HUMAN	EST HUMAN	INC	EST HUMAN	FOT LIMAN	Т	Т	Т	EST HUMAN	Т	EST_HUMAN	THUMAN	L	EST HIMAN	Т	Т	Т	Ę	EST HUMAN	EST HUMAN	Г	EST HUMAN
	Top Hit Acession No.	1.0E-100 AW075983.1		1.0E-100 AF135116.1		4557568	4567568 NT	5729867	1.0E-100 AU140214.1	1.0E-100 AU136800.1		7382479	1.0E-100 AA496841,1			Γ		3.1	1.0E-100 AL163203.2					-				1.0E-100 AW630487.1 E			
	Most Similar (Top) Hit BLAST E Value	1.0E-100	1.0E-100	1.0E-100	1.0E-100 X14690.1	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100 R10887.1	1.0E-100	1.0E-100	1 0F-100 /	1.0E-100 E	1.0E-100 E	1.0E-100 X04571.1	1.0E-100 E	1.0E-100	1.0E-100	1.0E-100	1.0E-100 AB040918.1	1.0E-100 AI972388.1	1.0E-100/A	1.0E-100 AU127720.1	1.0E-100 AB046846.1	1.0E-100 AB046846.1	1.0E-100	1.0E-100 AW630487.1	1.0E-100 AV732101.1	1.0E-100 B
	Expression Signal	0.59	1.33	1.28	0.8	0.94	0.94	1.67	5.64	1.97	1.37	6.0	1.19	130	1.13	1.13	6.76	71.7	4.8	0.68	0.68	3.62	2.78	1.82	7.61	2.11	2.11	1.68	1.68	0.40	1.47
	ORF SEQ ID NO:	30831	31323	31369	31461	31814	31815		32173	32224	32362	32622	32608	32008	32557	32558	32565	34261		34746	34747	34986		33520		35316	35317	36598	35599	35749	36230
	Exen SEQ ID NO:	18220				18850	18850	19113	19174	19224	19349	19587	19576	19576	19530	19530	19537	21123	21158	21603	21603	21820	22089	20404	22048	22138	22136	22394	2394	22254	23014
	Probe SEQ ID NO:	5421	5614	999 999 9	5747	5071	6071	88 88	9405	6457	929	0820	6742	6742	6786	6786	6793	8430	8466	8912	8912	6 132	9210	0333	9386	9483	2883	9743	9743	9905	10368

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	Top Hit Descriptor	Human endogenous retrovirus HERV-K, pol gene	MR0-BN0070-270300-008-h11 BN0070 Horno sapiens cDNA	Homo sapiens 14q32 Jaggad2 gene, complete cds: and unknown gene	Homo saplens 14q32 Jagged2 gene, complete cds; and unknown gene	Homo septens chromosome 21 segment HS21C047	QV2-PT0012-010300-070-404 PT0012 Homo sepiens cDNA	Homo sapiens golgin-like protein (GLP) gene, complete cds	zk89e03.r1 Soares_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE:489984 5'	2K89e03.r1 Soares_pregnant_uterus_NbHPU Hamo sepiens oDNA clone IMAGE:489984 5	Homo septens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	7q88h03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' saniler to TR:Q21997 Q21997 COSMID R151 [2] TR:OQLIACE:	Homo sablens SH3-domain binding probain 1 (SH3-RD1) mRNA	Homo saplens transcobalamin II; mecrocytic anemia (TCN2), mRNA	Homo sapiens SEC14 (S. cerewisiae) like 2 (SEC14L2), mRNA	Homo sapiens SEC14 (S. cerevisiae)-Illie 2 (SEC14L2), mRNA	Homo sapiens mRNA for KIAA0448 protein, partial cds	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA	Homo sepiens ventral enterior homeobox 2 (VAX2), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens phosphoribosykjykonamide formytransferase, phosphoribosykjykonamide synthetase, phosphoribosykaminolmidazole synthetase (QART) mRNA	Homo sepiens of cardiac alpha-myostn heavy chain gene	602156474F1 NIH_MGC_83 Hamo sepiens cDNA done IMAGE:4297291 61	4999e09.x1 Source_NFL_T_GBC_S1 Hamo septens cDNA clane IMAGE:1843336 3'	Homo sepiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	Homo septens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	Homo sapiens KIAA0669 gene product (KIAA0569), mRNA	Homo septens KIAA0589 gene product (KIAA0569), mRNA	Homo sepiens carboxypeptidase A1 (pencreatic) (CPA1) mRNA	RC3-ST0281-160600-016-h09 ST0281 Homo septens cDNA	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA	H. sepiens EWS gene, exon 5
מון ויווויש מום	Top Hit Detabase Source	N	EST HUMAN	NT	LN	LN	EST HUMAN	1	EST_HUMAN	EST_HUMAN	FN	EST HUMAN	L	LN.	14 NT	12	Z	INT	F	NT	14NT	N	EST_HUMAN	EST_HUMAN	NT	L	ΤN	אַן	노	EST_HUMAN	Ę	Ā
5	Top Hit Acession No.	Y10391.1	1.0E-100 BF327292.1	1.0E-100 AF111170.3	1.0E-100 AF111170.3		1.0E-100 AW875464.1	1.0E-100 AF268285.1	1.0E-100 AA115605.1	1.0E-100 AA115805.1	1.0E-100 AF240786.1	1.0E-100 BF448549.1	15732	11417974 NT	7110714	7110714	AB007915.2	7110734	7110734 NT	7657454 NT	4503914		1.0E-101 BF881218.1	Al221878.1	5921460 NT	5921460 NT	7882183 NT	7862183 NT	4502998 NT	BE843070.1	5729892	
	Most Similar (Top) Hit BLAST E Value	1.0E-100 Y10391.1	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-100	1.0E-101	1.0E-101		1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101 Z20656.1	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	_	\rightarrow	1.0E-101	1.0E-101 X72993.
	Expression Signal	2.2	6.27	4.52	4.52	2.11	1.59	1.48	1.57	1.57	6.67	1.51	3.67	4.62	1.75	1.75	1.62	5.88	6.88	1.99	1.6	1.22	14.28	1.63	1.40	1.46	1.52	1.52	1.62	1.79	1.71	28
	ORF SEQ ID NO:		36586	37319	37320	25443			37668	37669	37806		31071	30908	25639	25540	26087	28111	26112	20185	26273	28335	26396	28440	27012	27013	27/182	27183	27389	27510	27808	28076
	Exen SEQ ID NO:		23349	24017		12830	24230	24276	24340	24340	24471	25278	24668	25044	12302	12002	13447	13463	13463	13526	13603	13671	13729	13790	14324	14324	14482	14482	14673	14783	15582	15332
	Probe SEQ ID NO:	10458	10658	11328	11326	11356	11633	11681	11749	11749	11907	12031	12200	12792	75	75	671	8	88	754	833	804	8	- - - - - - - - - - - - - - - - - - -	1577	1577	1740	1740	1938	2 2 2 2 3 3 3	2349	2620

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Single Exon Dayles Evanous in Paris	Top Hit Descriptor	Homo seplens RIBIIR name (nortic) and 40	Home sessions DIDIL	Home parties rubility gene (perties), expn 12	Home exploring genomic downstream Rhesus box	MONASSASE NILL MOS AS U.	EST377830 MACE	Home sealers Diplice of the Company	Home equition bigging () and	France september 1 (1986 (partial), except 12	Home supreme ASTIAL gene, complete cds, eimilar to Drosophile ash2 gene	Lorino sapiens butyrophilm, subfemily 2, member A1 (BTN2A1), mRNA	FIGURE Sapients Dutyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	LO 1377 Z1Z MANGE resequences, MAGI Homo sapiens cDNA	ricilo septens oyopeasmic linker 2 (CYLN2), mRNA	numo sapiens cycoplasmic linker 2 (CYLN2), mRNA	namo saplens carbonic anhydrase VII (CA7), mRNA	Homo sepiens hypothetical protein FLJ22087 (FLJ22087), mRNA	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, atternetive splice form 4, pertial cds	Tham septens Nutropel-type zinc finger protein (PEG3) mRNA, atternative splice form 4, partial ods	WOOTIZXI NG CGAP Gas4 Homo sepiens cDNA clone IMAGE:2533487 3'	PC4 PT6843 200200 AG 52 CE POTTO BEDIENS CDNA clone IMAGE:3349901 5'	SOLOSIOS-ZOLOW-018-112 BT0313 Home sapiens cDNA	60113463454 NILL 2000 CV Hamp septens CUNA clone (MAGE:3345869 5'	801784888E1 NIH MAC AT HAIR BABIENS CONA GIONE (MACE: 3345889 5'	hh74g10.y1 NG_CGAP_GU1 Home septens CDNA done IMAGE:3996837 6* similar to gb:J03143	hit/401/3 NG COAP GUI Home septems CDNA done IMAGE:2868578 5' similar to ab:J03143	ACAGOBAT Socree pregnent whente North Home septems (DNA Alma MARCELIZACOR)	PIR:S54640 S54640 YD8335.03c protein - yeast;	Homo seplens mRNA for KIAA 1351 protein, partial cds	Fromo sepiens mRNA for KIAA1351 protein, partial cds	Trumen mixVA for pancreatic gamma-glutamytransferase	numen micha tor pancreatic gamme-glutamytransferase
Info Exon Pm	Top Hit Database Source	\ 	Į.	ΤΛ	TNOX	EST HUMAN	EST HUMAN	L	Į.	μ	TN.	FN	ENT LIMAN	NAT - IONG						T CHINAN	T	HIMAN	T	Т	Т		T	Т	HOMAN				
i.	Top Hit Acession No.	1.0E-101 AJ237744.1	1.0E-101 AJ237744.1	1.0E-101 AJ252312 1	183	1.0E-101 BF035327.1	1.0E-101 AW985558.1	1.0E-101 AJ237744.1	1.0E-101 AJ237744.1	1.0E-101 AB022785 1	5921480 NT	5021480 NT	1.0E-101 AW 985139 1	Ě	7427542	TA 420 724 NT	14848790 AIT	00/0101		Τ	T	T	T										
	Most Similar (Top) Hit BLAST E Vatue	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0E-101	1.0F-101	1.0F-101	4 OF 404 A FORESTA	1.0F-101 AF208020 4	1.0E-101 AW008475 4	1.0E-101 BE257384 1	1.0E-101 BF330759 1	1.0E-101 BE275821.1	1.0E-101 BE275821 1	1.0E-101 BF029174.1	1.0E-101 AW630070.1	1.0E-101 AW630070 1	107	1.0E-101 AAU30800.1	1 0F-101 AB037772 4	1.0E-101 X80069 4	1.0E-101 X00069 1	
	Expression Signal	1.09	1,09	13.73	1.98	2,27	1.93	1.49	1.49	3.69	1.16	1.16	1.22	3.68	3.68	127	1.01	5 67	5.57	7.48	1.79	7.43	0.84	78.0	2.88	0.67	0.67	8	083	0.83	17.13	17.13	
	ORF SEQ ID NO:		28193		28613		28790		28193	29245	30304	30305	30669	31651	31652	32372		32977	32978	33136		33398	33631	33632	33772	34050	34051	24744	35080	35081	33553	33554	
	Exon SEQ ID NO:			_ l	I	_ {		_1	_	16607	17697	17697	18041	18608	18698	18358	19859	19905	18905	20056	20147	20289	20508	20208 20208	20043	20915	20915	21599	21908	21908	20432	20432	
	Probe SEQ ID NO:	2747	2747	2955	3198	3235	3375	3396	3385	380	4974	4974	5235	5013	5913	රජිමර	7173	7220	7220	7376	7474	7023	7813	7843	7954	8221	8221	8008	8228	9229		9362	

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Single Exon Probes Explessed in Diam	Top Hit Descriptor	Homo sapiens protein phosphatase-1 regulatory subulint / (PPF 177) years, control	Homo sepiens HSC54 mRNA for heat shock cognate process of	Homo septens histone deacetylase 7 (HDAC7), mRNA	Homo saidens historie deecest/ase 7 (HDAC7), mRNA	Lance seviese hert domain and RLD 2 (HERC2), mRNA	and 2009 x1 Beretead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q1313/	Q13137 NDP52.; An Ant 6/15 NIH MGC 20 Homo sapiens cDNA clone IMAGE:3831241 5	A01277215F1 NIH MGC 20 Homo septens CDNA clone IMAGE:3618243 5	Homo sablens mRNA for Centeurin-alpha2 protein	AV710738 Cu Homo septens cDNA clone CuAAKD03 5'	OV3 NT0025-210600-236-h08 NT0026 Homo septens cDNA	ANSOLIOTET NIH MGC 70 Homo septens cDNA clone IMAGE:3903145 5	AVRA4817 GKC Hamo sablens aDNA clane GKCEEE11 5'	AVR04817 GKC Homo septens cDNA clone GKCEEE11 5'	Homo sapiens mRNA for KIAA0454 protein, partial cds	A1283770F1 NIH MGC 44 Homo saplens cDNA clone IMAGE:3605536 5	601283770F1 NIH MGC 44 Homo expiens cDNA clone IMAGE:3805536 5	wi63b08.x1 NCI CGAP_Kid12 Homo sepiens cDNA clone IMAGE:2397971 3' similer to contents within the	MERA MERA repetitive element ; AVZESAZ BM Homo sabiens cONA done BMFAUDO6 5'	1413407 rt Soares febal liver spiesen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5	vd13d07.r1 Soares fetal liver spieen 1NFLS Hamo sepiens cDNA clone IMAGE: 67021 5	AU124629 NT2RM4 Homo septens cDNA done NT2RM4000309 6	Homo sapiens phospholipid acramblase 1 gene, excn 1 and 5 flanking region	IRC-BT074-280499-014 BT074 Homo saplens cDNA	RC-BT074-260499-014 BT074 Homo saplens dDNA	on57h04.81 Soares NFL_T_GBC_S1 Homo expiens cDNA clone IMAGE:1580823 3 smiler to	SW:CAV2_HUMAN P51636 CAVEOLIN-2. [1];	Turno services LIDP charge/transferase 2 family, polypeptide B11 (UGT2B11) mRNA	Lizabiting Sparses heatis NHT Homo septems CDNA clone IMAGE:1408347 3'	RC6-ET0072-150800-011-F01 ET0072 Homo seplens cDNA	
e Exon Probe	Top Hit Database Source	5	LZ LZ					$\neg \tau$	NAME I	HOMAN	CICINAN	Т	T	٦	TOT HIMAN	EST MONOR	N I	EST HIMAN	110111	EST HUMAN	FOT THINKAN	EST HIMAN	ENT HIMAN	LN LN	MAN IL	EST HIMAN	EST LICENT	EST HUMAN	IN.	INT	EST HUMAN	TEST TOWNS
Singl	Top Hit Acession No.			80230	loasco//	N Secol/	11433046 NT						1.0E-102 BE783051.1	3E910555.1	17694817.1	1,7894817.1	AB007923.1	3E388063.1	3E388003.1	1.0E-102 AI762859.1	1.0E-102 AV755842.1	170393.1	170383.1	1.0E-102/AU124029.1	1.0E-10Z/AF 135/ 10:1	A1905037.1	1.0E-102/AIB05037.7	1.0E-102 AA970786.1	4507822 NI	45078222 NT	1.0E-102 AA868675.1	1.0E-102 BF359/243.1
	Most Similar (Top) Hit BLAST E Value	1 OF-102 AF067133.1	1 100 AD00 AD00 405 4	1.0E-102	1.0E-102	1.0E-102	1.0E-102	1.0E-102 AI459825.1	1.0E-102 BE729323.1	1.0E-102 BE386106.1	1.0E-102 AJ238994.1	1.0E-102 AV710738.	1.0€-102 €	1.0E-102 BE910555.	1.0E-102 AV694817.	1.0E-102 AV894817.	1.0E-102 AB007923.	1.0E-102 BE388063	1.0E-102 BE388003.	1.0E-102	1.0E-102	1.0E-102 170393.1	1.0E-10Z 170383.1	1.05-102	1.0E-10Z	\perp						1
	Expression Signer	1 87	0.	9.17	2.84	2.84	0.81	2.83	0.75	1.04	8.23	2.48	3.91	1.32	221	221	1.19	0.63	0.63	0.52	0.81	2.28	2.28	3.79			3.67	1.24	2.56	2.56		3.01
	ORF SEQ E	032.00	30/33		31414	31415	31420	31854	32785	32821	33014	33288		34032	34218	34219	34335		34668	35049	35017			35151			36229	36295				7 37287
	Exan SEQ 1D NO:		18092	18458	18492	18402	18498	18978	19728	L		L	1_	L	L		L		21521	<u></u>			21900	Ц	22929	L	7 23013	8 23074	L.	1_	1_	Ш
	Probe SEQ ID NO:		5287	5983	2698	5698	5704	8200	7038	7085	7255	7524	8122	8201	8392	8392	8501	8828	8829	9150	9181	9221	9221	9311	10281	10367	10367	10428	11008	11008	11280	11380

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	Top Hit Descriptor	tm58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13789 Q13789 ANONYMOUS.;	tm58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289.3' similar to TR:Q13769 Q13769 ANONYMOUS.;	Homo saplens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS239, DXS289, DXS270, DXS272 (DMD), transcript variant Dp427m, DNA	Hamo saplens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164,	DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA	Homo saplens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	EST377849 MAGE resequences, MAGI Homo sapiens cDNA	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'	tm58b05.x1 NCI_CGAP_Bm25 Hamo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;	tm68b05.x1 NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.	EST27193 Human Brain Homo saplens cDNA 5' end similar to None	AU140344 PLACE2 Homo septens cDNA clone PLACE2000374 5'	AU140344 PLACE2 Homo sepiens cDNA dane PLACE2000374 5'	760e03.x1 Soares, NSF_FB_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:3525964.3' similar to SW-PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1:	Homo septens triple functional domain (PTPRF interacting) (TRIO), mRNA	Homo sepiens triple functional domain (PTPRF interacting) (TRIO), mRNA	nd13c02.s1 NCI_CGAP_Ov1 Homo sepiens cDNA clone IMAGE:800162 3' straiter to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);	ae84d12.61 Strategene schizo brain 311 Homo septens dDNA cione IMAGE:9708713' straiter to ab:X03747. cds1 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-1 (HIMAN):	QV2-NN0045-230800-322-b03 NN0045 Homo sapiens cDNA	QV2-NN0045-230800-322-b03 NN0045 Hamo sapiens cDNA	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)	EST375749 MAGE resequences, MAGH Homo saplens cDNA
26	Top Hit Database Source	EST_HUMAN	EST_HUMAN	E		둗	۲	ΝΤ	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	L	L	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	TN	EST_HUMAN
5	Top Hit Acession No.	1.0E-103 AI590071.1	1.0E-103 Al590071.1	TIV COCCOM	202200	5032282 NT	11431100 NT	1.0E-103 AJ28980.1	1.0E-103 AW965776.1	1.0E-103 BE748158.1	1.0E-103 AI590071.1	1.0E-103 AISB0071.1	T31080.1	AU140344.1	1.0E-103 AU140344.1	1.0E-103 BF109244.1	6005921 NT	9005921 NT	1.0E-103 AA581086.1	1.0E-103 AA774980.1	3E935842.1	1.0E-103 BE935842.1		1.0E-103 AW963678.1
	Most Similar (Top) Hit BLAST E Value	1.0E-103	1.0E-103	200	201	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 T31080.1	1.0E-103 AU140344.	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103/	1.0E-103 BE935842	1.0E-103	1.0E-103 237976.1	1.0E-103 /
	Expression Signal	1.48	1.48	4	3	1.53	1.27	0.99	1.63	6.93	4.21	4.21	0.77	222	2.22	1.1	2.86	2.86	1.16	5.04	0.58	0.56	1.44	1.89
	ORF SEQ ID NO:	32396	32397	OL HOE		30580	30544	32716	32883	32860	33446	33447	34019	34354	34355	34439	34845	34846	34891	34941	34995	34996	35811	35859
	Exen SEQ ID NO:	19380	19380	4.704R		17916	17949	19670	19815	19918	20335	20335	20881		21211	21296	21695	21695	21738	21777	21832	21832	22808	22847
	Probe SEQ ID NO:	6618	6618	6747		6747	6872	6935	7127	7233	7871	787.1	8187	8510	8519	880.4	9005	9002	9046	8088	9162	9162	8928	0666

Page 430 of 536 Table 4 Single Exon Probes Expressed In Brain

WU 0	1/5/2/5		1	Ţ	Т	T	T	T	T-	Г	Т	1	T	Τ-	Т	Т	Т	" "	T	7	ተ	Ť"	7"	PO	CT T	/U	Ş0 T	1/(000	67 T	T
i able 4 ngle Exon Probes Expressed in Brain	Top Hit Descriptor	au51g04.y1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE:2518326 5' similar to TR:015046 015046 KIAA0338;	002d08.95 NCI_CGAP_Lu5 Homo septens cDNA clone IMAGE:1522283 5' similer to TR:062084 Q62084 PHOSPHOLIPASE C NEIGHBORING:	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA	Homo sapiens AXL receptor tyrostne kinase (AXL), mRNA	Homo sapiens NOD1 protein (NOD1) gene, excres 1, 2, and 3	Homo sepiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	Homo septens mRNA for partial OCT/plean-A2 protein	Homo sapiens mRNA for partial OCT/plexin-A2 protein	AU136283 PLACE1 Homo sepiens cDNA clone PLACE1003923 5	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30	7e88a10x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29 t3 MER29 tabelithe element	Homo sepiens hypothetical protein FL J20454 (FL J20454) mRNA	Homo sapiens gene for AF-8, complete cds	DKFZp664H1072_r1 564 (synonym: htbr2) Homo sepiens cDNA clone DKFZp564H1072 5	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo septens cDNA clone DKFZp564H1072 51	Homo saplens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA	2022008.s1 Strategene colon (#937294) Home septens cDNA clone IMAGE:587626 3' similar to ob. 714116, met CD50 (3' YCOPROTTEIN PRECI IRSO, ALI IMAN).	001577460F1 NIH MGC 9 Hamp septems CDNA clane IMAGE:3926438 5	RC1-CT0249-110000-214-f12 CT0249 Hamo saplens cDNA	RC1-CT0249-110500-214-f12 CT0249 Homo sepiens cDNA	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA	Homo sepiens KIAA0440 protein (KIAA0440), mRNA	Homo sapiene KIAA0440 protein (KIAA0440), mRNA	Human Iymphocytic antigen CD59/NEM43 mRNA, complete cds	H. sepiens gene encoding phenypyruvate tautomerase ii	EST2/1858 Adrenal gland fumor Homo sapiens cDNA 5' and	Homo sepiens mRNA for KIAA1276 protein, pertial ods	Homo sepiens mRNA for KIAA1276 protein, pertial cds	Homo sepiens mRNA for KIAA1172 protein, pertial cds	Humen mRNA for fibronectin (FN precursor)
gle Exon Prol	Top Hit Defabese Source	EST_HUMAN	EST HUMAN	INT.	IN T	F	NT	LN	LN	EST_HUMAN	NT	EST HUMAN	L'Z	N	EST HUMAN	EST HUMAN	N.	FST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	O NT	TN	TN	TN	NT	EST_HUMAN	TN	N	Z	۲
Sin	Top Hit Acession No.	1.0E-103 AI878956.1		124061	2406		3.1			1		1.0E-103 BE644811.1	38291	1.0E-103 AB011399.1	1.0E-104 AL037549.3	1.0E-104 AL037549.3	4502428 NT					5031570	7862125	7862125 NT	134671.1						
	Most Similar (Top) Hit BLAST E	1.0E-103	1.0E-103 AI792759.1	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 X87831.2	1.0E-103 X87831.2	1.0E-103	1.0E-103 L43610.1	1.0E-103	1.0E-103	1.0E-103 A	1.0E-104	1.0E-104	1.0E-104	1.0E-104 AA132975.1	1.0E-104 BE744628.1	1.0E-104 BF334221.1	1.0E-104 BF334221.1	1.0E-104	1.0E-104	1.0E-104	1.0E-104 M34671.1	1.0E-104 Y11151.1	1.0E-104 AA319436.1	1.0E-104 AB033102	1.0E-104 AB033102.1	1.0E-104 AB032908.1	1.0E-104 X02781.1
	Expression Signal	9.2	3.56	2.04	2.04	222	2.22	1.3	1.3	2.8	10.74	2.41	2.11	2.83	3.73	3.73	2.18	3,68	2.57	1.38	1.38	1.08	1.11	1.11	7.41	2.74	2.04	0.79	0.79	0.78	3.93
	ORF SEQ ID NO:	35998	38583	30008	3000	39677	30678	36717	36718	37340	36421	37867		31091	25878	25677	27328	27853	27606	27829	27830	27893	27965	27068	28285			28986	28967	20315	20712
	Exan SEQ ID NO:	22786	23326	23424			23434	23476	23478	24037	23190	24339	24494	24620	13030	13039	14618	14919	14923	15091	15091	15158	15224	15224	15641	15683	16145	1834	16341	16874	17083
	Probe SEQ ID NO:	10138	10634	10737	10737	10748	10748	10793	10703	11347	11423	11748	11837	12128	227	227	1881	2190	2201	2360	2369	2438	2507	2507	2874	847	3388	3687	3587	3924	4 4 4

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WU	01/5/2/5			_									_							44.0		_	نے عیرا	,] ,	PÇ	T/	ÜŞ	01	<u>/0(</u>)66 سا	7
Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo saplens chromosome 21 unknown mRNA	Homo sapleris chromosome 21 unionown mRNA	Homo saciens death recent 8 (DR8), mRNA	Human Down Syndrome region of chromosome 21 DNA	Human Down Syndrome region of chromosome 21 DNA	Homo seplens all 3 mRNA for Aurora/pi/1-related kinase 3, complete cds	W03b12x1 NCI_CGAP_KI412 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN :contains element TR7 remaititue element	W03b12x1 NCI_CGAP_Kid12 Homo sepiens cDNA clone INMGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN :contains element TR7 remettle alement	Homo sergiers PDZ demain-confeshing question production and account of Account.	601150451F1 NIH MGC 19 Home seniors concernating leads (LCC31731), micro-	6015045(F) NIH MGC 19 Home explana control (MACE) 3000000000000000000000000000000000000	Homo sepiers adeptive related profess constants and a selection (Appendix Constants)	UI-HBIG-BOW-D-09-0-11 81 NC CCAP Sinks Home and the control of the	Ineq16a11x1 NCI CGAP 1.02 Homo series china Acres NAACE 32861763	298b05.81 Sources feetal liver spileon 1NFIS St Home services CNA close 11AA DE Jacobs 2	ye8302.1 Source infant brain 1NB Home services of the Appeal Add CE 224.0 F	Homo sepiens Tho Isoform mRNA, complete cals	Homo septens Trio Isoform mRNA, complete cds	II.3-HT0619-080900-249-F07 HT0619 Homo seciens CDNA	IL3-HT0619-080900-249-F07 HT0619 Homo seplens cDNA	xd78d02x1 Sogres_NR_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116 Q24116 HYPOTHETICAL 29.4 KD PROTEIN	xd76d02x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2803523 3' similar to TR:Q24116 (024116 HYPOTHETICAL 29 4 KD DROTTEIN	Hamo suplems historic general Model - DNA	801581503F1 NIH MCC 7 Home gentlene colon Amerika Colonocata #1	601581503F1 NIH MGC 7 Hamp sepiens CDNA clane IMAGE-3933977 5	AV728070 HTC Homo sapiens CONA close HTCRYARZ FI	11308 F.	25		V
gle Exon Pro	Top Hit Database Source	Z	Ę	¥	F	Z.	N	EST HUMAN	EST HUMAN	ZINT	EST HUMAN	EST HUMAN	NT.	EST HUMAN	EST HUMAN		EST HUMAN	E	E	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	IN LN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N	5	EST_HUMAN
Sin	Top Hit Acession	1.0E-104 AF231920.1	1.0E-104 AF231920.1	7657038 NT	143379.1	J43379.1	1.0E-104 AB017332.1	1.0E-104 AI768797.1	1.0E-104 AI768797.1	965	1.0E-104 BE314182.1	1.0E-104 BE314182.1	557			1.0E-104 AA682308.1					F352841.1	1.0E-104 AW103848.1	1.0E-104 AW 103848.1			T.				11427757 NT	
	Most Similar (Top) Hit BLAST E Value	1.0E-104	1.0E-104 /	1.0E-104	1.0E-104 U43379.1	1.0E-104 U43379.1	1.0E-104	1.0E-104	1.0E-104 /	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104 T74219.1	1.0E-104 AF001395.	1.0E-104 AF091395.1	1.0E-104	1.0E-104 BF352841.1	1.0E-104 A	1.0E-104 A	1.0E-104 AF113514.1	1.0E-104 BE791713.1	1.0E-104 BE721713.1	1.0E-104 AV728070.1	1.0E-104 AU130755.1	1.0E-104 U66535.1	1.0E-104	1.0E-104 BE720191.1
	Expression Signal	1.23	1.23	1.08	1.28	1.28	1.12	9.51	9.51	0.75	3.31	3.31	2.03	0.83	5.23	9.0	1.31	4.27	4.27	4.4	4.4	0.85	0.85	0.71	2.83	283	1.29	4.51	4.41	0.92	2.07
	ORF SEQ ID NO:			30441			31630	32141	32142	32322	32663	32664		34330	34915	34897					33530	35503	35504	35698	35852	35853	36160	36204	36327		37221
	SEQ ID NO:	Ш				_ 1	18682	19144		19316	19621	19621	19813	21187	21754	21833	21854	21893	21883	20412	20412	22306	22306	22497	22641	22641	22946	22986	23096	23110	23930
	Probe SEQ ID NO:	4570	4570	5106	5850	5850	5897	6375	6375	6551	6706	8708	7125	8495	5906	9163	9184	9214	9214	34	8341	9654	9654	9847	58833	5666	10299	10339	10450	10464	11288

PCT/US01/00667

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Homo sepiens anyloid bets (A4) precursor protein (protesse nextn-ll, Alzheimer disease) (APP), mRNA EST20609 Spieen I Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit Homo supiens ribosomai protein S6 kinasa, 90kD, polypeptide 5 (RPS6KA5), mRNA 801312181F1 NIH_MGC_44 Homo supiens cDNA clone IMAGE:3058976 5 601434491F1 NIH MGC_72 Hamo septens cDNA clane IMAGE:3919511 5 602141215F1 NIH_MGC_46 Homo saplens cDNA clone IMAGE:4302507 6 6015668006F1 NIH_MGC_Z1 Home septens cDNA clone IMAGE:3841681 5 601566806F1 NIH_MGC_21 Homo septens dDNA done IMAGE:3841681 5 Homo sepiens potasstum channel eubunit (HERG-3) mRNA, complete cds Hamo sepiens potassium channel subunit (HERG-3) mRNA, complete cds Top Hit Descriptor RC0-HT0885-310700-021-b09 HT0885 Homo sepiens cDNA Homo sapiens Meist (mouse) homolog (MEIS1) mRNA Homo saplens chromosome 21 segment HS21C080 Human mRNA for KIAA0128 gene, pertial ods EST HUMAN EST_HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN EST HUMAN Database 五四五 Source 눋 Ę 뉟 4502166|NT 4505150 NT 11434720 Top Hit Acesslon 1.0E-105 AL163280.2 1.0E-105 BE891766.1 1.0E-104 BE393892.1 1.0E-105 AF032897.1 1.0E-105 AF032897.1 1.0E-105 AA318360.1 1.0E-104 BE731976.1 1.0E-104 BF684288.1 1.0E-104 BE731978.1 BE720191.1 1.0E-105 D50918.1 1.0E-105 1.0E-105 1.0E-104 1.0E-104 Aost Simila H (do L) BLASTE 11.13 1.92 0.91 1.83 1.44 1.42 8,99 1.75 4.96 2.07 Expression Signal 25988 27366 25440 37505 37506 37772 25722 25987 27649 ORF SEQ D NO 13360 14656 14915 15047 23930 24189 24381 24982 15514 12827 13360 14554 SEQ ID 24189 Š ÿ 2322 1814 1919 2186 11590 11590 272 416 580 12702 11268 11299 11791 SEQ ID ÿ

PCT/US01/00667 Hamo sepiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3 Hamo septens bramodomein adjecent to zinc finger domein, 28 (BAZ2B), mRNA Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZZB), mRNA 801677278F1 NIH_MGC_21 Hamo sapiens cDNA clone IMAGE:3980019 5 801901028F1 NIH_MGC_19 Hama saplens cDNA clone IMAGE:4130334 5 601901028F1 NIH_MGC_19 Homo septens cDNA clone IMAGE:4130334 5 801446823F1 NIH_MGC_65 Hamo sapiens cDNA olane IMAGE:3850156 5 601445823F1 NIH_MGC_65 Home sablens cDNA clone IMAGE:3850158 5 Homo saplens E6-AP ublquiffn-protein ligase (UBE3A) gene, exen 2 Homo saplens Retine-derived POU-domain factor-1 (RPF-1), mRNA Homo saplens GTPass activating protein-like (GAPL), mRNA EST363689 MAGE resequences, MAGB Homo saplens cDNA EST373761 MAGE resequences, MAGG Hamo septens cDNA EST378088 MAGE resequences, MAGI Homo sepiens cDNA Homo sepiens GTPsse activating protein like (GAPL), mRNA Homo sapiens mRNA for KIAA0796 protein, pertial cds Homo saplens chromosome 21 segment HS21 C008 Homo sepiens plakophilin 4 (PKP4), mRNA Human mRNA for dbl proto-oncogene EST HUMAN EST_HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN HUMAN EST 6806894|NT 11419196 NT 11419196|NT Ę 눋 <u>5</u> 7304922 NT 7304022 NT 11420134 1.0E-105 AW951634.1 1.0E-105 AW961688.1 1.0E-105 AW 988015.1 1.0E-105 BE902616.1 1.0E-105 AB018339.1 I.0E-105 BF314302.1 1.0E-105 AL163208.2 1.0E-105 BF314302.1 1.0E-105 BE868881.1 BE868881.1 AF016704.1 .0E-105 AJ229041.1 1.0E-105|X12556.1 1.0E-105 1.0E-106 1.0E-105 1.0E-105 1.0E-105 1.0E-105 1.0E-105 1.0E-105 3.65 3.65 0.05 900 0.97 0.74 2.89 0.88 70. 0.88 424 đ 2.07 30516 30515 32709 32944 33579 32485 33500 32486 28760 30058 30059 30377 30428 30681 29447 18118 19465 20454 17428 17810 18053 19465 19983 16105 16105 17428 17613 17762 17961 17961 19870 16821 15772 7758 5247 6804 6804 6885 6885 7184 3346 4694 488 4886 5091 6927 407 3006

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	Top Hit Descriptor	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR32	W850c10.xt NCI_CGAP_Bm25 Home septens cDNA clone IMAGE:2500628 3' similar to SW:ACSA PENCH P36533 ACETY _COENTYME A SYNTHETAGE	RC1-CX10008-070100-011-015 CXK0008 Homo services CNNA	UI-H-Billo-abi-b-12-0-UI st NCI (CGAP Sub) Home services china clean IVA CE (224,755.5)	QV2-070062-140300-083-d09 070062 Homo sepiens cDNA	QV2-0T0062-140300-063-d09 OT0062 Homo septems cDNA	801443755F1 NIH_MGC_85 Homo seplens cDNA clone IMAGE:3847884 51	601443755F1 NIH MGC 65 Homo sepiens cDNA clone IMAGE:3847884 51	Homo sapiens SMARCA4 Isoform (SMARCA4) gene, complete cds. atternatively spiliced	Homo septiens COL4A8 gene for e8(IV) collegen, exon 31	Homo saplens Ran binding protein 11 (LOC51194), mRNA	w/74f07.xt Soeres_thymus_NHFTh Homo saplens cDNA clone IMAGE:2535301 3' similar to TR:P87892 PR0TEASE:	7018c10x1 NCI_CGAP_KId11 Homo sepiens aDNA clone IMAGE:3574291 3' similar to TR:P97680 P97680 RIN4	Homo seciens neve for Smed 3 error 2 error 3	Homo sepiens gene for Smed 3, econ 2 and 3	UI-HE-BNO-side-07-0-U.rl NIH MGC 50 Homo senies cDNA close IMAGE 3078348 F	1978-01.x1 NCI_CGAP_Utf Homo sepiens cDNA clone IMAGE-2215008 3'	EST377629 MAGE resequences, MAGI Homo sapiens cDNA	Human dihydrofolate reductase pseudogene (psi-hd1)	Human diliydrofolate reductase pseudogene (psl-hd1)	Homo sapiens soluble neuropilin-1 mRNA, complete cds	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds	ng41c05.s1 NCI_CGAP_Co3 Homo sepiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element :	ng41c05.s1 NCL_CGAP_Co3 Homo sepiens cDNA done IMAGE:837352 3' similar to contains element	MR0-HT0165-140200-008-d10 HT0165 Homo serviens cDNA	Homo sapiens dutatrione S-transferase theta 1 (GSTT1) mRNA	1801140783F1 NIH MGC 19 Hamp septens CDNA come INA GE 3F02481 F	q176h10.x1 Soares_NhHMPu_S1 Homo septens cDNA clone IMAGE:1878307 3'	Homo sapiens glutafilone S-transferase theta 1 (GSTT1), mRNA
	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	Z	LN.	LN.	EST HUMAN	NAM! H HARN	L	NT	EST HUMAN	EST HUMAN	EST HUMAN	LX.	TN	N	K	EST HUMAN	EST HUMAN	EST HUMAN	Ā	EST HUMAN	EST_HUMAN	Z
	Top Hit Acession No.	1.0E-105 T05087.1	1.0E-105 AW007194.1	1.0E-105 AW840817.1	1.0E-105 AW016879.1	1.0E-105 AW882372.1	1.0E-105 AW882372.1	1.0E-105 BE867793.1	1.0E-105 BE867783.1	1.0E-105 AF254822.1	D63548.1	7705936	1.0E-105 AW027554.1	1.0E-105 BF430921 1	1.0E-105 AB004924 1	1.0E-105 AB004924.1	1.0E-106 AW 603208.1	1.0E-106 AI565065.1	1.0E-106 AW985558.1	J00146.1	J00146.1	1.0E-106 AF145712.1		1.0E-106 AA527446.1	1.0E-108 AA527448.1	1.0E-106 BE144286.1	04184	1.0E-106 BE280201.1		04184
	Most Similar (Top) Hit BLAST E Value		1.0E-105	1.0E-105	1.0E-105	1.0E-105	1.0E-105	1.0E-105	1.0E-105	1.0E-105	1.0E-105 D63548.1	1.0E-105	1.0E-105	1.0E-105	1.0E-105	1.0E-105	1.0E-106	1.0E-106	1.0E-106	1.0E-106 J00146.1	1.0E-106 J00148.1	1.0E-106	1.0E-106 U48724.1	1.0E-106	1.0E-108	1.0E-106	1.0E-108	1.0E-106	1.0E-106 AI276526.1	1.0E-108
	Expression Signal	6.55	1.41	0.68	2.82	0.0	0.0	0.68	0.68	5.73	1.59	2.38	2.58	1.43	1.73	1.73	1.39	1.79	2.68	0.75	206	1.33	3.48	4.71	4.71	2.31	2.89	1.82	3.24	1.91
	ORF SEQ ID NO:	33750	34129	34663		34054	34955	35247	35248	36778	37146	37204	37494	37592	37753	37754		25854	25947	28000	28000	26948	27138	27245	27246	27578	27778	28064	28210	26842
	SEQ ID NO:	20622	19802	21518	21639	21791	21791	22077	22077	23531	23880	23912	24179	24270	24415	24415	12962	13013	13313	13371	13371	14262	1440	14536	14536	14849	15040	15322	15466	14159
	Probe SEQ ID NO:	7927	7628	8828	8648	9103	9103	9467	9467	10850	11195	11250	11580	11675	11831	11831	147	200	623	<u>\$</u>	285	1515	1697	1796	1798	2118	2315	2810	2761	2828

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Table 4
Single Exon Probes Expressed in Brain

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Hymn centons of the Millians O	House equals gluiauliding or a an side as others 1 (GSTT1), mRNA	House equals involved for NIAA1326 protein, partial cds	House easiers. It was a recommendated by the second	Home series handless protein FLJ11273 (FLJ11273), mRNA	Horne explains injurement protein re-1/12/3 (F-L/112/3), mRNA	Hans septemble for KIAA 1279	Harm explains in the Art of Arthritish (200 public dds - Harm explains in the Arthritish (200 public dds - Harm explains promise and Arthritish (200 public dds - Harm explains promise and Arthritish (200 public dds - Harman explains promise and Arthritish (200 public dds - Harma	ESTABLES IN U.S. C. MINNEY OF MINNEY AND AND AND AND AND AND AND AND AND AND	ESTRESSE IN OF THE MACIN HOME REPIERS CONA	TOOL OF WINNEL TOOL OF THE BLOOK A DISTRICT OF THE SECOND TO THE SECOND	MED COMPARE A IN-TIBLE I, MENA	H. septens mRNA shriller to D29783 mouse mRNA for setzure-related gene product 6. Shares domains with Plate.	H. septions mRNA shiller to D20763 mouse mRNA for seizure-related gene product 6. Shares domeins with BMPs. Tolloid Sushi meast product.	a/24b09.s1 Sogress testis, NHT Home saplens cDNA done 1391225 3' similar to gb:X12433 PROTEIN	1. 1. 2. (1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	AU 1301 13 N1 ZNP3 From Begiens cDNA clone NT2RP3000274 5'	20/28412 of Segretary Indian September CUNA Gone N 2RP/3000274 5	AU143428 V70AA1 Home sections and the Control of th	AU143428 Y79AA1 Home sepiens CINA close 179AA1001912 5	602154012F1 NIH MGC 83 Home serviews CDNA closes MACE: 2020027 E1	601439670F1 NIH_MGC_72 Hamp seciens cDNA clone IMAGE-3024641 F	Homo seplens xylosytransferane XT2) mBNA	Homo seplens xylosytransferase II XT2) mRNA	S11 Homo saplens cDNA clone IMAGE:989732 3' similar to gb:X65873			Home earliese excline earliese at (2012)		HEMBA1000129 5'
ngle Exon Pro	Top Hit Detabase Source	TW.	NT	1	Į.	LN L	LZ.	Į.	LN L	FST HIMAN	EST HIMAN	N_	FOT HIMAN		Į.	MANUEL TOR	EST LITTAN	EST HIMAN	EST HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	¥	N _T	EST HIMAN	.=.	T HI MAAN	T TOMOS		T_HUMAN
ō	Top Hit Acesslon No.	4504184 NT	1.0E-108 AB037747 1	1.0E-108 AB037747 1	FN 2902208	8922965 NT	1.0E-106 AB008681.1	1.0E-108 AB033104.1	1.0E-106 AB033104.1	1.0E-108 AW974650.1	1.0E-106 AW974650.1	5729729INT	1.0E-106 BE144286 1	1.0E-106 AL050253.1	1.0E-108 AL050253.1	1.0E-106 AA781155 1	1.0E-106 AL 1130113 1	1.0E-106 AU130113.1	1.0E-106 AA434168.1	1.0E-106 AU143428.1	1.0E-106 AU143428.1	F679574.1		11545913 NT	11545913 NT		2847		25503	11425503 NT	П
	Most Similar (Top) Hit BLAST E Value	1.0E-106	1.0E-108	1.0E-108	1.0E-106	1.0E-106	1.0E-106	1.0E-108	1.0E-106	1.0E-108	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-108/	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-108 BF679574.1	1.0E-106 BE897112.1	1.0E-106	1.0E-106	1.0E-106 AA663779.1	1.0E-108	1.0E-106 BE292722.1	1.0E-108	1.0E-106	1.0E-106 AU116850.1
	Expression Signal	1.91	5.23	523	2.18	2.18	0.81	1.18	1.18	7.95	7.95	1.05	7.	1.09	1.09	2.61	0.58	0.58	0.58	1.3	1.3	4.89	0.77	17.68	17.68	5.16	5.33	1.21	9.20	9.29	0.67
	ORF SEQ ID NO:	26843	28357	28358	28588	28589			28839	793391	29392	29410	20024	30469	30470	30750	31480	31481	31533	31637	31638	31755	31860	32083	32084	33031	33084	33161	33275	33276	33491
-	SEQ ID NO:	3 14159		15707	15939	Ц				16763	16763	_!	17297	17853	17853			18555	18605	18689	18680	18792	18892	Cene	19096	19955	20002	20080	20182	20182	20378
	Probe SEQ ID NO:	2828	2942	2942	3178	3178	3367	3434	3434	4017	4017	4035	4582	6135	5135	5285	5764	5764	5816	2804	300	8 8	2003	233	823	7271	7324	7402	7511	7611	7714

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Top Hit Descriptor	801594331F1 NIH_MGC_9 Homo sepiens cDNA done IMAGE:3948463 5'	801594331F1 NIH_MGC_9 Homo sepiens cDNA done IMAGE:3948463 5	ar68a07.x1 Barstoad aorta HPLRB6 Homo sapiens cDNA done IMAGE:2127732 3' similar to gb:X06233	CALGRANULIN B (HUMAN);	601282717F1 NIH_MGC_44 Homo septems cDNA clone IMAGE:3604463 5	601282717F1 NIH_MGC_44 Hamo sapiens cDNA clone IMAGE:3604463 6	ty62805.x1 NCL_CGAP_KId11 Homo sepiens cDNA clone IMAGE:2283632 3's smiles to SW:ICAS_HUMAN CO5084 69 KD ISLET CELL AUTOANTIGEN;	CW4-LT0059-150200-098-e06 LT0059 Homo sepiens cDNA	oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354/90 3	oc67e08.s1 NC_CGAP_GCB1 Hamo septens CUNA clone IMACH: 1334750 3	cn03e04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn03e04 random	Inn41f02.x1 NCL_CGAP_KId11 Homo sepiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3 TAR1 PTR5 receitive element:	1. 4480 - 4 MO COAD KIA44 Home contains china chara IMAGE:2180889 3' similar to contains MSR1.ts	Interior. In the control of the cont	601282387F1 NIH_MGC_44 Home saplens cDNA clone IMAGE:3804217 5	601671674F1 NIH MGC 20 Homo septens GUNA Garie IMAGE 3834403 5	60-167-167-4F1 NIH MGC ZO Hamo sapiens alina diama invariante diamana	Inp57b10.81 NCI_CGAP_BIZ Homo septems count date awards. Tologo 2	Inp67b10.s1 NCI CGAP BIZ Homo septens curva come invade I course of	TKUJ-CI (0316-201 (96-03 1-811 C.103 to maino sapara o como DKFZ0434F0712 51	Home seriers chromosome 21 segment HS21 C002	601453461F1 NIH MGC 98 Homo septens cDNA clone IMAGE:3857366 6	601453461F1 NIH MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5	Human ryanodine receptor mRNA, complete ods	Human ryanodine receptor mRNA, complete cds	601109219F1 NIH_MGC_16 Hamo sapiens cDNA done IMAGE:3348997 5	RC5-BN0192-100500-021-B02 BN0192 Homo septens cDNA	RC5-BN0192-100500-021-B02 BN0192 Homo saplens cDNA	moth11x1 NIH_MGC_17 Home explens cDNA clone IMAGE:2361644 5	601433087F1 NIH_MGC_72 Homo sapiens CDNA clone IMAGE:3918524 5
Top Hit Detabase Source	EST_HUMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	MAMIL TOO	אולאוסט ופש	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	FO L TOWAR	EST HIMAN	EST HUMAN	Z	Z	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN
Top Hit Acession No.	1.0E-106 BE741408.1	1.0E-106 BE741408.1		1.0E-106 AJ523086.1		1.0E-106 BE387950.1	1.0E-108 AI654123.1	1.0E-106 AW838831.1	1.0E-106 AA825307.1	1.0E-106 AA825307.1	1.0E-108 A 750447.1	- Cancer 1 4	1.0E-100 AI4/8008.1	1.0E-106 AH79589.1	1.0E-108 BE389234.1	1.0E-106 BF027310.1	1.0E-106 BF027310.1	1.0E-106 AA604417.1	1.0E-106 AA604417.1	1.0E-106 AW363299.1	1.0E-106 AL039886.1	1.0E-100 AL 103202.2	1.0E-10A BE032755 1	1.0E-106 J05200.1	1.0E-106 J05200.1	1.0E-106 BE257385.1	1.0E-106 BE010882.1	1.0E-106 BE010882.1	1.0E-108 AW410405.1	1.0E-106 BE894488.1
Most Similar (Top) Hit BLAST E Value	1.0E-106	1.0E-106		1.0E-100	1.0E-106	1.0E-106		L														┙	1							
Expression Signal	8.44	8 44		1.38	0.47	0.47	3.64		3.28	3.28	1.28		1.8	<u>60</u>	1.19	1.09	1.09		6.22				7.4						8.77	
ORF SEQ ID NO:	33707	33708		33897			3443	34788		34890	35021		35169	35170	Ŀ	35841		36003					30/30		١					31068
Ewn SEQ ID NO:	20579	20570	2003	20768	21219	21219	21,200	21641	21735	21735	21858	1	21996	21998	22551	22832	22632	22789	22789			_1	\perp	23480 2368	┸	1	1	1	1	
Probe SEQ ID NO:	7884	100	8	8074	8577	8527	Br807	8050	9045	9045	88.8		8329	8330	8902	888	9984	10141	10141	10185	10358	10470	10812	70001	10005	11384	11532	11532	11981	12/03

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	601433087F1 NIH MGC 72 Homo saniens cDNA close IMA CE 3048E24 E	RC1-CT0249-090800-024-405 CT0249 Home series CNA	Homo sablens Xa bseudosuthsomal harion: samment 1/2	Human IFNAR gene for inherferon alpha/beta recentor	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA	Homo sablens NY-REN-25 entities mRNA partiel cds	Human IFNAR gene for interferon alpha/beta receptor	Anders seeing september in the control of the contr	Homo saciens BAZ18 mRNA for brancdomain adjacent to sinc finger dymeir 18 complete cus	QV2-HT0540-120900-358-605 HT0540 Homo seriens CDNA	Homo saplens cathebsin Z precursor (CTSZ) gene, exm. 3	Homo saplens mRNA for KIAA0453 nortal colo	Homo sablens mRNA for KIAA0463 protein, partial par	Human dipeblidy peolidase IV (CD28) gene, man 20	PM1-CN0031-190100-001-d03 CN0031 Homo seniens c:DNA	PM1-CN0031-190100-001-d03 CN0031 Homo sepiens cDNA	601567619F1 NIH MGC 21 Homo serviens CDNA clone IMAGE: 3242200 51	601567619F1 NIH MGC 21 Hamp septens CDNA clane IMAGE: 3842300 K	PM1-CN0031-190100-001-d03 CN0031 Homo sepiens cDNA	PM1-CN0031-190100-001-d03 CN0031 Homo seciens cDNA	Homo sepiens SMT3 (suppressor of mif two 3, yeast) hamalog 2 (SMT3H2), mRNA	Homo sapiens myotubularin (MTM1) gene, excn 9	EST381116 MAGE resequences, MAGK Homo sapiens cDNA	601442538F1 NIH_MGC_65 Homo saplens cDNA clone IMAGE:3846494 51	Homo sapiers general transcription factor IIIC independent (albha airbina airbina) / Chico.	MANN services assess from the services of the	ILHERNAGE OR ALL MILL MC ED L	ULHF-BNO-eff-COROLII 1 NIH MOC 50 Home colons CONA Company 111 OF 1	wh56h04.x1 NGL CGAP Kid11 Homo services china class 10.10 Character 20.10010 5	fh09d11.x2 NIH MGC 17 Hamp sapiens cDNA done IMAGE-2024524 F	AU122469 MAMMA1 Homo sepiens cDNA clone MAMMA1002433 57
gle Exon Pro	Top Hit Database Source	EST HUMAN	EST HUMAN	LN	NT L	SS NT	LZ	L L	LΝ	L	EST HUMAN	N	Z.	ĽN.	N	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	Ψ	N-	EST_HUMAN	EST_HUMAN	Ę	5	EST HIMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN
Sin	Top Hit Acession No.	1.0E-106 BE894488.1	1.0E-106 BE095905.1	1.0E-107 AJ271735.1	(80459.1	4826963	1.0E-107 AF155103.1	(80450.1	1.0E-107 AF154121.1	1.0E-107 AB032253.1	1.0E-107 BF087405.1	1.0E-107 AF136275.1	1.0E-107 AB007922.2	1.0E-107 AB007922.2		1.0E-107 AW842451.1	1.0E-107 AW842451.1	E732460.1	E732460.1		1.0E-107 AW842451.1	5902097 NT		_		11431469 NT	114314BO NT					П
	Most Similar (Top) Hit BLAST E Value	1.0E-106	1.0E-106	1.0E-107	1.0E-107 X60459.1	1.0E-107	1.0E-107	1.0E-107 X80459.1	1.0E-107	1.0E-107	1.0E-107 E	1.0E-107	1.0E-107	1.0E-107	1.0E-107 U13729.1	1.0E-107	1.0E-107	1.0E-107 BE732460.1	1.0E-107 BE732460.1	1.0E-107 A	1.0E-107	1.0E-107	1.0E-107 AF020671.1	1.0E-107	1.0E-107 BE867469.1	1.0E-107	1.0E-107	1.0E-107 AW 503913.1	1.0E-107 AW 503913.1	1.0E-107 AI765078.1	1.0E-107 AW410961.1	1.0E-107 AU122469.1
	Expression Signal	3.32	4.6	4.42	1.29	4.03	1.89	1.52	11.55	0.73	3.77	1.55	66.0	0.99	0.95	1.45	1.45	1.2	1.2	3.89	3.89	2.63	5.14	0.88	3.2	1.46	1.45	1.42	1.42	1.48	9.0	0.95
	ORF SEQ ID NO:	31069					26028	28305	26379	28873	26996	27187	27283	27284	27671	27822	27823	27991	27992	28421	28422	28502	29190	31242	31495	32506	32507	33023	33024	33183	33469	35213
	Exon SEQ ID NO:				\Box			13635				- 1		ı	Į	1	- 1	15250	ı		15773	15861	16558	18335	18566	19484	19484	19947	19947	20106	20354	22041
	Probe SEQ ID NO:	12103	12408	228	258	607	916	886	948	1255	1562	1746	1832	1832	2205	2362	2362	2535	2535	3007	3007	8	0000	Š	5775	6823	6823	7263	7263	7429	7890	9287

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Single Exon Probes Expressed in Brain

ze45e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381944 3' similar to contains THR.b' Homo saplens solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA h12a11.x1 NCI_CGAP_GU1 Home septens cDNA clone IMAGE:2972080 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3BP-1; Homo septens solute certier ferrily 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA g10d06.x1 NCI_CGAP_CLL1 Hamo saplens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI Homo sepiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexpkinase mRNA, complete cds (MOUSE); ob25b10x1 NIH_MGC_14 Hamo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S 802123963F1 NIH_MGC_56 Hamo sepiens cDNA done IMAGE:4281039 5 601066681F1 NIH_MGC_10 Home sepiens cDNA clone IMAGE:3452829 5 Home sepiens HSPC049 protein (HSPC049), mRNA Home sepiens HSPC049 protein (HSPC049), mRNA 601177018F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:3532348 5 601444922F1 NIH_MGC_65 Homo septens cDNA clone IMAGE:3848980 5 601444622F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 6 Homo sepiens potassium channel subunit (HERG-3) mRNA, complete cds Homo sapiens potassium channel subunit (HERG-3) mRNA, complete ods Homo sepiens familial mental retardation protein 2 (FMR2) gene, exon 20 Hamo sapiens neuroendocrine-specific protein (NSP) gene, exen 4 Top Hit Descriptor ROO-HT0372-241199-031-d03 HT0372 Homo septems cDNA Homo saplens KIAA0187 gene product (KIAA0187), mRNA Human hepatocyte nuclear factor 4-alpha gene, exen 2 Human hepatocyle nuclear factor 4-alpha gene, exen 2 PO5095 ALPHA-ACTININ 3, NON MUSCULAR; Homo sapiens PSN1 gene, alternative transcript Homo saplens NF2 gene THR repeditive element; 쁑 EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN Database **EST HUMAN** EST HUMAN 西班 Source 4506970 NT 4505970 NT 11419701 NT 11419701 NT 눋 Ę z 눋 눋 E 7681979 NT 눋 Ę Ż Top Hit Acession 1.0E-107 BF666511.1 1.0E-108|AW684438.1 1.0E-107 BE540550.1 1.0E-107|AA001415.1 BE296042.1 1.0E-108 BE206694.1 1.0E-108 AF032897.1 BE869016.1 1.0E-107 AI392850.1 1.0E-108 AF032897.1 1.0E-108 AJ008005.1 AW384094.1 1.0E-108 AF012623.1 호 1.0E-108 AF264717.1 BE869016.1 1.0E-108 AF284717.1 1.0E-108 Y18000.1 1.0E-107 L49141.1 1.0E-108 U72961.1 1.0E-108 U72961.1 1.0E-108 1.0E-107 .0E-108 Most Similer 1.0E-107 1.0E-107 .0E-108 .0E-108 1.0E-107 1.0E-108 (Top) Hit BLASTE Value 3.18 14.26 6.66 5.97 1.36 8 5.86 2.66 1.87 4.97 5.97 0.71 218 2.18 0.71 1.74 2.8 1.15 6.13 6.13 Expression Signal 36794 36405 ORF SEQ 37768 36807 37252 36406 37769 26367 27883 28755 29507 28756 30883 30955 31790 31791 20853 29854 30113 30241 30954 ÖΝQ 23297 23954 SEGID 23546 24427 23560 23178 15149 23178 24427 13702 16103 16878 25328 16103 17225 13991 18828 17225 17623 18191 18239 18239 18626 Š 17484 18828 SEQ ID 1000 2003 10866 11843 2428 3344 11283 1242 10880 11367 12043 4138 11843 3344 11367 935 4480 4480 4752 4896 5440 5440 6048 8 5837 ö

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Top Hit Descriptor	Homo sepiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2e, and 2b), CAV1 (exons 1 and 2)	PM4-CT0403-240700-001-c10 CT0403 Homo saplens cDNA	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4	Home saplens E6-AP ubiquith-proven ages (UBE3A) gens, excit 4	Homo sapiens G protein-coupled receptor, femily C, group 5, member B (GPRC30), mrava	Hamo sapiens delta-6 fatty acid desaturase (FAUSUS) mrvva	601113471F1 NIH MGC 16 Horno septens CLINA CIGHE IMAGE: 3034004 3	602043384F1 NCI_CCAP_Effet Home squerts curve invace—4 to tool 2	80204334F1 N.J. CGAP. Bino/ nono sepens culvividate invidente color	Home septens connective tissue grown that protein precuisal, mixery, curied we	ULHE-BMO-ads-4-12-C-ULT NIH MGC 38 Homo septens curve civils invacing to	UI-HE-BM0-eds-6-12-0-UI:r1 NIH_MGC_38 Home sapiens cunn crone invace::300z6/6 5	Home capiens ETS-family transcription factor EHF (EHF) mixthA, complete cos	y/35h10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273233 3 similar to FIR.443773	A45773 kelch protein, long form - fruit fly;	601038/08F1 NIH MGC 10 HORD SECTINA CATIS INVICE: 241-201 5	Homo sepiens mRNA for Gogl-essociated microutibule-tanging protecting the control of a sharrefluence	Homo septiens calcium channel alphane subulint (CACIVALE) gene, excus 7-15, and pared cus, accounting spliced	EST378258 MAGE resequences, MAGI Homo sapiens cDNA	AV708790 ADC Homo septiens cDNA clone ADCAEE03 5	AV708790 ADC Homo saplens cDNA clone ADCAEE03 5'	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA	Homo sapiens COL4A6 gene for a6(IV) collagen, exch 23	Homo sapiens mRNA for FLJ00037 protein, partial cds	602018571F1 NCI_CGAP_Brn97 Homo septens cDNA done INACE:4134247 o	IL2-UM0077-260400-079-D06 UM0077 Homo sapiens CUNA	Human mRNA for KIAA0220 gene, partial cds	Homo saptens refliculocabin 1, EF-hand calcium binding domain (KCN1), mruna	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA	Homo sapiens mRNA for KIAA0669 protein, partial cos	Homo sapiens mRNA for KIAA0889 provein, pertral cas	Homo sapiens nucleotar phosphoprotein B23 (NPM1) mknA, complete cas
Top Hit Database Source	NT	EST_HUMAN	NT	LΝ	FN	F.	EST_HUMAN	EST_HUMAN	EST HUMAN	L	EST HUMAN	EST HUMAN	NT		EST HUMAN	EST HOMAN	Ę	<u> 5</u>	EST HUMAN	EST HUMAN	EST HUMAN	NT	N	Z	EST HUMAN	EST_HUMAN	NT	NT	INT	NT	뉟	님
Top Hit Acession No.	U133289.1	1.0E-108 BF334851.1	(F016706.1	(F016706.1	11431857	4758333	1.0E-108 BE252807.1	1.0E-108 BF528912.1	1.0E-108 BF528912.1	1.0E-108 AF083500.1	1.0E-108 AW 408694.1	1.0E-108 AW 408694.1	1.0E-108 AF203977.1		444974.1	1.0E-108 BE535227.1	712490.1	4 00 400 400 23301 4	1.0E-108 AW966185.1	1 0F-108 AV708790 1	1.0E-108 AV708790.1	11441465	D63539.1	1.0E-108 AK024447.1	1.0E-108 BF346356.1	1.0E-109 AW803116.1	D86974.1	11438391	4507712	1.0E-109 AB023216.1	1.0E-109 AB023216.1	M28699.1
Most Similar (Top) Hit BLAST E Value	1.0E-108 AJ133289.1	1.0E-108	1.0E-108 AF016706.1	1.0E-108 AF016706.	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108		1.0E-108 N44974.1	1.0E-108	1.0E-108 Y12490.1	10 4 10 4	1 05-108	4 OF-108	1.0E-108	1.0E-108	1.0E-108 D63539.1	1.0E-108	1.0E-108	1.0E-109	1.0E-109 D86974.1	1.0E-109	1.0E-100			1.0E-109 M28699.1
Expression Signal	1.27	0.92	0.63	0.63	5.82	3.55	1.18	0.84	0.84	1.68	0.48	0.48	0.75		0.54	1.73	1.98	7	2 82	000	22	1.67	1.68	2.41	8.32	0.87	76.0	1.59	69.9	26.8	26.8	10.97
ORF SEQ ID NO:	31918	31660	32290	32291	32811	33098	33137	33164	33165		33838	33839			34823	33481			30920				37359			25488		25667				
SEQ ID	18946	18697	19287	19287	19748	20020	20057	20082	20082	20658	20709	20709	21636		21674	20368	<u> </u>			1	1	L	L	<u> </u>	L	<u> </u>	L	<u> </u>	1_	L	13364	
Probe SEQ ID NO:	6160	6285	6521	6521	7907	7339	7377	7405	7405	7963	8014	8014	8945		8984	10585	10731		10998	8C711	11204	11343	11405	12204	12583	4	8	220	454	584	584	1180

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	Top Hit Descriptor	Homo sepiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	601186822F2 NIH_MGC_15 Hamo sapiens cDNA clane IMAGE:2959636 51	601186922F2 NIH_MGC_15 Hamo saplens cDNA clane IMAGE:2959636 5	Homo sapiens mRNA for KIAA0018 protein, pertial cds	Homo sepiens chromosome 21 segment HS21C084	Homo sapiens SNF5/INI1 gene, exon 6	owo5a01.xt Sceres_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;	ow85a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo seplens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;	Homo sapiens guanyate cyclase activator 1A (retina) (GUCA1A) mRNA	J2816F Human fetai heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43	CM3-NN0009-190400-150-f10 NN0009 Homo septens cDNA	CM3-NN0009-190400-150-f10 NN0009 Homo saplens cDNA	Homo sapiens retind dehydrogenese homolog isoform-1 (RDH) mRNA, complete cds	Homo sapeths adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10	Homo sapeins adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10	MR0-HT0209-110400-108-e04 HT0209 Homo sepiens cDNA	Homo sapiens mRNA for KIAA0809 protein, partial cds		_	nu63c12 s1 NG_CGAP_Pt22 Homo sepiens cDNA clone IMAGE:1218282 3' similar to SW:GTT2_HUMAN P30712 GLUTHATHIONE S-TRANSFERASE THETA 2;	nu63c12s1 NCI_CGAP_Pr22 Homo sepiens cDNA clone IMAGE:12182623' similar to SW:GTT2_HUMAN	P30712 GLUTHATHIONE S-TRANSFERASE THETA 2;	Homo sapiens guenylete cyclase activator 1A (retina) (GUCA1A) mRNA	Homo seplens KIAA0377 gene product (KIAA0377), mRNA	ye48e06.r1 Soeres Infant brain 1NIB Home sapiens cDNA clone IMAGE:53057 5	801186922F2 NIH_MGC_15 Hamo septens cDNA done IMAGE:2959636 5	801188922F2 NIH_MGC_15 Homo sepiens cDNA clone IMAGE:2959636 5	AU137282 PLACE1 Hamo sapiens cDNA done PLACE1006159 5'	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 6'
	Top Hit Database Source	LN	EST_HUMAN	EST_HUMAN	NT	NT	NT	EST HUMAN	EST HUMAN	LN LN	EST HIMAN	EST HUMAN	4 1	NT	NT	F	EST_HUMAN	5	Ę	EST HUMAN	EST HUMAN	<u> </u>	EST_HUMAN	NT	TN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN
) 	Top Hit Acession No.		1.1			2		1022328.1	1022328.1	4504206 NT	}	W 893192 1	1.0E-109 AW 893192.1	1.0E-109 AF240698.1	A37928.1	A37928.1	1.0E-109 BE146144.1	1.0E-109 AB011181.2	1.0E-109 AB011181.2	N655417.1	1 0F-109 AA682274.1		1.0E-109 AA682274.1	4504206 NT	7862083 NT	215400.1	1.0E-109 BE293673.1	1.0E-109 BE293673.1	1.0E-109 AU137282.1	1.0E-109 BF673718.1
-	Most Similar (Top) Hit BLASTE Vatue	1.0E-109 M28689.1	1.0E-109 BE293673.1	1.0E-109 BE293673.1	1.0E-109 D13843.2	1.0E-109 AL163284.2	1.0E-109 Y17123.1	1.0E-109 Al022328.1	1.0E-109 A 022328.1	1.0E-109	1 OE 100 Ne5100 1	1.0E-109 AW893192	1.0E-109	1.0E-109	1.0E-109 M37928.1	1.0E-109 M37928.1	1.0E-109	1.0E-109 A	1.0E-109	1.0E-109 Al655417.1	1 OF-109		1.0E-109	1.0E-109	1.0E-109	1.0E-109 R15400.1	1.0E-109	1.0E-1001	1.0E-109/	1.0E-109
	Expression Signal	4	3.31	3.31	3.3	1 78	1.88	3.98	388	207	23	3 14	3.14	14	6.0	0.0	2.59	1.42	1.42	3.88	20		1.02	2.48	1.88	1.27	1.30	1.39	0.81	1.06
	<u>η</u> Φ. Ω	١								1	1	1		1												,				
<u></u>	ORF SEQ Expa	26598	26967	26968				28084								28964		29357	29358	29497			20513		L		1			Ш
-		13933 26598			14605 27315	14965 27705			15340		0000	3034 13020 20404			16303	16303	16575	18723	16723	16869		200	4141 1883 29513	17109	L			47775	17976	Ш

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wo	01/57275			-	_				_	_	7	_	Ŧ		_	_				r	انساد			74.	<u>.</u>	-	P	CT/	ŲS	01	/00)66	7
Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sapiens placental protein 11 (serine proteinese) (P11) mRNA	RC1+170615-200400-022-drk HT/0615 Home senses CDNA	CM1-UT0038-080000-300-h07 LTT0038 Home senions ANIA	RC1-HT0815-200400-022-404 HT0815 Homo sentens chiva	Homo saplens mRNA for KIAA1561 protein partial cds	Homo sapiens AT-binding transcription factor 1 (ATBF1) mRNA	601809495F1 NIH MGC 18 Homo seniens cDNA close IMARCE: 4040270 F	801809495F1 NIH MGC 18 Hamp sapiens CDNA clone IMACE-4040775 5	601145017F2 NIH_MGC_19 Homo saplens cDNA clone IMAGE:3180229 5	Novel human gene mapping to chomosome 13	PM0-BT0340-091299-002-e05 BT0340 Homo sepiens cDNA	7818H01 Chromosome 7 Fetal Brain cDNA Library Homo sepiens cDNA clone 7818H01	601479417F1 NIH_MGC_68 Homo sapiens oDNA clone IMAGE:3882124 5'	601479417F1 NIH_MGC_68 Homo septens cDNA clone IMAQE;3882124 5	ILO-HT0205-071189-142-g01 HT0205 Homo septens cDNA	7890g08.11 Sogres retina N2b61-R Homo septens cDNA clone IMAGE:222110 5' similar to SP:A53491 A53491 BUMETANIDE.SENSITIVE NA.K.C. COTTOANSDOTTED CONT.	601289780F1 NIH MGC 8 Home serving child class IMAGE-28-20020 F	601289760F1 NIH MGC 8 Homo sepiens cDNA clone IMAGE Actions F	HSC/1EC121 normalized infant brain cDNA Homo sepiens cDNA close c-1ec12	601063030F1 NIH MGC 10 Homo septens cDNA clone IMACE:3446500 F	601063030F1 NIH MGC_10 Homo septens cDNA clone IMAGE:344050p F	602080724F2 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4245341 5	Homo sepiens KIAA0744 gene product: histone descendase 7 (KIAA0744) mBNA	Homo sepiens KIAA0744 gene product: histone descelviese 7 (KIAAA744)	AU121370 HEMBB1 Homo septens cDNA clone HEMBR1002930 5	Homo sepiens Chedlak-Higashi syndrome 1 (CHS1) mRNA	2008/12.r1 Sceres_fetal_lung_NbHL19W Home sapiens cDNA clone IMAGE:301439 6' similar to PIR:S43969 S43089 n64-bats stress_antilaried property transfer.	Homo septems single-minded (Direconhile) homoton 1 (SIL14) DNA	602039003F1 NCI CGAP Brids Homo saniens CDNA close INACE: 4188782 F1	602039003F1 NCI CGAP Brids Homo sanions CDNA clone IMACE:4186753 5	Homo sepiens SNF5/INIT gene excu 6	Homo sepiens SNF5/INI cere excu 6
gle Exon Pro	Top Hit Databese Source	ZZINT	EST HUMAN	EST HUMAN	EST HUMAN		IN T	EST HUMAN	EST_HUMAN	EST_HUMAN	ΝŢ	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	5		HUMAN	NT	EST HUMAN	Г	T HUMAN	Г	Т	Ę
Sin	Top Hit Acession No.	48	1.0E-109 BE179356.1	1.0E-109 BF379688.1	1.0E-109 BE178358.1	Γ	12574	1.0E-109 BF182707.1											-					7862279 NT	7682279 NT		4502838 N		418618				
	Most Similar (Top) Hit BLAST E Value	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109 AL040784.1	1.0E-109 A	1.0E-109 A	1.0E-109 E	1.0E-109 BE787540.1	1.0E-109 BE145672.1	1.0E-109 H84860.1	1.0E-109 BE397068.1	1.0E-109 BE397068.	1.0E-109 F08804.1	1.0E-109 BE540909.1	1.0E-109 BE540909.1	1.0E-109 BF694831.1	1.0E-109	1.0E-109	1.0E-109 AU121370.1	1.0E-109	1.0E-109 W16610.1	1.0E-109	1.0E-109 BF339540.1	1.0E-109 BF339540.1	1.0E-109 Y17123.1	1.0E-109 Y17123.1
	Expression Signal	3.09	1.11	0.64	1.8	0.97	3.99	6.28	5.28	0.67	1.48	0.99	277	8.42	8.42	0.56	1.91	0.63	0.63	264	1.71	1.71	15.79	1.55	1.55	1.8	272	11.6	1.46	1.27	1.27	2.1	2.73
	ORF SEQ ID NO:	30662		31580				33232	33233	33451	33898	34014	201100	ı		34/11	34990	35101	35102	35218	36606	38607	38638	36818	36810	37013	37336	37291	37602	37773	37774	27714	27714
	SEQ ID NO:		18318					[┙		1	Z1247	27572	27323	200	21825	21929	21929	22048	23364	23384	23399	23568	23568	23739	24032	23990	24280	24432	24432	14976	14978
	Probe SEQ ID NO:	6230	5520	5838	5907	7140	7464	7466	7400	7874	8073	3 2	0000	3 8	200	0/80	9137	9250	9250	88	10673	10673	10710	10888	10888	1000	11342	11383	11685	11848	11848	12112	12328

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Top Hit Detachase Source	Home emises cana for AF-8 complete cds					HUMAN				•	HUMAN	T HUMAN				ZAAN	T		HUMAN		T HUMAN	HUMAN						Tri 2408.x1 NCI_CGAP_Bm25 Hamo septens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN		EST_HUMAN AV714276 DCB Homo septens cDNA clane DCBCGE01 6	EST_HUMAN AV714276 DCB Hamp sepiens cDNA dane DCBCGE01 6'		EST_HUMAN AU137923 PLACE1 Hamp septens GUNA dans PLACE100/511 5
Top Hit Acession D	T14		7549804 NT	5803073 NT	5803073 NT		7549804 NT	84550.1 NT	5031620	3032263.1 NT	1	1	4503098 NT	11438041 NT	11438041 NT				U117812.1 EST	7662441 NT		E621069.1 EST	11419323 NT	114193Z3 NT	55112.1 NT	08888.1 NT	08888.1 NT			1	1	4	-
Most Similar (Top) Hit BLAST E	100,	1.0E-109 ADO 1.1389.	1.0E-110	1.0E-110	1.0E-110	1.0E-110 C04498.1	1.0E-110	1.0E-110 U84550.1	1.0E-110	1.0E-110 AB032263.	1.0E-110 BE379477.	1.0E-110 BF508896.	1.0E-110	1.0E-110	1.0E-110	4 OF 440 BE049858	1011-301	1.0E-110 AI017213.1	1.0E-110 AU117812.	1.0E-110	1.0E-110 BE299406.	1.0E-110 BE621069.	1.0E-110	1.0E-110	1.0E-110 M55112.1	1.0E-110 U08888.1	1.0E-110 U08888.1		1.0E-110 AI560289.1	1.0E-110 AV714276.		1.0E-110 AB020675.	
Expression Signal		2.00	1.85	4.71	4.71	0.7	2.28	1.54	0.8	9.0	1.19	1.6	٢	1.49	1.40		80.	2.14	3.9	2.7	2.63	0.8	8.61		8.08	0.8	8.0		0.74	6.8	6.9	3.21	0.83
ORF SEQ ID NO:		31047	25444	25482	25483					26674				28603) A	29951			30642				32395				32983	L			
Exen SEQ ID NO:		24813	12831	12864	12864	12905	12831	13298	13912	1_	1_	L					16//0	17328					1_	1_		1_	1	L	19909			<u> </u>	20143
Probe SEQ ID NO:		12443	က	88	38	2	107	514	1157	1256	1914	2051	2845	3189	3180		4031	450	4608	4018	6212	5630	9699	9292	8617	7002	7002		7224	7325	7325	7355	7469

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	 8	T					T.																			<i>አ</i> \$	T					
Top Hit Descriptor	be68f01.y1 NIH_MGC_20 Homo saplens cONA clone IMAGE:2905561 5' similar to TR:077258 077258	EG:114D9.2 PROTEIN.;	QV2-LT0053-020400-119-e04-LI 00053 From Septemb Control	Homo sapiens galactorinase 2 (GALK2), mirry	H.sapiens mRNA for myotonic dystrophy protein kinds in a Co. 2840.483 F.	601565604F1 NIH MGC 21 Hamo septens CLINA Clarte INANCE, 30-1033 5	1801565804F1 NIH_MGC_21 Home sapiens GUNA Gane INA CEL SOFTENS OF	2w67q02.r1 Soares testis_NHT Homo saplens cDNA clone IMAGE:781298 5 similar to 17.01143010	G1145816 FKBP54;	601439/84FT NIH MGC / Z FAIN SEPTING CONTRACTOR SEPTING SEPTIN	ILC-DIOLOG-O-COT BIT OF THE COMPLETE COLOR	Homo separatis gene to rue v, comprome NHPU Homo septens conditione IMAGE:1711222 3'	qc31c12X1 Souldes Meginenic description qc31c12XX1 Souldes Meginenic description qc31c12XX1 Souldes Meginenic description qc31c12XX1 Souldes Meginenic description qc31c12XX1 Souldes qc31c12XX1 Soulde	PMS-NN1082-140800-3004 12 11 1 CGAP Subs Home sapiens CDNA clone IMAGE:3085784 3	Url Diragos room of the markets and	Human nbosoma proced Loss in the Company of the Com	ANA RESTATE IN MICE 68 Home sapiens cDNA clone IMAGE:3862086 6	Home eachers cat eve syndrome critical region gene 1 (CECR1), mRNA	Himan cardiac alpha-mycsin heavy chain (MYH8) gene, exons 32 to 34	Homo seriens KIAA0555 gene product (KIAA0555), mRNA	Homo explans colleden type IX alpha 1 chain (COL9A1) gene, exons 29, 30, 31, and 32	Homo septens DKFZP434D156 protein (DKFZP434D156), mRNA	Human enkephalin B (enkB) gene, econ 4 and 3' flank and complete cds	Homo sapiens phosphorylase kinase, alpha 1 (muscle) (PHKA1), mRNA	1801443680F1 NIH MGC 65 Homo septens cDNA clone IMAGE:3847655 5	Janoba12 x1 NCI CGAP Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M28893 KAS-	RELATED PROTEIN RAL-A (HUMAN);	DKFZp434C1815_r1 434 (synonym: httes3) Homo septens curve durie Dnr 247575151515	UI-HBWO-eff-03-0-UI.81 NG CGAP Subs Homo sapiens GUNA Cross IMMOLIZI 250220	III 2-NT0101-280700-114-E03 NT0101 Homo saplens cDNA	W68401.x1 NCI_CGAP_Kid12 Home eaplens cDNA clone IMAGE:2398465 3' similar to gb:J04813	CYTOCHROME P450 IIIA5 (HUMAN);
Top Hit Detabase Source		EST HUMAN	EST HUMAN	Z	LN.	EST HUMAN	FST HUMAN		EST_HUMAN	EST HUMAN	EST_HUMAN	LN.	EST HUMAN	EST_HUMAN	EST HUMAN	Į,	Z	ESI HUMAN	Z	1	Z	Z 14	12		MAN LI MAN	THOU I SH	EST HUMAN	EST HUMAN	FST HIMAN	EST HIMAN	ES L. IONALIA	EST HUMAN
Top Hit Acession No.				2732		-		E134501.1	1.0E-110 AA446529.1	1.0E-110 BE897218.1	1.0E-110 AW062258.1	1.0E-110 AB011399.1	1.0E-110 A1127761.1	1.0E-110 BF364546.1	1.0E-110 BF508896.1	U43701.1	4758807 INI	1.0E-111 BF035327.1	8383082 N	1.0E-111 M25142.1	768217/INI	1.0E-111 AF038126.1	7 6000	1.0E-111 KUZZOS 1	T COCH	1.0E-111 BE86/808.1	1 0F-111 AI344679.1	4 0F-111 Ai 040762 1	1.01-111 AWOORAB 1	AW Zaroto.	1.0E-111 BF-300220.1	1.0E-111 AI761228.1
Most Similar (Top) Hit T BLAST E		1.0E-110 BE302504.1	1 OF-110 A	4 OF-110	4 OF-410 V12337.1	4 01 440 1	100	1.05-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-110	1.0E-111 U43701.1	1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.0E-111	1.05-111						1	١	1	1
Expression Signal	+	7.88	0,0	2 45	200	3 6	3.73	3.75	245	4.54	11.71	1.44	1.35	3.25	54.	10.84	1.05	2.38	5.13	3.82	1.43	1.02	1.08	4.38	8.36	1.00	90				2.99	0.62
ORF SEQ E		35087	70000	20000	30001	362/8	36816	36817	36418								25645		26154	26338	27060				30057	31249					3 33104	33198
SEQ ID		2	21813	27.23	22809	23330	23.847	23567	23187	24496	24578	24720	1	L	1_	. _	L		13500	13673	14371	14962	16892		17425	18341		- 1		19624	, 20028	3 20110
Probe SEO ID		300	1534	878	10221	10648	10887	10887	11430	11030	12084	1220	13348	12420	700.0	170	ğ	718	726	808	1624	2234	4150	4295	4691	5544		5942	6580	6029	7347	7433

PCT/US01/00667

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cn07a11.x1 Normal Human Trabecular Bone Cells Homo saplens cDNA clone NHTBC_cn07a11 random Homo saplens meningioma (disrupted in belanced translocation) 1 (MN1), mRNA Homo sepiens cone sodium-calcium potassium exchanger spiloe variant (NCKX) mRNA, complete cds Homo sepiens besic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory 2879g03.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 2370g03.rl NCI_CGAP_GCB1 Homo saplens cDNA clone IMAGE:703732 5' similer to TR:G1256410 ee58g02.s1 NCI_CGAP_GCB1 Homo sepiens dDNA done IMAGE:825170 3' similer to gb:L09235 UI-H-BI4-ect-g-04-0-UI.s1 NCI_CGAP_Sub8 Home septens cDNA done IMAGE:3086023 3 UI-HBI4 eat-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo septens oDNA clone IMAGE:3086023 3 231101.r1 Scenes, pregnerit, uterus, NbHPU Homo septens cDNA clone IMAGE:503545 5' Human thrombopoletin receptor (MPL) gene, exons 1,2,3,4,5 and 6 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN); Homo septens nuclear factor of activated T-cells, cytoplesmic 2 (NFATC2), mRNA 601847132F1 NIH_MGC_65 Hamo saplens cDNA clone IMAGE:4078303 5 protein (neity) and survival motor neuron protein (smn) genes, complete cds Homo sepiens acetyl-Coenzyme A cerboxylese beta (ACACB), mRNA Homo sepiens HTRA serine probase (PRSS11) gene, complete cds Human staroldoganic acute regulatory protein (StAR) gene, excn 5 Human staroldogenic acute regulatory protein (StAR) gene, excn 5 Homo sapiens mRNA for neureoin Leipha protein, complete ods Top Hit Descriptor QV2-BT0817-270900-398-606 BT0817 Homo sepiens cDNA 01250410 11-ZINC-FINGER TRANSCRIPTION FACTOR.; AV708482 ADC Homo septens cDNA clone ADCAOB08 5' G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. Homo sepiens mRNA for FLJ00045 protein, partiel cds Homo seplens protein x 0001 (LOC61185), mRNA Homo saplens RGH1 gene, retrovirus-like element Homo sapiens Trio isoform mRNA, complete cds Human beta4-integrin (ITGB4) gene, excn 13 Human mRNA for integrin alpha-2 subunit Human mRNA for integrin alpha-2 subunit ZINC FINGER PROTEIN 135 Single Exon Probes Expressed in Brain SWISSPROT EST HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST HUMAN **EST HUMAN** Database 世紀 Source F Þ 4501854 NT È 뉟 K Ž 눋 b 눋 11420516 NT 11417901 11431896 Top Hit Acession 1.0E-111 AA278868.1 1.0E-111 AV708482.1 1.0E-111 AB035356.1 1.0E-112 BF509039.1 1.0E-112 AF157623.1 1.0E-111 AA504160.1 1.0E-112 BF509039.1 1.0E-111 AK024453.1 1.0E-111 AA131248.1 1.0E-111 AAZ78968.1 AF091395.1 1.0E-111 AI751071.1 1.0E-111|AF177987.1 BF214902.1 BF333210. 1.0E-112 U29103.1 D10083.1 1.0E-111 U68150.1 1.0E-111 U66533.1 1.0E-112 U29103.1 1.0E-111 U80017.1 X17033.1 X17033.1 1.0E-111 1.06-111 1.0E-112 1.0E-111 1.0E-111 1.0E-111 .0E-111 1.0E-111 1.0E-111 1.0E-111 (dob) BLASTE Value 8.84 2.2 2.4 1.51 1.56 12.55 12.55 1.86 12.9 12.9 0.49 3.72 1.29 86. 8.65 4.25 0.79 1.57 90 0.73 0.62 0.73 3.28 Expression Signer 37376 31040 30509 28003 26004 28030 35917 37802 26001 34409 36902 33816 34825 35066 36038 33279 33815 33912 33967 34513 34621 ORFSEQ Ö N Q 13374 13395 13396 23649 24068 24800 13372 13800 22700 17914 20833 21366 21399 21400 21474 21474 21676 21896 22820 13374 20185 24464 20688 21271 SEQ ID ö 88 1040 8782 8782 8986 10080 10973 12672 8 598 91 981 8708 10052 10172 11465 11897 12424 7514 8088 8139 8579 4728 8707 9217 7993 SEQ ID ÿ

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo saplens KIAA0440 protein (KIAA0440) mRNA	Homo seplens KIAA0440 protein (KIAA0440) mRNA	WISOFIDEXT NCI CGAP KId12 Homo septiens CDNA clone IMACE: 2400841 21	601442874F1 NIH MGC 65 Home serviens c/NA clowe IMAGE-3948859 F1	Homo sapiens glutamate receptor, lonotropic, kalnate 1 (GRIK1) mRNA	wk45b12.x1 NCI_CGAP_Pr22 Homo eaplens cDNA done IMAGE;2418335 3' similar to gb:M81650_ma1 SEMENOGELIN 1 PROTEIN PRECI IRSOR (HI IMAN)	MR2-870590-090300-113-09 RT0590 Homo sentens -7NA	Homo sablens alutamata recentor innormole kalada 4 (CRIK4) DAIA	Homo saplens mRNA for KIAA1411 profess partial cds	Homo saplens mRNA for KIAA141 mortal cale	W35d07.r1 Soares melanocula 2NbHM Homo canians child charalista Courses	Homo seplens NOD1 broken (NOD1) mene, errors 1,2 and 10 an	801594717F1 NIH MGC 9 Homo content content that the IMAGE source at	802152849F1 NIH MGC 81 Home entires of NA Alma MAGE 1202125	801142755F1 NIH MGC 14 Home explain CONA Line INVOC. 1220120.	60114275551 NIH MGC 14 Home services CONA close IMA CE GROSSIO ST	802131405F1 NIH MGC 81 Home seniens cDNA Alma IMAGE 3200300 5	Homo sapiens solute carrier family 6 (neurotransmitter fransconter rmvire) member 7 /c1 CeA7/DNA	Homo sacians soluting carrier family 8 (neurotronomittee temperature).	60184508951 NIH MGC 55 Home seeless DNA Alexandria, Lydon B), member 7 (SLCGA1), mraya	AU118051 HEMBAI Home sentence CONA close HEMBAI 100272 5	601443151F1 NIH MGC 65 Home seniens cDNA Alone IMA CE-291738E	801443151F1 NIH MGC 65 Home septens cDNA close IMA GE 384728 F	730g07.x1 Sogres_NSF_F8_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:3523020 3' similar to TR-09W35 DOWNS5 CONWS5 CONTENT	WR3-SN0008-100-N-10-N-10-N-10-N-10-N-10-N-10-	Horno sentene mRNA for secretary model less mains equites to les	801155323F1 NIH MGC 21 Homo septems CONA close (MAGE-3138080 F)	qk24c08.y6 NCI_CGAP_Kid3 Homo septens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES;	
T gle Exon Prol	Top Hit Database Source	Ž	L'	EST HUMAN	EST HUMAN	5 NT	EST HUMAN	EST HUMAN	IS NT	ĽΝ	N	EST HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	7 NT	ĮN 7	EST HUMAN	Т	Т	Т		Т	Т	T HUMAN		1
Sin	Top Hit Acession No.	7662125 NT	7002125 NT	1.0E-112 AI766925.1	1.0E-112 BE868859.1	Ĕ	1.0E-112 AI826511.1	1.0E-112 BE076073.1	Ž	1.0E-112 AB037832.1					F672815.1	E273103.1	1.0E-112 BE273103.1	F574235.1	1877	11416777		Γ				Π				
	Most Similar (Top) Hit BLAST E Value	1.0E-112	1.0E-112		1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112 N46046.1	1.0E-112 AF149773.1	1.0E-112 BE741666.	1.0E-112 BF672815	1.0E-112 BE273103.1	1.0E-112 B	1.0E-112 BF574235.1	1.0E-112	1.0E-112	1.0E-112 BF213358.1	1.0E-112 AU118051.1	1.0E-112 BE867635.1	1.0E-112 BE867635.1	1.0E-112 BF111413.1	1.0E-112 AW963327.1	1.0E-112 AJ249900.1	1.0E-112 BE280479.1	1.0E-112 AI792603.1	
	Expression Signal	4.39	4.39	1.37	1.1	1.15	2.0.	0.74	1.39	4.9	4.9	40.74	1.04	1.43	0.68	0.71	0.71	1.13	1.87	1.87	0.56	1.73	209	209	2.15	2.86	3.37	1.92	1.59	
•	ORF SEQ ID NO:	27117	27118	27857			28770	29253	12862	89008			31730	31889	32134	32308	32309	32607	32995	32996	33507	33919	34694	34695	35849	36611	36796	36981	37053	
	Exan SEQ ID NO:	14423	14423			15842	16115		17300	17437				18932	19138	18304	19304	19575	19921	19921	25120	20787	21547	21547	22444	23368	23548	23711	23779	
	Probe SEQ ID NO:	1679	1679	2194	2612	3078	3355	3864	4565	4704	4704	5581	5985	6155	6369	6539	6639	6741	7236	7236	7728	8083	8858	8856	9783	10877	10868	11040	11109	

Page 445 of 536 Table 4 Single Exon Probes Expressed in Brain

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	qi/24c08 y5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1866902 5' similar to TR:Q64362 Q64362 FUSED TOES:	PM0-CT0237-141099-001-h02 CT0237 Homo saciens cDNA	qk24c08.y5 NG_CGAP_Kd3 Homo sepiens cDNA clone IMAGE:1888902 5' similar to TR:Q64362 Q64362 FUSED TOES;	qk24c08.y5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869602 5' similar to TR:Q64362 Q64362 FUSED TOES:	8095f01.x1 Schiller meningioma Homo saplens dDNA clone IMAGF-1953625.3	8095101 xt Schiller merindtome Homo septens cDNA clone IMAGE-1953625 3	Human X-linked phosphoglycerate kinase gene, exon 8	ao95101.x1 Schiller meningloma Homo sapiens cDNA clone IMAGE:1953625.3	Homo saplens ol F4E-transporter mRNA, complete cds	UI+HBW1-eni-f-03-0-UI.s1 NCI CGAP Sub7 Homo saplens oDNA clone IMAGE 308/2878 3	Homo sapiens PLP gene	Homo sepiens mRNA for putative RNA halicase, 3' end	Homo sepiens gene for cholecystoldnin type-A recentor, complete cds	Homo septens activating transcription factor B (B-ATF), mRNA	Homo septens activating transcription factor B (B-ATF) mRNA	601469465F1 NIH MGC 67 Hamo saplens cDNA clone IMAGE:3872538 5'	AU127214 NT2RP2 Hamo septens cDNA clone NT2RP2000807 5'	AU140291 PLACE2 Homo seplens cDNA clone PLACE2000274 5	Homo saplens P-glycoprobain (mdr1) mRNA, complete cds	Homo sapiens UDP-N-acetyl-alpha-D-gelactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA	Homo sepiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA	Homo sepiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript varient B, mRNA	Homo services of trainate recentry functionals Nameth & Company (Company Company)	OTO SEPTEMBER INCOMES PRODUCTION OF SEPTEMBER OF CHINAL MICHAEL OF CHINAL MICHAEL SEPTEMBER OF CHINAL MICHAEL MICHAEL OF CHINAL MICHAE	601152078F1 NIH MGC 19 Homo serlens CONA close MARCE SERVES F	601152078F1 NIH MGC 19 Homo septens oDNA close MAGGE 3508267 F	EST371030 MAGE resequences, MAGE Homo sapiens cDNA	Homo sepiens hypothetical protein FLJ11006 (FLJ11006), mRNA
gle Exon Pro	Top Hit Detabese Source	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LΝ	EST_HUMAN	NT	EST_HUMAN	NT	NT	N	Ę	5	EST_HUMAN	EST_HUMAN	EST_HUMAN	ΤN	-	5	ļ	-		EST HUMAN	EST HUMAN	EST_HUMAN	Ţ
Sing	Top Hit Acession No.	1.0E-112 AI792603.1	-	1.0E-112 AI792603.1	1.0E-112 AI792603.1		1.0E-113 AI365586.1						1.1		5453562 NT	5453562 NT			1.0E-113 AU140291.1 E	1.0E-113 AF016535.1	11525737 NT	9961249 NT	9961249 N	6006002 NT	9009002 N				2819
	Most Similar (Top) Hit BLAST E Value			1.0E-112	1.0E-112	1.0E-113	1.0E-113	1.0E-113 M11965.1	1.0E-113 AI365586.1	1.0E-113 AF240775.	1.0E-113 L	1.0E-113 /	1.0E-113	1.0E-113 D85606.1	1.0E-113	1.0E-113	1.0E-113 E	1.0E-113	1.0E-113	1.0E-113 A	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113 BE282161.1	1.0E-113 BE262161.1	1.0E-113 AW958960.1	1.0E-113
	Expression Signal	1.59	8.8	1.92	1.82	5.37	5.37	7.99	2.08	1.44	1.02	26.34	1.92	0.91	2.18	2.16	2.97	7.66	4.17	1.47	262	0.68	0.68	0.8	0.8	0.78	0.78	0.56	0.48
	ORF SEQ ID NO:		37085	37734	37736		26153		26966	27382	27551	27913	28536	30300	30335	30336		30909	31554	31580	31725	31806	31807	31974	31975	32979	32980	33347	34629
	Exan SEQ ID NO:		23806	24399	24399		_				4	_			_1			_	ı	18848	18761	18843	18843	18998	18988	19906	19006	20242	21482
	Probe SEQ ID NO.	11109	11139	11810	11810	725	725	921	1532	1832	2088	2456	3127	4066	2008	5008	5165	5405	5832	2861	5979	200	7606	6224	6224	7221	7221	7573	8780

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hh81a09.y1 NCI_CGAP_GU1 Homo septens cDNA done IMAGE:2969176 5' similar to TR:060327 060327 hh81a09.y1 NCI_CGAP_GU1 Homo sepiens cDNA done IMAGE:2969176 5' similar to TR:060327 060327 nc80b03.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1; nc80b03.11 NCI_CGAP_GC1 Homo septens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1; yd15c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);contains Alu repetitive element, UI-HF-BNO-akt-b-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5 UI-HF-BNO-akj-b-12-0-UI.r1 NIH_MGC_50 Hamo sapiens cDNA clane IMAGE:3077328 5 Homo sapiens glutamate receptor, tonotropic, N-methyl D-espertate 2A (GRIN2A) mRNA Homo sepiens glutamete receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13 602247740F1 NIH_MGC_62 Hamo sapiens cDNA clone IMAGE:4333280 5' 602247740F1 NIH_MGC_62 Hamo sepiens cDNA clone IMAGE:4333280 5' 601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5 601297709F1 NIH_MGC_19 Hama saplens cDNA clone IMAGE:3627554 5 801105529F1 NIH_MGC_15 Homo saplens cDNA clone IMAGE: 2988365 5' 601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5 Human interferon-alpha receptor (HulFN-alpha-Rec) mRNA, complete cds Homo sapiens rhabdold tumor deletion region protein 1 (RTDR1), mRNA Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA Top Hit Descriptor Homo sepiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 RC1-FT0134-280600-021-d02 FT0134 Homo saplens cDNA Human erg profein (ets-related gene) mRNA, complete cds Homo sepiens transmembrane protein 2 (TMEM2), mRNA Homo sepiens nucleoporin-like protein 1 (NLP_1), mRNA Homo sepiens mRNA for KIAA1276 protein, pertial cds Homo sapiens RAN binding protein 7 (RANBP7), mRNA Homo sapiens RAN binding protein 7 (RANBP7), mRNA Homo sepiens mRNA for KIAA1276 protein, pertiel cds Single Exon Probes Expressed in Brain KIAA0584 PROTEIN: KIAA0584 PROTEIN; **EST HUMAN** EST_HUMAN **EST HUMAN** EST_HUMAN **EST HUMAN EST HUMAN** EST_HUMAN EST HUMAN Top Hit Databese EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** Source ż 눋 눋 11429367 NT 8923087 NT ż 6679073 NT F 뉟 600600211 6006002 5453997 Top Hit Acession 5453997 7657529 1.0E-113 AW500517.1 1.0E-113 AW630291.1 1.0E-113 AW630291.1 BE382842.1 1.0E-113 AW 500519.1 1.0E-113 BE382842.1 1.0E-113 BE772967.1 BE292968.1 1.0E-113 AA580720.1 BF691687.1 1.0E-113 AA580720.1 1.0E-114 AB033102.1 1.0E-114 BF206374.1 BF691687.1 1.0E-114 AB033102.1 1.0E-114 AF149773.1 1.0E-113 M21535.1 1.0E-114 T70551.1 1.0E-114 X04086.1 1.0E-114 J03171.1 1.0E-113 1.0E-113 1.0E-113 1.0E-113 1.0E-113 1.0E-113 1.0E-113 I.0E-113 Most Similar 1.0E-114 1.0E-114 1.0E-114 H (de) **BLAST E** Value 3.06 0.45 0.83 0.81 0.55 0.55 2.84 284 1.39 1.32 1.32 1.39 6.8 5.09 4.27 1.28 281 Expression Signal 36386 34830 ORF SEQ 35802 35803 36388 37020 37393 35683 36387 37019 31974 37394 25492 31975 26712 27104 25491 28537 28581 3483 37011 37177 28377 29731 ÖNQ 21682 SEQ ID 23746 21968 22588 23160 24082 22381 18998 18998 23890 24082 22481 23161 23737 23746 13808 14039 14413 15883 15932 16745 12871 12871 SEQ ID 8992 8992 9730 9830 9950 9950 0514 10515 9301 10515 11067 11481 11078 11076 11181 11181 ğ 1049 82 2807 3128 11481 1667 2807 3169 3997 4358 11227

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Top Hit Descriptor	601122173F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:3346099 5'	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA	Home series seem domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain	(TM) and short cytoplesmic domain, (semephorin) 54 (SEMASA) mRNA	Homo sepiens dethrin, heavy polypeptide-like 1 (CLTCL1), transcript varient 2, minute.	H.sepiens isoform 1 gene for L-type calcium channel, exon 20	Homo septens spera/ostbonectin, owov and kazal-like domains proteogrycan (testitioan) (SPOCK) mRNA	Homo sepiens HCMOGT-1 mRNA for sperm sntigen, complete cds	AU134187 OVARC1 Homo saplens cDNA clone OVARCTUD1444 3	AU134167 OVARC1 Home sapiens cLWA cione OVARC1001444 5	Hamo sapiens NF2 gene	Homo sapiens NF2 gene	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha z (GABRAZ) mixta	gy68d06.x1 NCI_CGAP_Bm25 Hamo septens curva cidne invalvexv in tox 3	QA88006 X1 NCI. CGAP. BITLS Train Species Curva corresponding	Human neutral cell agnesion molecula cupo ilinuita, collippado cua	Homo sapiens mit/NA for KI/AA/cod protein, par les cus	Homo septiens mikina to husakusot process, par see cue	716912.X1 Source_NSF_F8_9W_OT_PA_F_S1 Hamo septens curva date image_s220047 5 3011118 TR:Q9UHN6 Q9UHN6 TRANSMEMBRANE PROTEIN 2.	dq03f05.x1 NIH_MGC_2 Homo septens cDNA clone IMAGE:2840/44 D	Homo explens tyrosine kinase ppotocaro (SKC) gane, exchii zana parua cus	Human caruloplasmin mKNA	601449752F1 NIH MGC 55 Hamo sepiens CUNA Gare IMAGE 3033300 3	Homo sepiens chromosome 21 segment HS210U2/	MR0-HT0559-250200-002-d07 HT0559 Homo sapiens CUNA	ber3g12.y1 NIH_MGC_20 Home septens cDNA clone IMAGE:2906086 5' simiter to gb:X17205 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element,	compare (MCCSE),	Hono sapiens carcium created apara in sciouri (spore) and in the property carcium created apara in sciouring carcium created and in the property carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium created and carcium c	
Top Hit Defabese Source	EST HUMAN					Ę			EST_HUMAN	T HUMAN	NT	LN		HUMAN	HUMAN	۲N	Z	NT	EST_HUMAN	EST HUMAN	Z		EST HUMAN	NT	EST_HUMAN	ş	EST HOMAN	Ā	
Top Hit Acession No.	1 0E-114 BE275324.1	TM COSSOS	20000	4506880 NT	9257201 NT	726298.1	4759163 NT	1.0E-114 AB041533.1	1.0E-114 AU134187.1	1.0E-114 AU134187.1	Y18000.1	Y18000.1	4557600 NT	1.0E-114 ABB3139.1	1.0E-114 AI363139.1	U63041.1	1.0E-114 AB011133.1	1.0E-114 AB011133.1	1.0E-114 BF109832.1	1.0E-114 AW327455.1	1.0E-114 AF077754.1	1.0E-114 M13536.1	1.0E-114 BE870004.1	1.0E-114 AL163227.2	1.0E-114 BE171984.1		1.0E-114 BE302668.1	1.0E-114 AF223391.1	
Most Similar (Top) Hit BLAST E Value	1.0E-114	1	1.0E-114	1.0E-114	1.0E-114	1.0E-114 Z26298.1	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114 Y18000.1	1.0E-114 Y18000.1	1.0E-114	1.0E-114	1.0E-114	1.0E-114 U63041.1	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114	1	-		
Expression Signal	105		8	128	0.97	0.64	0.62	0.95	1.02	1.02	8.3	8.3	2.62	1.92	1.92	3.81	6.93	6.93	0.49	6.83	2.8	1.03	1.08	1.5	0.7		3.15	1.71	
ORF SEQ ID NO:	30400	1	30//2	30776	1		30534		32894	١	32041				33890	34437	34505	34506			33555		35905					36714	
Exon SEQ ID NO:	47783	3	18119	18119	18308	18912	47074	19458	19826	19826	19968	L		١.	20761	21294	_	1_				L	1.	1_	L		23378	1	
Probe SEQ ID NO:	1000	5	5315	53.45	8025	6134	8088	1/18	7130	7130	7182	7482	100	2008	7908	8602	8005	8885	9081	9314	8363	9448	10039	10061	10439	} }	10687	10789	

Page 448 of 536 Table 4 Single Exon Probes Expressed in Brain

ORF SEQ Expression (Top) Hit Top Hit Acession Database ID NO: Signal Value	36715 1.71 1.0E-114 AF223391.1 NT	37094 3 1.0E-114 AV733454.1 EST	37095 3 1.0E-114 AV733454.1 EST_HUMAN	37719 1.7 1.0E-114 4758673 NI	37759 1.32 1.0E-114 11526317 NT	3.42 1.0E-114 11418047 N	30998 4,93 1.0E-114 11034650 NT	30899 4.93 1.0E-114 1105-014	25464 2.89 1.0E-110	26585 2.03 1.0E-115 4505550 N	2.33 1.0E-115 455788/ N	25733 2.23 1.0E-115 AW804759.1 ESI_HUMAN	0.99	20007	25940 0.99 1.0E-116 AI39206.1 EST_HUMAN	26201 1.36 1.0E-115 5174702 NT	26202 1.36 1.0E-115 5174702 NT	28204 40.4 1.0E-115 4503794 N	26985 1.26 1.0E-115 AF229180.1 NI	28986 1.26 1.0E-115 AF 22818U.1	27285 1.01 1.0E-115 U78027.1 NT	27541 0.06 1.0E-115 AB007902.1 NT	27758 2.13 1.0E-115 AF231124.1 NT	1.39 1.0E-115 AW804759.1 EST HUMAIN	28518 6.22 1.0E-115 AJ245822.1 NI	28519 6.22 1.0E-115 A.1245922.1 INT	28875 1.6 1.0E-115 AJ277892.1 NI	28397 3.67 1.0E-115 AB002348.2 N	29742 3.27 1.0E-115 6912559 NI	29768 3.6 1.0E-116 4/38Z/WI	29996 2.64 1.0E-115[AL098857.1 [N.1
ORF SEQ ID NO:	36715	37094	37095	37719													L							3							
SEQ ID	38472	L		_	<u> </u>		Ц			12942	12946	13092	l _	13307	13307	┸	上	13543	<u> </u>	14298	3 14572		L	55 15623	3 15878	L		79791	30 17107	33 17140	28 17363
Probe SEQ ID NO:	101	11145	11145	11796	11834	12334	12577	12577	2	127	131	288		575	£33	7697	780	1	1552	1552	1833	2078	2238	2855	3113	3113	3465	4021	4369	4403	4628

Page 449 of 536 Table 4 Single Exon Probes Expressed in Brain

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	Novel human mRNA from chromosome 1 which has similarities to BAT2 and	Homo saplens chromosome 21 secment HS2/C2/68	Homo saciens chromosome 21 segment HS21CDRs	EST382416 MAGE resequences. March Hormo serviens cDNA	802/18348F1 NIH MGC 58 Homo saniens cDNA close 1MA CC: 4278739 £1	Homo sapiens similar to ER to nucleus signalling 1 (H. saniens) (1 OCS2433)	Homo sepiens similar to ER to nucleus signalling 1 (H. sepiens) (1 OCG2423) mRNA	au64g01.x1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE.2519568 3' similar to gb1.07807 DYNAMIN-1 (HUMAN);	au84g01.x1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE:2519568 3' similar to gb1.07807 DYNAMIN-1 (HUMAN):	Homo sapiens sperm surface protein (HSS) mRNA	Homo septems soom surface product (HSC), misuca	Homo sections similar to ribosomal brutain 200 (H. carisons) (1.00-2004)	Homo septems KIAA0054 cene product Helicage KIAA00643 m DAAA	Homo sapiens KIAA0054 cene product: Helicase (KIAA0054), IIINNA	yd80b08.r1 Soeres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP:DPOG YEAST P15891 DNA POI YAFRASE CANAMA	0231808X1 Soares total fetus Nb2HF8 Sw Home seniens child.chose NAACE:167804.4.9	0231808x1 Sogres total fetus Nb2HF8 9w Home sapiens cDNA close IMAGE-187804.4 3	Homo sepiens mRNA for KIAA0395 protein, pertiel cds	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA	RC8-ET0081-130700-011-G01 ET0081 Hamo sepiens cDNA	Homo sepiens eukanyotic translation initiation factor 4B (EIF4B), mRNA	601816352F1 NIH_MGC_56 Hamo sapiens cDNA clone IMAGE:4050108 5'	Human mRNA for KIAA0338 gene, pertial ods	Human mRNA for KIAA0338 gene, partial cds	1989909.X. Some NET TOBY 84 U	th 2e07.x1 NGI_CGAP_CLT How experies CDNA clare INAGE: 2118036 3' similar to TR: 0161.29 0161.29 PHENYLALANYL TRNA SYNTHETASE	xc32f08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA P10463 CALCYPHOSINE *	Homo sapiens UDP-glucosecg/coprotein glucosytransferase 1 (HUGT1), mRNA
gle Exon Pr	Top Hit Database Source	H	Ę	NT	EST HUMAN	IB .		F	EST_HUMAN	EST HUMAN	N L	LX	LZ.	Ę	¥	EST HUMAN	EST HUMAN	EST HUMAN	F	EST_HUMAN	EST HUMAN	2 NT	EST_HUMAN	Ę.	NT TOT	EST HIMAN	EST HUMAN	ST HUMAN	NT
SIn	Top Hit Acession No.	1.0E-115 AL096857.1	1.0E-115 AL163268.2	1.0E-115 AL163268.2	1.0E-115 AW970335.1	1.0E-115 BF865387.1	11425128 NT	11425128 NT	1.0E-115 AI928799.1	1.0E-115 Al928799.1	11426786 NT	11426786INT	11426038 INT	7861883 NT	7661883 NT		-			1.0E-115 BE830187.1		1.05-115 11434772		1.0E-116 AB002336.1				1.0E-116 AW671644.1	27
	Most Similar (Top) Hit BLAST E Value	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115 T86774.1	1.0E-115	1.0E-115 Al076598.1	1.0E-115	1.0E-115	1.0E-115	1.0=-115	1.05-115	1.05-115	4 OE: 44E AISSHOTS 4	1.0E-115 AI221878.1	1.0E-115 AJ524687.1	1.0E-115 A	1.0E-115
	Expression Signal	2.64	3.51	3.51	1.62	0.78	1.96	1.96	1.34	1.34	0.97	79.0	9.84	2.04	2.04	0.83	1.54	1.54	8.22	13.71	13.71	2,15	9 5	2220	7	-	0.82	7.62	1.33
	ORF SEQ ID NO:	29997				30802	31143	31144	31313	31314	31916	31917	32061	32198	32199	32521	32835	32936	33068	33885	33886	34048	27000	35/43	36284	36285	36293	36549	36797
	Exen SEQ ID NO:							18253	18400			18945			19202	19497					20/04			22540	23084	23064	23072	23310	23549
	Probe SEQ ID NO:	4628	484	4848	5263	5338	5454	545	5604	5604	6168	6168	6302	6434	6434	6835	7178	7178	7308	8080	8060	21 10	200	0000	10418	10418	10426	10617	10869

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Page 450 of 536 Table 4

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| Top Hit Descriptor | hq54c10.x1 NCI_CGAP_Pen3 Homo sepiens cDNA clone IMAGE:3123186 3' similar to TR:088378 O88378 PRP4 PROTEIN KINASE HOMOLOG; | hq54c10.x1 NCI_CGAP_Par3 Homo saplens cDNA clone IMAGE:3123186 3' similar to TR:088378 O8837/
PRP4 PROTEIN KINASE HOMOLOG: | Homo saplens calcium channel, voltage-dependent, alpha 1E surkunit (CACNA1E) mRNA | 601111744F1 NIH MGC 16 Homo sepiens cDNA clone IMAGE 3352370 F | QV3-0T0085-200300-137-h12 OT0065 Homo sapiens cDNA | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds | 601121347F1 NIH MGC 20 Homo sepiens cDNA clone IMAGE JORRB75 F. | Homo eaplens synaptolenin 1 (SYNJ1), mRNA | Homo sapiens synaptojanin 1 (SYNJ1), mRNA | Homo sapiens pericentrin (PCNT) mRNA | Homo septiens pericentrin (PCNT) mRNA | Humen apolipoprotein B-100 (apol3) gene, expris 17 and 18

 | Human apolipoprotein B-100 (apoB) gene, exons 17 and 18 | Homo saplens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA | Human offactory receptor off17-201-1 (OR17-201-1) gene, offactory receptor off17-32 (OR17-32) gene and offactory receptor pseudo off17-01 (OR17-01) pseudocene, complete ode | Homo saciens mRNA for KIAA0700 protein partial cds

 | 801513337F1 NIH_MGC_71 Homo seplens cDNA clone IMAGE:3914800 5 | Homo saplens DiGeorge syndrome critical region, centromeric end
 | Home sepiens DiGeorge syndroms critical region, centromeric and | Homo sepiens sodium phosphate transporter 3 (NPT3) mRNA | PM-BT135-070499-016 BT135 Homo septens cDNA | qn19d04x1 NG_CGAP_Lu5 Homo sapiens cDNA done IMAGE:1898695 3' similar to contains element
MER25 repetitive element; | 252407.r1 Sogres_seriescent_fibroblasts_NbHSF Homo sapiens cDNA done IMAGE:323245 5' similar to SW-MDHM MOLISE passate MA ATE DELIVIDE CENTRE MITCHINGTON CONTROLLS
CONTROLLS CO | Homo sepiers mRNA for KIAA1636 protein pertial cds | Homo sablens mRNA for KIAA1636 protein partial cris
 | 801302281F1 NIH MGC 21 Homo saciens cDNA clone IMAGE:3636764 5' | MR2-HT0379-210200-102-b04 HT0379 Homo sapiens cDNA |
| Top Hit
Detabase
Source | EST_HUMAN | EST HUMAN | LN LN | EST HUMAN | EST_HUMAN | ¥ | EST HUMAN | N F | F | LN | TN | N

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 | EST_HUMAN | LZ.
 | 5 | 5 | EST_HUMAN | EST_HUMAN |
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| Top Hit Acession
No. | BE045890.1 | BE045890.1 | 4502528 | L | | _ | 3E275502.1 | 4507334 | 4507334 | 5174478 | 5174478 |

 | | 5453941 | |

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| Most Similar
(Top) Hit
BLAST E
Value | 1.0E-115 | 1.0E-115 | 1.0E-115 | 1.0E-115 | 1.0E-115 | 1.0E-115 | 1.0E-118 | 1.0E-116 | 1.0E-118 | 1.0E-116 | 1.0E-116 | 1.0E-116

 | 1.0E-116 N | 1.0E-118 | 1.0E-116 L | 1.0E-116

 | 1.0E-118 | 1.0E-116 L
 | 1.0E-116 L | 1.0E-116 | 1.0E-116 A | 1.0E-116 A | 1.0E-116 W
 | 1.0E-116 A | 1.0E-116 A
 | 1.0E-116 B | 1.0E-116 BE158133.1 |
| Expression
Signal | 1.54 | 1.64 | 2.27 | 2.53 | 1.63 | 2.16 | 1.98 | 2.21 | 1.76 | 2.55 | 2.55 | 2.6

 | 2.6 | 1.95 | 1.36 | 2.84

 | 1.53 | 4.87
 | 4.87 | 2.43 | 1.57 | 0.87 | 4.4
 | 1.8 | 1.8
 | 0.78 | 1.55 |
| ORF SEQ
ID NO: | 37174 | 37175 | 37281 | 37699 | 37767 | | 25969 | 26216 | | 27447 | 27448 | 27552

 | 27553 | 27767 | | 27915

 | 28183 | 28582
 | 28583 | 29713 | 30156 | 30627 | 31619
 | 31862 | 31863
 | 31934 | |
| Econ
SEQ ID
NO: | 23888 | 23888 | 1 1 | | 24426 | 24481 | 13341 | 13555 | 13009 | 14726 | 14726 | 15585

 | 15585 | 15030 | 15083 | 15178

 | 15533 | 15934
 | 15834 | 1708 | 17534 | 18005 | 18674
 | 18895 | 18895
 | 18961 | 19189 |
| Probe
SEQ ID
NO: | 11225 | 11225 | 11374 | 11775 | 11842 | 11920 | 559 | 783 | 83 | 1980 | 1990 | 88

 | 88 | 2306 | 2340 | 2458

 | 2738 | 3171
 | 3171 | 4345 | £88 | 5197 | 888
 | 6117 | 6117
 | 9184 | 9421 |
| | Exon ORF SEQ Expression ID NO: Signal RLAST E No. Source NO: Value | Exon ORF SEQ Expression ID NO: Top Hit Accession Signal Top Hit Accession No. Top Hit Accession No. Top Hit Accession Source Source Top Hit Accession No. Top Hit Accession No. Top Hit Accession Source Source Top Hit Accession No. Defabloss 23888 37174 1.54 1.0E-115 BE045890.1 EST_HUMAN PRP4 PROTEIN KINASE HOMOLOG: | Exon
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	Top Hit Descriptor	C02944 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC0567	AV718314 DCB Hamo septens cDNA done DCBBCG06 5	EST62885 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2	EST62685 Jurkat T-cells V Homo saplens cDNA 5' end similar to similar to keratin 2	CM-BT043-090239-075 BT043 Homo saplens cDNA	601338268F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:3680680 5'	qh09c05.x1 Soarse_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:1844168 3' similer to gb:X63741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA	Homo sapiens partial mRNA for xylosyltransferase I (XT-I gene)	Homo septens partial mRNA for xylosyltransferase ((XT-I gene)	QV4-HT0401-281289-063-c09 HT0401 Homo sepiens cDNA	CM2-CT0482-300800-349-e06 CT0482 Homo sapiens cDNA	qq41e04x1 Soares_NhHMPu_S1 Homo sapiens cDNA done IMAGE:1935102 3' similar to WP:B0495.7 OE01765 :	DKFZp762L1110 r1 762 (synorym: hmel2) Homo saplens cDNA clone DKFZp762L1110 5'	Homo sapiens acetyl-Coarzyma A carboxylase alpha (ACACA), mRNA	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15	Homo sapiens lymphocyte activation-essociated protein mRNA, complete cds	Human apolipoprotein B-100 (apoB) gene, expn 10	EST369769 MAGE resequences, MAGE Homo sapiens cDNA	op32c11.s1 Sogres_NFL_T_GBC_S1 Homo septiens cDNA clone IMAGE:1578548 3'	EST189414 HCC cell line (matestasis to liver in mouse) Il Homo septens cDNA 6' end similar to ribosomal profesiol 20	Homo saciens collegen, type IV, alpha 5 (Abort syndrome) (COL4A5), mRNA	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'	H. seplens mRNA for TPCR16 protein	H.seplens mRNA for TPCR16 protein	Homo saplens Scar2 (SCAR2) gene, partial cds	Homo sapiens Scar2 (SCAR2) gene, partial cds	Homo sepiens mRNA for KIAA0866 protein, complete cds	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA	601582857F1 NIH MGC 20 Hamo sepiens aDNA dane IMAGE:3832214 5
יסי וווסאם פונ	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	LΝ	TN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	NT	TN	L	LN	EST HUMAN	EST_HUMAN	NAMINE TOTAL	L	EST HUMAN	Z	LZ.	LZ	TN	NT	NT	EST HUMAN
<u> </u>	Top Hit Acession No.	1.0E-116 C02944.1	1.0E-116 AV716314.1	1.0E-116 AA354258.1	1.0E-118 AA354258.1	1.0E-118 Al904151.1	1.0E-116 BE565507.1	1.0E-116 AI216352.1	11418646 NT	1.0E-116 AJ277441.1	1.0E-116 AJ277441.1	1.0E-116 BE158913.1	1.0E-116 BF335849.1	1.0E-116 AB87140.1		828638	1.0E-117 AF124393.1	1.0E-117 AF123320.1	1.0E-117 M19816.1	1.1	1.0E-117 AA978114.1	1 DE-447 AA348793 4	59564	1.0E-117 AL042120.1			1.0E-117 AF134304.2	1.0E-117 AF134304.2	1.0E-117 AB020673.1	6012461 NT	1.0E-117 BE730508.1
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	Expression Signal	1.19	5.74	1.37	1.37	96.0	1.66	1.61	1.52	0.74	0.74	0.78	2.4	2.85	1.86	1.67	96.0	1.02	1.51	1.54	1.64	9.4	2.03	2.95	1.27	1.27	10.03	10.03	3.57	0.73	3.01
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	SEQ ID NO:	19544	19790	20961	20961	21071	21528	21687	22228	22818	22818	22894	23281	23750	25287	13328	15559	14489	14562	14938	16024	16720	17040	17273	17408	17408	17491	17491	17614	17854	18070
	Probe SEQ ID NO:	6844	7102	8267	8267	8378	8836	2668	8573	10170	10170	10248	10586	11080	12625	545	1055	1747	1823	2208	3282	3071	4310	4538	4674	4874	4759	4759	4887	5138	5264

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Top Hit Describtor	Postocada Combellium II Homo septens cDNA 5' end similar to similar to zinc finger domain	EST 20111 Cet exemit it fam of experts (shp) gene, 3' end of cds	Homo saplens nuclear hormone receptor (ship) gene, 3' end of cds	AV747778 DCB Homo saplens cDNA clone DCBBAE01 6	AV717788 DCB Homo saplens dDNA clone DCBBAE01 5	WINSERDYX NCI CGAP BIR25 Homo sepiens CDNA done IMAGE:2468629 3' SIMIKET TO I R. U. 5003	O75065 KIAA0477 PROTEIN.;	Home septens neural call adhesion molecule 1 (NCAM1), mRNA	Houlin september 1000 Hours september ODNA	CARP 1043 380299 075 BT043 Homo sepiens oDNA	Himmen gene for very low density lipoprotein receptor, exon 11	NATIFACA17F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3843748 5	Homo seciens damme-eminobutyric acid type B receptor 2 (GABABR2) mRNA, compress cus	Humo sariens Droscohla Kelch like protein (DKELCHL), mRNA	Human mRNA for KIAAD191 gene, partial cds	Homo eaplens protein (peptidyl-protyl dis/trans leomerase) NIMA-interacting 1 (PIN1), minns	Home serviers protein (peotidy-proty cis/trans isomerase) NIMA-interacting i (File I), illicator	Homo septems mRNA for MEGF8, pertial cds	Homo sapiens mRNA for MEGF8, partial cds	601186203F1 NIH_MGC_8 Homo septems dDNA clone IMAGE:3344296 3	Homo saplens ATP-binding cessette, sub-family A (ABC), member 3 (ABCA3), mRNA	Homo saplens ATP-binding cassette, sub-ramily A (Abo.), montes	Homo saplens HSPC151 mRNA, complete cds Homo saplens DNF clone DKFZp4341056 5	DKFZp4341036 71 434 (syndyin: nees-) (bkFZp4341036 71 434 (syndyin: nees-) (bkFZp4341036 71 434 (syndyin: nees-)	Homo sepiens hypothetical protein (UUSZOZIBJO1:1), m. C., (SIX1) mRNA	Homo sapiens sine oculis indirector (1000schime) con MAGE:3604019 5	601281947F1 NIH_MGC 44 France September 2012 April 2004019 5	601281947F1 NIH MGC 44 Homo septens conv. cons. IIIA CE-2804010 6	Т	Т	Human breakpoint cluster region (BCR) gene, complete cds	Human breakpoint cluster region (BCR) gene, complete cds	Homo sapiens PRKY exon 7	
Top Hit Database Source		EST HUMAN	LN	IN	EST HUMAN	EST TOWAR	EST HUMAN	NT.	Z	EST HUMAN	ESI HUMAIN	IN I	HOLL HOME	Z	Z	N 12	IN COLUMN	E L	Z	EST HUMAN	LN	LN	I. 1	EST HUMAN	1		EST HUMAN	EST HUMAN	FST HUMAN	EST HIMAN	17	LV.	LN	
Top Hit Acession No.							1950145.1	없	10834989 NT			1	1.0E-117 BE733922.1	1.0E-117 AF099033.1	11420222 N	D83776.1	11424633	11424835 NT	1.0E-117/AB011541.1	1.0E-117 AB011541.1	4501848INT	4501848 NT	1.0E-118 AF161500.1	4 DE-118 AI 045854.1	T057016 NT		RF389705	4 AC 449 DE380705 1	DESCRIPTION 1	1.0E-118 BE308700.1	i۱	1.0E-118 00/000.1	1.0E-118 00/000.1	
<u>a</u> = u	Value	1.0E-117 AA323348.1	1.0E-117 L76571.1	1.0E-117 L76571.1	1.0E-117 AV717788.1	1.0E-117 AV717788.1	1.0E-117 AI950145.1	1.0E-117	1.0E-117	1.0E-117	1.0E-117 AI904151.1	1.0E-117 D16524.1	1.0E-117	1.0E-117	1.0E-117	1.0E-117 D83776.1	1.0E-117	1.0E-117	1.0E-117	1.0E-117	1.0E-117	1			_	1		1		1			╛	
Expression Signal		0.86	5.01	5.01	1.75	1.75	338	2.28	2.20	0.56	0.56	2.25	207	29	1.11	1.77	2.68	2.68	3.32	3.32	14.73		2.02		Z.13									4.04
ORF SEQ ID NO:		30574	33108	33109	33212	33213	33800	34039	34040	34141	L		L					L	37196	37197				1						5 27695		0 28189		77
	ö	17027	2003	20031	20122	20122		200/3	7000	2100	21004	21868	22338	L	L	1_	1	<u>L</u>	L	<u>_</u>			Ц			\perp		14955	7 14955	7 14955	15054	4 15450		2 15867
10	ö	US68	3 62	3 2	7446	7446		7878	2 6	2 6	2 2	3 8	9880	0848	10460	10765	1000	10001	11243	11243	11369	11587	11687	8	g	504	88	1222	7227	7222	2329	2744	2744	3102

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	Top Hit Descriptor	abo1f05x1 NCI_CGAP_Kd5 Hamo sepiens cDNA done IMAGE:1916769 3'	another of NCI CGAP Kide Homo sablens obnA done IMAGE:1916769 3'	Human mRNA for ribosomes protein, complete ods	The section KIAANA78 rane product (KIAA0478), mRNA	nuclear ending channel cannot subunit (CACNG4) gene, excn 3	notice seques calculum channel gamma 4 automit (CACNG4) gene, exon 3	TIGHTO SEATON TO SET IN THE NAME OF THE PROPERTY OF THE PROPER	Total Saprate Communication (NELN), mRNA	Usana methe filmets transmembrane conductance regulator (CFTR) gene, exch 4	Light contains Table 4 (TBX4), mRNA	Line series Thou 4 (TRX4) mRNA	United services franches and properties of the Common State of the	Hame sequents leaves transforming growth factor beta binding protein 2 (LTBP2) mRNA	House superior many transformation mouth factor beta binding protein 2 (LTBP2) mRNA	Home separate leave in the security of the security of the security of the DKFZp43400127 5	DNF 2043-0012, 1143 (synonym: hies3) Homo sepiens cDNA clone DKFZ043400127 5	UNITED SANCOLIST 1 121 (STREET) TREET 3 (CZORF3), mRNA	PACS 41620E1 NIH MGC 46 Homo explens CDNA clone IMAGE:4302749 5	COLUMN MAC 67 Homo serviers CDNA done IMAGE:3872247 5	OU 1408 1401 1 1111 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CVV-BT0263-090200-097-H03 BT0283 Homo suplems cDNA	CASANT I Scenes NIHIMPU S1 Homo septems cDNA clone IMAGE:811789 5	2598407.rt Soares NirHMPu_S1 Homo saplens cDNA clone IMAGE:811789 5	Himman mRNA for KIAA0383 gene, pertiel cds	Human mRNA for KIAA0383 gene, partial cds	Home services latent transforming growth factor bota binding protein 2 (LTBP2) mRNA	Home sentens latert transforming growth factor beta binding protein 2 (LTBP2) mRNA	POSTAZARATE NIH MIGC 19 Hamo sapiens CDIVA clane IMAGE:3160502 5	COLITYCOM TO THE CONTROL HUTE HOMO Septens CONA clone DKFZp586K1824	Home sanians hynothetical protein (DJ328E19.C1.1), mRNA	TIGHTS SEPTING 1970 AND AND AND SEPTING CONA Clone DKFZp5470017 5	7217A0 C CGAP BITZ3 Homo sapiens CDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR;
	Top Hit Database Source	FOT HIMAN	Τ	Т	ž!	Ž	Z	IN.	N.	I N	Z	Z	z !	EZ.	1N	LN	EST HUMAN	EST HUMAN	N. POL	EST TOWAR	EST HUMAN	ESI HUMAIN	FSI HOMAN	EST HIMAN	- LA	Z	N 1	1 N 1	INIZ	ESI HUMAN	ES! HUMAN	S N I	ES HOMAIN	EST_HUMAN
	Top Hit Acession No.	T			23000.1	3/83		1.0E-118 AF142624.1	11422054 N	1N4C0ZZ411	M55109.1	11425900 N	11425900 N	11420784 NT	4557732 NT	4667732 NT	1.0E-118 AL043761.1	1.0E-118 AL043761.1	11431050 N	1.0E-118 BF085272.1	1.0E-118 BE781223.1	1.0E-118 BE062855.1	1.0E-118 BE062855.1	1.0E-118 AA443024.1	1.0E-116 AA443024.1	1.0E-118 AB00Z381.1	1.0E-118 AB002361.1	450/732 IN I	4567732 N	1.0E-118 BE263134.1	AL048474.2	185/016 N	1.0E-118 AL138321.1	1.0E-118 BF195407.1
	Most Similar (Top) Hit BLAST E Value	4077	1.0E-118 AI34/094.	1.0E-118 Al347694.1	1.0E-118 DZ3050.1	1.0E-118	1.0E-118 A	1.0E-118 /	1.0E-118	1.0E-118	1.0E-118 M55109.1	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.05-116	1.0E-118	1.0E-118							ł
	Expression Signal		4.67	4.67	4.77	0.0	1.87	1.87	0.94	0.94	1.24	0.83	0.83	1.40	1.44	1.44	1.12	1.12	5.63	0.88	2.17	6.58	6.58	1.37	1.37					4.95		1.53	86.0	1.88
	ORF SEQ ID NO:		28605	28606	29439	30028	30800	30801	31247	31248	31395	31491	31402	31578	32368	32360	32738			33512	33693	34118						34455	34456	34787	34806	35327	3 35731	36134
	SEQ ID		15953	15953	16811	17393	18140	18140	18340	18340	18477	18563	18563	18640	19355	L		L		L	L	20976	20976		أسا			L	L	21624	21656	<u> </u>	3 22536	\$ 22822
٠	Probe SEQ ID NO:		3190	3190	4067	4659	5337	5337	5543	5543	5684	6772	5772	5853	6592	6582	6997	6997	7500	7733	7872	8282	8282	8288	8288	8573	8573	8621	8621	8833	808	9493	9886	10274

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igo Exori I coso Expressed III Dialil	Top Hit Descriptor	2848e10.xf NG CGAP, Kid11 Hamo septens dDNA done IMAGE:2772888 3' similar to SW:BODG HUMAN 075836 GAMMA-BUTYROBETAINE.2-OXOGLUTARATE DIOXYGENASE	UI-H-BW0-eio-e-07-0-UI.s1 NCI CGAP Sub6 Homo sepiens cDNA clone IMAGE:2729772 3'	802141529F1 NIH_MGC_46 Hamo septens cDNA clone IMAGE:4302798 5	Homo sapiens protein with polygluternine repeat, calcium (ca2+) homeostasis endoplasmic reticulum protein (ERPROT213-21), mRNA	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sepiens cDNA 5 and strailer to dynein, light chain 1, cytoblesmic	801499514F1 NIH MGC 70 Homo saplens cDNA clone IMAGE 3801563 51	601499514F1 NIH_MGC_70 Homo suplens cDNA clone IMAGE:3901563 57	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA	QV0-UM0091-120900-385-b12 UM0091 Homo saplens dDNA	Homo suplens chloride channel CLC4 (CIC4) mRNA, complete cds	Homo sapiens CGI-105 protein (LOC51011), mRNA	Homo sapiens mRNA for KIAA0930 protein, partial ods	Homo sepiens hypothetical protein FLJ10052 (FLJ10052), mRNA	on10b05.s1 NCI_CGAP_Lu5 Homo sepiens cDNA done IMAGE:1556241 3' similar to WP:E04F6.2 CE01214;	Homo saplens glutamate receptor, bondropic, kainate 1 (GRİK1) mRNA	AU133399 NT 2RP4 Homo septens cDNA clone NT 2RP4001891 57	Human neurofibronnin (NF1) gene, complete cds	RC1-NN0073-250800-018-g06 NN0073 Hamp sapiens cDNA	AV683731 GKC Hamo sepiens cDNA clone GKCDHB03 5	DKFZp782M0710_r1 782 (synonym: hmel2) Homo saplens cDNA clone DKFZp762M0710 5	DKFZp762M0710_r1 762 (synonym: hmel2) Homo saplens cDNA clone DKFZp762M0710 5	qb77c09.x1 Soarse_fetal_heart_NbHH10W Homo sepiens cDNA clone IMAGE:1706128 3' similer to	Homo saplers matrix metallocroteinese 28 (MMP28) mRNA complete cats	Homo sepiens metrix metalloproteinase 28 (MMP28) mRNA, complete cds	tm23f10.xt Sogres_NFL_T_GBC_S1 Hamo septens cDNA clane IMAGE:21574513'	Human c-feafips proto-oncogene	EST386298 MAGE resequences, MAGM Hamp sapiens cDNA	601592005F1 NIH_MGC_7 Hamo sepiens aDNA dane IMAGE:3946081 5	601280564F1 NIH_MGC_39 Hamo sapiens cDNA clone IMAGE:3622526 5'
אין ווייאין פוש	Top Hit Detabase Source	EST HUMAN	EST HUMAN	EST_HUMAN	F	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	LN	TN	LN	EST_HUMAN	E	EST_HUMAN	TN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	H 0	NT NT	NT	EST HUMAN	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.	1.0E-118 AW271289.1	1.0E-118 AW296351.1	1.0E-118 BF685214.1	11055988	1.0E-118 AA315007.1	1.0E-118 BE908678.1	1.0E-118 BE908676.1		1.0E-118 BF093687.1		05607		8822205	1.0E-119 AA916760.1	4504116	7.					1.0E-119 AL134903.1	4 001 440		1.0E-119 AF315883.1	1.0E-119 AI476732,1		1.0E-119 AW974193.1		1.0E-119 BE615150.1
	Most Similar (Top) Hit BLAST E Value	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119 M89914.1	1.0E-119	1.0E-119	1.0E-119	1.0E-119	10.0	1.0E-119	1.0E-119	1.0E-119	1.0E-119 X06282.1	1.0E-119	1.0E-119	1.0E-119
	Expression Signal	0.46	0.65	1.61	1.8	10.23	1.68	1.68	1.61	1.61	76.0	1.61	5.97	1.57	0.8	1.42	2.5	21.82	3.11	1.83	0.63	0.63	,	0.92	0.92	0.85	2.62	4.69	1.5	1.18
	ORF SEQ ID NO:	1229E	00898	37155	37186	37201	37457	37458	37461	37462	26173	26433	27374	28606		28325	30688	30701	30706	30830	31201	31202	24778	31940	31941	31987	32135	32148	33070	34390
	Econ SEQ ID NO:	23012	23077	23869	23899	23908	24147	24147	24150	24150	13514	15558	14662	15884	15996	10084	18050	18072	18076	18150	18301	1830	1884	18967	18967	19013	19139	19149	19993	21252
	Probe SEQ ID NO:	10365	10431	11206	11236	11246	11548	11548	11551	11551	741	1014	1926	3099	3234	3934	5253	8873	5270	5347	5503	5563	8 038	9190	6190	6230	8370	8380	340	8580

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qf43a11.x1 Soares_testis_NHT Homo saplens cDNA clone IMAGE:1752764 3' similar to TR:Q13458 Hamo septens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds yy40g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273768 5 Homo sepiens aqueporin 4 (AQP4), spiloe variant b, mRNA Homo sepiens synaptojanin 1 (SYNJ1), mRNA Homo sepiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds Homo sepiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds Homo saplens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17 Homo septens partial IL-12RB1 gene for IL-12 receptor betat chain, exons 16-17 Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17 Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO. qd61f03.x1 Soeres_testis_NHT Homo sepiens cDNA clone IMAGE:1733981.3' 8832705.r1 NCI_CGAP_GCB1 Homo sapiens aDNA clans IMAGE:814977 5 602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5 602183994F1 NIH_MGC_42 Hamo septens cDNA clone IMAGE:4300174 57 802183994F1 NIH_MGC_42 Hamo septens cDNA clone IMAGE:4300174 57 Homo sapiens dishitegrin and metalloprotease domain 10 (ADAM10) mRNA Homo septens glutamete receptor, tonotropic, keinate 1 (GRIK1) mRNA Homo sapiens Sod mRNA for stearcyl-CoA desaturase, complete cds Homo saplens hypothetical protein FLJ10206 (FLJ10206), mRNA Homo saplens hypothetical protein FLJ10206 (FLJ10206), mRNA Fop Hit Descriptor RC3-CT0212-240999-011-f03 CT0212 Homo sepiens cDNA Homo sepiens intersectin 2 (SH3D1B) mRNA, complete cds Homo sepiens intersectin 2 (SH3D1B) mRNA, complete cds Homo sapiens KIAA0477 gene product (KIAA0477), mRNA Human TBXAS1 gene for thromboxane synthase, exon 7 Homo sapiens stanniocalcin (STC) gene, pertial cds Homo sapiens stanniocalcin (STC) gene, partial cds Human P-glycoprotein (MDR1) gene, exons 6 and 7 Human P-glycoprotein (MDR1) gene, exons 6 and 7 Human gene for neuroflement subunit M (NF-M) Homo sepiens syneptojanin 1 (SYNJ1), mRNA Homo sepiens gene for AF-6, complete cds Homo sepiens gene for AF-6, complete cds Single Exon Probes Expressed in Brain **EST HUMAN** EST HUMAN EST_HUMAN Top Hit Detabase HUMAN EST_HUMAN EST HUMAN EST HUMAN EST_HUMAN Source EST 11036643 NT Ż 눋 눋 4507334 NT Ę E 4557250 NT 늘 4507334 NT Top Hit Acession 11425837 11425837 4755124 4504116 1.0E-119 AW847519.1 1.0E-119 AA465124.1 1.0E-119 AB032261.1 1.0E-119 AJ297701.1 1.0E-120 AF248540.1 1.0E-119 AJ297701.1 1.0E-119 AJ297701.1 1.0E-119 BF569571.1 1.0E-119|AI149796.1 1.0E-120 AF248540.1 1.0E-120 AF167708.1 1.0E-120 AB011389.1 1.0E-120 AB011399.1 1.0E-120 AF056490.1 .0E-120 AF056490.1 1.0E-120 AI190903.1 1.0E-120 AF098463.1 1.0E-120 AF098463.1 1.0E-120 BF568222.1 1.0E-120 N44873.1 1.0E-120 BF568222 1 1.0E-120 M29428.1 1.0E-120 M29428. 1.0E-120 D34619.1 1.0E-120 Y00067.1 1.0E-119 1.0E-119 1.0E-119 1.0E-120 1.0E-120 1.0E-120 BLASTE 1.0E-120 Most Simila **堂(do_L)** .0E-120 Value 1.15 4.18 2.38 0.71 0.71 2.38 2.16 1.43 2.49 2.49 0.92 0.92 1.50 6.31 231 3.08 1.21 5.24 1.95 1.95 Expression 0.0 16.61 16.61 36263 ORF SEQ 35683 36317 36318 36390 36913 28440 27033 27250 27566 27985 26439 26832 27585 29693 36914 29692 20083 29984 38401 30468 32110 32111 33236 31357 ÖNQ SEGE 22458 23080 2852 22794 23089 23163 23660 23660 13100 23826 13778 14343 25326 13778 14152 14539 14831 15247 13180 17349 17349 14831 **1**86 17064 18444 19120 20490 19123 Ö 17851 **24** 10006 10443 10443 9807 10401 11159 1018 1018 3302 10146 10985 10985 12198 8 1405 1799 2100 2188 4325 10517 2531 5640 597 4614 5133 5649 6350 6350 7471 ÿ

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	Most Similar Top Hit Acession Database BLASTE No. Source	1.0E-120 Y00067.1 NT	1.0E-120 BF337599.1	1.0E-120 AB033057.1	1.0E-120 AB033057.1 NT	1.0E-120 AB007964.1 NT	1.0E-120 AB007984.1 NT	1.0E-120 AB007834.1 NT	1.0E-120 BE392102.1 EST HUMAN	1.0E-120 BE392102.1 EST HUMAN	1.0E-120 BF308641.1 EST HUMAN	1.0E-120 AU133205.1 EST HUMAN	1.0E-120 AL049801.1 NT	1.0E-120 AI904151.1 EST_HUMAN	1.0E-120 AB029000.1 NT	1.0E-120 BE296387.1 EST_HUMAN	1.0E-120 BE887619.1 EST_HUMAN	1.0E-120 BE867619.1 EST_HUMAN	1.0E-120 U94774.1 NT	1.0E-121 Y18000.1	1.0E-121 AU134963.1 ESI HUMAIN	1.0E-121 5032192 N I	1.0E-121 AB011153.1 INI	4755139 NT Homo sapiens incettal polyphosphatase, type I, 107kD (INPPAA), splice variant e, mRNA	4755139NT	1 OF 124 M95988 1	1 0F.121 M95988 1	4 OF 424 78831.1	1 0F-121 Y19208.1	TA 05 424 V40208 4	4 OF 424 AD037758 4 NT	4 0E-121 AB037758 1 NT	TAN CASTRACTO TO TO	1.0E-121 AF150150.2
Sill ISI	p Hit Acession No.									1					_	-						32192		4755139	4755130	:1					7			7
		1.0E-120 YO	1.0E-120 BF	1.0E-120 AE	1.0E-120 AE	1.0E-120 AE	1.0E-120 AE	1.0E-120 AE	1.0E-120 BE	1.0E-120 BF	1.0E-120 BF	1.0E-120 AL	1.0E-120 AI	1.0E-120 AI	1.0E-120 AI	1.0E-120 Bi	1.0E-120 BI	1.0E-120 BI	1.0E-120 U	1.0E-121 Y	1.0E-121 A	1.0E-121	1.0E-121 A	1.0E-121					1 OF 124 V				١	
	Expression Signal	522	243	0.85	0.85	2.33	2.33	1.17						0.54	2.55	3.72				1.08			2.81	1.33										7.35
	ORF SEQ ID NO:	33613	34063	34135	34136	34138	34139	34182			35492		36525		35831	37015	37311	37312	37567	25534		26130	27001	27407	_	27445								23060
	⊇	20400	20824	20907	20907	21001	21001	21045	22063	22063	22297	22312	22329	22443	22624	23741	24007	24007	24247	12898	13165	15549	14315	14694		14684	14/00	34/8	14820	1584	15844	16281	16281	16419
	Exen SEQ ID NO:	18	iإ×	i ¤	10	12	"			L	L_	L	L	9792	9766	L	11316	11316	11850	F	88	707	1568	1958	⊢	1928	3 3	150	88	3079	3070	3525	3525	3866

PCT/US01/00667

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Top Hit Descriptor	The State Dark Dark Carriers and Chron MAGE:20054173	7001 XI NCI COGAT TRUIT TAILS SEPTICES COSTS COS	H. Saplens E.C1 gare (exc.) 17	9908XT NCL CGAP LUZ+ FIGURE SEPTIME CONTROL MAGE: 2049820 5	601140485F1 NIH MIGG. B Harro Sapratas Culta Carlo IIIVano.	Human glucose transporter (SLU 14) gene, compress con	Homo saplens Xq pseudoeutosamer region, seguinani 22.	RC3-NNV088-2/U404-011-102 NNV000 FIGURE CDNA	RCS-NINO000-2/ 04:00-01 1:02 W COCO (GABA) A receptor, alpha 2 (GABRA2), mRNA	Homo Sapara y Ballinia an incompany or some	Homo septens UNA to protective in synthese each 8	Homo septens DINA 10 prosecution is printed and septens con 5's similar to TR:075457 075457 CYTOSOLIC	PHOSPHOLIPASE A2-GAMMA: PHOSPH	ia05g05.y/ Human Panchedic Isless from Saprens Color o	Homo sapiens COX11 (yeast) homolog, cytochirune c oxuasee assembly promit (1978) # PASS allele.	who explens UDP-glucuranceydransrerase aby processor (COLED-Y)	complete das	MAG01.s1 Spares fetal fiver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'	741140330 HEMBA1 Homo septems CDNA clone HEMBA1006536 5	Long capture T. cell hundrome investion and metastasis 1 (TIAM1), mRNA	Homo sepiens intersectin short isoform (ITSN) mRNA, complete cds	Homo septens T-cell (Imphoma invasion and metastasis 1 (TIAM1), mRNA	Homo saplens intersectin short isoform (ITSN) mRNA, complete cds		Human kappa-Immunoglobulin germine pseudogene (Chr22.4) variable region (subgroup V kappa II)	omo saplena cysteine-rich repeat-containing protein containing protein	Homo saplens collegen, type XII, eigna 1 (COL 12x I), III VAN	Homo septens collegen, type XI, aprila 1 (COLTA1), interesting	601497032F1 NIH_MGC_70 Home sapiens curve cione liverue: 3088336 3	601896173F1 NIH MGC_19 Home septent Curva Curva IMAGE:4125234 5	O SOUTH AND THE PROPERTY OF TH
Top Hit Detebese Source		T HUMAN	П	\neg	T HUMAN	Į.		HOMAN	HOMAN			Į.	EST HUMAN P	3858.1 EST_HUMAN P	П			WALL OF THE PARTY	1	LICENSE						L			T HUMAN	П	EST HUMAN
Top Hit Acession No.		-		0.1	1				1.0E-121 AW898086.1	1436217			1.0E-121 AW583858.1	1 0E-121 AW 583858.1	11427788		1.0E-121 AF064200.1	7330334 N	N59624.1	1.0E-121 AU119320.1	5	E00478	110201	1.0E-122 AF114488.1	1.0E-122 M20707.1	1.0E-122 AF167706.1	11418424 NT	11418424 NT	1.0E-122 BE906024.1	1.0E-122 BF316170.1	1.0E-122 BF316170.1
jg ≠ m	anis A	1.0E-121	1.0E-121 X91937.1	1.0E-121 BE222250	1.0E-121 BE271424.	1.0E-121 M91463.1	1.0E-121 AJ271736.	1.0E-121	1.0E-121	1.0E-121	1.0E-121 D84122.1	1.0E-121 D84122.1	1.0E-121	1.0E-121	1.0E-121		1.0E-121	1.0E-121	1.0E-121 N59624.1	1.0E-121	1.0E-122	١	1	1.0E-122					1)	1.0E-122
Expression Signal	_	2	3.24	76.0	0.85	16.0	0.68	1.78	1.78	211	2.45	2.45	1.24	1 24	2.95		1.28	3.46	2.53	2.83	228	2.63	214	3.99	4.28	1.28	1.35	1.35			5.21
ORF SEQ I		20663	30259	30510	31167	32294		30537	30638	33960	33664	33865	35615				36616		36844	37269			25787		28814						Ш
Exon SEQ ID	<u> </u>	17035	l	1	1	1_	1	L	L	1	1_	L	l		22.402		23374	_	23597	上		13128	13147	13631	13050	1		1	14400	1	11
Probe SEQ ID	<u> </u>	4208	4919	218	5474	8524	8788	9888	9888	7838	7842	7842	0758	8	8738	2/02/	10683	10880	10917	11309	281	327	348	862	2,4		000		18/	2495	2495

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1/57275 ————																100	*	-	e de la companya de l	·	PCT/	Ų	SQ1	/00)66	57 • •	-
Top Hit Descriptor	Homo sapiens FYVE domain-conteining dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds	Homo sapiens amyloid beta (A4) precursor protein (protesse nedn-il, Atzheimer disesse) (APP), mRNA	UI-HF-BNO-all-a-03-0-UI-TI NIH_MGC_50 Home sapiens cDNA done IMAGE:30/3646 3	601113567F1 NIH MGC 16 Homo sapiens CDNA cione IMAGE:3334232 5	601113567F1 NIH MGC 18 Hamo eaplens CLYNA Clane IMANCE: 3534232 3	BA49106.81 Sogres testis NH1 Homo saparis Cuiva dans imake: 1408538 3	Homo saplens mRNA for doublesex and mabos readed transcriptor lactor (Christia)	Homo saplens forther gent tarves (Urosophila) norther (Little Central Personalize to	gyszho7.x1 NCI_CGAP_Britzs Home septens GUNA Gode Invace.2013/3/3 shinine id SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.;	gyg2h07.x1 NCI_CGAP_Bm23 Homo seplens cDNA clone IMAGE.2013757 3' smillar to sw:.MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.	Novel human gane mapping to chomosome X, isoform of dbl (proto-oncogene)	EST367904 MAGE resequences, MAGD Homo septems cDNA	Homo sapiens gene for B120, excn 10	Homo septens phosphomennonvites 1 (PMM1), mRNA	602018058F1 NCI CGAP Bm6/ Homo septens curva cicne IMACE: 4153670 5	602018058F1 NCI CGAP BITTO Home sapients contraction of the contraction of	Homo septens chromosome 21 segment no 210048	HOTO SECTION IN THE TREE PROPERTY INVOLVED THE CHILD WAS A CONTRACT OF THE CONTRACT OF	Homo sapiens phosphaidylinositol 4-phosphaie 5-kmase, type II, beta (Fil-on.c.b) IIInvin, and tangened products	Homo sepiens phosphaddylinositol-4-phosphate 5-kinase, type II, bota (PIP6K2B) mkNA, and translated products	Homo sepiens pertial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02	Human amelogenin (AMELY) gene, 3' end of cds	Human amologenin (AMELY) gene, 3' end of cds	Human amelogenin (AMELY) gene, 3' and of cds	Homo sapiens RAB9-Ike protein (LOC31209) mKNA	Homo sapiens gluteminy-peptide cyclotransterase (gluteminy cyclase) (kind i), minus	Homo sapiens retinadehyde-binding protein (CKALBP) gene, comprete cus
Top Hit Databese Source	N	ÑŢ	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	NT	N	EST_HUMAN	EST HUMAN	M	EST_HUMAN	Ę	LN1		EST HUMAN	LN.	LN1	¥	8 NT	Ę	N	NT	Į.	Z	7NT	¥
Top Hit Acession No.	1.0E-122 AF264717.1	4502186	AW504645.1	1,0E-122 BE256039.1				11424216	1.0E-122 Al359618.1	1.0E-122 Al359618.1		1.0E-122 AW955834.1		18187	1.0E-123 BF345274.1	1.0E-123 BF345274.1	1.0E-123 AL163249.2	5803114	4505818 NT	4505818	1.0E-123 AJ388641.1	W55419.1	M55419.1		7705962	691281	34219.1
Most Similar (Top) Hit BLAST E Value	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-122/	1.0E-122	1.0E-122	1.0E-122	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123 M55419.1	1.0E-123 M55419.1	1.0E-123 M55419.1			1.0E-123 L34219.1
Expression Signal	14.1	5.04	1.46	1.36	7.1	0.73	0.65	121	1.19	1 19	1.05	217	1.88	6.8	1.74	1.74	5.4	2.5	5.58	5.58	0.0	2.7		2.7	3.62	0.95	1.56
ORF SEQ ID NO:	28280			31170	١			34761							28181		26415	26422	<u> </u>				L			28657	30847
Econ SEQ ID NO:	15612	17526	17658	18275	18275	19801	21387	21617	21902	24002	22682	23588	24046	24509	13523	13623	13754	13761	13966	1	1		L.	L	L	1	L
Probe SEQ ID NO:	8	4796	4930	5478	8658	7113	8695	8926	8223	823	10034	10008	11358	11958	751	751	885	<u>\$</u>	1218	2 2 2	1438	200	2002	2082	2313	3245	5361

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	Top Hit Descriptor	Homo sapiens retinaldehyde binding protein (CRALBP) gene, complete cds	801591108F1 NIH MGC 7 Hamo sapiens cDNA clone IMAGE:3945433 5	AU118435 HEMBA1 Hamo septens cDNA clone HEMBA1003591 5"	yd84e03.r1 Soeres fetal fiver spleen 1NFLS Home sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14e80 PROTEIN KINASE YAK1	Human growth hormone releasing hormone gene, expn 7	Human hBRAVO/Nr-CAM precursor (hBRAVO/Nr-CAM) gene, complete cds	Homo septens heperan sulfate (glucosemine) 3-O-sulfotransferase 2 (HS3ST2), mRNA	Homo seplens 2-5 bilgoedenylate synthetase 2 (OAS2), mRNA	601152815F1 NIH_MGC_19 Hamo septens aDNA clane IMAGE:3509162 5	AU131881 NT2RP3 Hamo sepiens aDNA done NT2RP3003409 5	AU131881 NTZRP3 Homo saplens cDNA done NTZRP3003409 5	RC4-BT0311-261199-012-e07 BT0311 Homo saplens cDNA	Homo septens mRNA for KIAA0454 protein, pertial cds	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabeflaz) mRNA, complete cds	802086791F1 NIH MGC 83 Homo segiens cDNA clone IMAGE:4250879 5'	602086791F1 NIH_MGC_83 Homo septens cDNA clone IMAGE:4250879 51	Homo sapiens T-cell lymphome invasion and metastasis 1 (TIAM1) mRNA	Homo sepiens T-cell lymphome invesion and metastasis 1 (TIAM1) mRNA	Homo septens DNA for amylold pracursor protein, complete cds	Homo saplens chromosome 21 segment HS21C046	281b04.r1 Strategene schizo brain S11 Homo sepiens cDNA clone IMAGE:728719 5 similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)	281b04.11 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 6300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVRAL ELEMENT)	Human putative ribosomal protein S1 mRNA	Homo sepiens T-cell lymphome Invesion and metastasis 1 (TIAM1) mRNA	Homo sepiens hypothetical protein (HSPC068), mRNA	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete ods	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds	Homo sapiens mRNA for nucleolar RNA-helicase (noH61 gene)	801491715F1 NIH_MGC_69 Hamo septens cDNA dane IMAGE:3893954 5	Homo sapiens glutamete receptor, Ionotropic, kainete 1 (GRIK1) mRNA
21 11000 218	Top Hit Database Source	N	EST HUMAN	EST_HUMAN	EST HUMAN	N	N F	N N	NT LV	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	Z	Þ	EST HUMAN	EST_HUMAN	뒫	F	Þ	IN	EST_HUMAN	EST HUMAN	Z	Ŋ.	IN	IN	NT	Į.	EST_HUMAN	Ā
	Top Hit Acession No.		1.0E-123 BE799746.1	1.0E-123 AU118435.1	153196.1			11525833	36439	1.0E-123 BE263001.1		1.0E-123 AU131881.1		1.0E-123 AB007823.1		1.0E-123 BF677292.1	1.0E-123 BF677292.1	4507600			1.0E-124 AL163246.2	1.0E-124 AA397551.1	1.0E-124 AA397551.1		4507500	7705446					4504118
	Most Similar (Top) Hit BLAST E Value	1.0E-123 L34219.1	1.0E-123	1.0E-123	1.0E-123 H53196.1	1.0E-123 U42224.1	1.0E-123 U55258.1	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123/	1.0E-123	1.0E-123 U09823.1	1.0E-123	1.0E-123	1.0E-124	1.0E-124	1.0E-124 D87675.1	1.0E-124 A	1.0E-124	1.0E-124	1.0E-124 AF155654.1	1.0E-124	1.0E-124	1.0E-124 AF274892.1	1.0E-124 AFZ74892.1	1.0E-124 AJ131712.1	1.0E-124 BE879524.1	1.0E-124
	Expression Signal	1.58	1.62	2.59	1.2	1.25	2.87	1.62	1.3	2.18	29.0	. 0.67	1.13	2.43	15.48	4.66	4.68	2.19	2.19	2.99	284	2.68	2.68	7.84	1.61	1.94	4.95	4.95	220	3.05	0.85
	ORF SEQ ID NO:	30848	31191	32145	32688	32698	32849	33061	33312	33324	33636	33637		35193	35239	37637	37838	25708	25709		25898	26092	26083	26174	28223	26321	28747	28748	27263	27512	28774
	Exon SEQ ID NO:	18163	18293	19146	19643	19652	19783	19985	20212	20221	20511	20511	21126	22023	22067	24314	24314	13070	13070	13076	13259	13450	13450	13515	13562	13653	14074	14074	14548	14786	16118
	Probe SEQ ID NO:	5361	5494	6377	6905	6915	7094	7302	7542	7851	7818	7816	8433	9269	9405	11720	11720	262	262	388	43	675	676	742	062	88	1325	1325	1808	R S	3338

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	Hang saniens A TD-care the investrity re-utfancy Calculation 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	Homo sabiens ATP-sensitive inwentity rectifying N-chainnel subunit (NCN-06/BIRT) gene, exch	H. seniens lactate dehartmosasses Brans arms 4 and 2/EC 4.4.017	Homo sabiens T-cell fumbhorns truesion and malestests 4 /TIA1/4 - DNA	Homo sablena dichemente mooreter involvenia di Colica - Di a	Homo sablens cene for 8120 even 14	Human (bronecth cere extra time III more of (EDII) execused	Homo saplens hypothetical by the El 140300 (Fl 140300) DAIA	Homo sapiens IO moiff containing GTDsea activation module 4 (100.4.54)	802124844F1 NIH MGC 56 Home seniors chiva Appen 14 A CC 120462 E1	AV711283 Cu Home septema china della chema Culada Denta invincio. 120 1050 5	Omo sanjens tihimithi shakka wasan w	Minusculus mRNA for house general medical control (Urosophila fat facets related) (USP9X), mRNA	SONDARZZIES NIEU WOG S L	S00043774F1 NIU MCC & U.S. SQUARE CON CONTRACTOR SA	COURT OF THE PROPERTY OF THE PROPERTY CAN CAN CAN CAN CAN CAN CAN CAN CAN CAN	Redefinds at Strategene HeLa cell 83 937216 Homo sapiens cDNA clone IMAGE:855897 3'	hg94a09.x1 NG_CGAP_KId11 Homo septiens cDNA done IMAGE:2953240 3' similar to TR-O05162	095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE	hg94e09.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2933240 3' similar to TR:095162	WC43003.XI NCI CGAP P/28 Home sentens - DNA Alexandra Al			AV645633 GLC Homo sepiers CDNA dans GLCACAL 3	Homo seplens cerc/50 centrearms ensoring the contract of the contract of the centre of	Homo septens certific central associated product minuty, compete cus	WIGSTOLKT NOT CGAP KINTO Homo seniens cDNA clone INACE: JAnneou 2:	W63f02x1 NC CGAP Kid12 Home seriente cDNA close MA CELLOCOCA 21	UI-HE-BNO-alz-b-04-04 II II NIH MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III II III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 Home sentens CONA June 1840 CE 2-4-04-04 III III MOC 50 CE 2-4-04-04 III III MOC 50 CE 2-4-04-04 III MOC 50 CE 2-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4	Homo seciens feuche-rich alloma hackwared 4 (1 Cit) with A	Human muscle glycogen phosphorylase (PYCM) pens arms 8 thm wh 47	hj05c08.x1 Soares_NFL_T_GBC_S1 Home sardens cDNA clane IMAGE.2980906 3'
gle Exon Prol	Top Hit Database Source	LN	LN	Į.	L	6 NT	Ę	Ę	N-	Ľ	EST HUMAN	EST HUMAN	L	L	EST HIMAN	EST HIMAN	TO LOUIS	ES HOMAN		EST_HUMAN	EST HIMAN	Т	Т	Т	Г	Т		EST_HUMAN	EST HUMAN	HUMAN	Т	Ę	EST HUMAN
Sin	Top Hit Acession No.				4507500	4504116	=		3022337	4506786 NT	1.0E-124 BF698135.1		0654	11717.1	Ī		Ī	18854		1.0E-124 AW612106.1	1.0E-124 AW612106.1				Γ						2087		П
	Most Similer (Top) Hit BLAST E Value	1.0E-124 S78684.1	1.0E-124 S78884.1	1.0E-124 X13794.1	1.0E-124	1.0E-124	1.0E-124 /	1.0E-124 M18178.1	1.0E-124	1.0E-124	1.0E-124 E	1.0E-124 A	1.0E-124	1.0E-124 Y11717.1	1.0E-124 B	1.0E-124 BE271295 1	4 OE 424 A ARSOSS4 4	1.0E-124		1.0E-124 A	1.0E-124 A	1.0E-124 AI799864.1	1.0E-124 AI799864.1	1.0E-124 AV645633.1	1.0E-124 AV645633.1	1.0E-124 AF022855.1	1.0E-124 AF022855.1	1.0E-124 AI767133.1	1.0E-124 AI767133,1	1.0E-124 AW503755.1	1.0E-124	1.0E-124 U94778.1	1.0E-124 AW665663.1
	Expression Signal	1.25	1.25	1.54	-	1.34	19.	1.13	12.12	0.92	6.94	0.91	96.0	2.95	400	90.0	800	8.07		1.28	178	0.61	0.61	231	2.31	0.62	0.52	7.57	7.57	1.57	1.44	1.61	3.51
	ORF SEQ ID NO:	28895	28896	29033	29269	29432	30061		30647	31293	31514	31823	32099	32695	32786	32787	33220	33982		34195	34196	34907	34908	35223	35224	35309	35310	35342	35343	35630		36905	37265
	Exon SEQ ID NO:		16239	· 16393							18588	18856	19109	19640	19729	19729	20128	20850	1 6	21002	21055	21749	21749	22052	22052	22130	22130	22161	23.64	22422	23487	23652	23964
	Probe SEQ ID NO:	3482	3482	3640	3880	4058	4696	4881	5215	5586	5797	6077	6339	6912	7037	7037	7452	8158	200	7922	8362	0906	0906	838	0686	9477	2477	8098	809	9771	10804	10976	11305
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z181604.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' strullar to TR:G300482 z181604.r1 Stratagene achizo brain S11 Homo sepiens cDNA cione IMAGE:728719 5' struller to TR:G300482 hv69e08.x1 NCI_CGAP_Lu24 Homo septens cDNA done IMAGE:3177686 3' similar to TR:Q25058 Q25058 N/39808.x1 NCI_CGAP_Lu24 Hamo septens cDNA done IMAGE:3177886 3' struller to TR:Q25058 Q25058 #19e03.x1 NCI_CGAP_Gas4 Home sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662 119e03.x1 NOL_CGAP_Gas4 Homo saplens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662 Homo sepiens Bruton's tyrosine kinese (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein zk33c07.s1 Soeres_pregnent_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to 2463307.81 Soares_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE:486540 3' similar to 201g09.r1 Scense_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:429568 5 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT); G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) 9b.X65867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN); Homo sepiens KIAA0744 gene product; histone descetylase 7 (KIAA0744), mRNA 601577981F1 NIH_MGC_9 Homo sapiens cDNA done IMAGE:3928685 5' Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA Top Hit Descriptor Homo sepiens celcineurin binding protein 1 (KIAA0330), mRNA HA0086 Human fetal liver cDNA library Homo sapiens cDNA HA0086 Human fetal liver cONA library Homo sapiens cONA Homo sepiens KIAA0022 gene product (KIAA0022), mRNA Homo seplens mRNA for KIAA1083 protein, partial cds Homo seplens mRNA for KIAA1172 protein, partial cds Homo saplens chromosome 21 segment HS21C010 Homo seplens Usurpin-elpha mRNA, complete cds Homo sepiens Usurpin-alpha mRNA, complete cds Homo saplens ALR-like protein mRNA, partial cds (L44L) and FTP3 (FTP3) genes, complete ods Homo sapiens inhibin, alpha (INHA) mRNA Homo sepiens inhibin, alpha (INHA) mRNA Single Exon Probes Expressed in Brain FIBROPELLIN IA; FIBROPELLIN IA : YKRS PROTEIN. YKRS PROTEIN. EST HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** EST HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST_HUMAN Detabase Top Hit Source ٤ 11417862 NT 11417862 NT 눋 눋 Ę 4504696 NT 7661867 NT 4504696|NT 7882279 Top Hit Acession 1.0E-124 AA397551.1 .0E-124 AB029016.1 1.0E-125 BE219510.1 1.0E-124 AA397551.1 1.0E-125 BE219510.1 1.0E-125 AB032908.1 1.0E-125 BE743922.1 1.0E-125 AA042813.1 1.0E-125 AA042813.1 1.0E-125 AL163210.2 1.0E-125 AF015450.1 AA011278.1 1.0E-124 AI446455.1 1.0E-125 AF284750.1 1.0E-124 AI448465.1 1.0E-125 AI110858.1 AF015450.1 1.0E-125 AI1 10656.1 1.0E-126 U78027.1 1.0E-124 1.0E-125 1.0E-125 1.0E-124 1.0E-125 1.0E-125 1.0E-125 Most Similar 1.0E-125 BLASTE 当(金) Value 6 4 1.18 2.28 4. 5.47 0.89 0.91 8 88.0 1.61 1.56 1.59 <u>E.</u> Expression Signal 36452 36453 28092 30729 25804 26043 26134 27242 31026 30730 25603 26280 28405 26545 27105 ORF SEQ 28083 27258 27259 28058 27816 27967 28057 ÖΖΩ SEO ID 23219 23219 13450 24823 25279 12828 13743 14544 13450 12961 13408 13408 13485 13870 15575 15225 25279 12961 13115 13887 14533 **454** 15080 15317 15317 Ö 11452 628 SEQ ID 11462 12029 12029 12454 148 4 311 623 2 978 1783 2508 12706 12708 417 1131 1988 1804 2604 2002 2358 8

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275	-	П	188		8	П	T	Т		Π	T	T	T	T	T	_	7 June -				US01	/0 <u>0</u>)66 	7	٦-	
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Top Hit Database Source	EST_HUMAN	EST_HUMAN	N N		EST HUMAN		NAM LI IMAN	NAME OF THE PARK	NOW I SEE	EST HUMAN	EST HUMAN	ESI HUMAN	ESI HOMAIN	Z P	EST HIMAN	123	뒫	5	EST HOMAN	ESI TIOMES	EST HUMAN	MT TOWN	Z Z	١£		
Top Hit Acession No.	E018009.1	1.0E-125 AA042813.1	11420114	41167411	1.0E-125 BE219510.1	1.0E-125 BE219510.1	11436448	1.0E-125 BE175189.1	1.0E-125 BE892660.1	1.0E-126 AI679904.1	1.0E-125 BE738055.1	1.0E-125 BE562528.1	1.0E-125 BE582528.1	X03427.1	1.0E-125 X03427.1	1.0E-125 BE515100.1	1.0E-125 U90288.1	1.0E-126 U80288.1	1.0E-125 BE181640.1	1.0E-125 BE181640.1	1.0E-125 AI585998.1	1.0E-125 BE794576.1	1.0E-125 AB002286.1	AFU43450.1	114233	ADDITOR:
Most Similar (Top) Hit BLAST E Value	1.0E-125 BE018009.1	1.0E-125	1.0E-125	1.0E-125	1.0E-125	1.0E-125													Ш				1			
Expression Signal	46.0	0.92	2.09	2.09	1.48	1.48	3.16	0.91	3.76	0.74	0.8	1.63				0.55	0.90	_		6.83						3.94
ORF SEQ ID NO:	28425	28228		29884	25803	25804	L	31517		31811				32450	32460	33483	34273	34274		34857	5 35207	7 36215	7 36253	8 36514		37026
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Probe SEQ ID NO:	3008	3830	4513	4513	4971	4074	5783	5802	5842	7007	3004	888	6486	9	6964	7706	8444	8444	9016	9016	88	10350	1039	10581	10758	11081

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WO 01/57275

	7275	Т	\neg	7		_		Γ	[_	-	T	İ					T	1/6	T	T	00667	٦	
	Top Hit Descriptor		Homo sanians myosin, heavy polyperotide 1, skeletal muscle, adult (MYH1), mRNA	Line and A hindre maken II (PABP2) gene, complete eds	Construction of the Constr	KCC-S 10180-250-200-10-01-01-01-01-01-01-01-01-01-01-01-0	QV3-B I USOS-UZVIZUO-U SAGUS EL I COOS I I GIRIO CAPITA CONTRA A C	CASAB LUSSASSASSASSASSASSASSASSASSASSASSASSASSA	Homo sapiens Cuching Innered Cuch Innered	H. saplens gene for eighnat - at text in the same of the saplens gene at the saplens gene at the saplens saple	Homo septens hypothetical protein Fuzzono (1 220048), mRNA	Hond sapers injuriance process: (PANRES) mRNA	Homo sapiens rounding product to the same 1 (GRIK1) mRNA	Hamb separation and the separation of the separa	20/2013, 13 of all appears of the control of the co	20/ 2003.1 Ditaggale para ce (not in the para ce para para para para para para para par	In september death receiptor 6 (DR6) mRNA	Hornic separatis Godul Foxopia (1919)	AX/8000.11 SUBLES INSTRUCTION SERVERS CON COME IMAGE:3928685 5	Publication of Science feed lines enlared INFLS Homo septems CDNA clone IMAGE:86527 3'	PROZDILZSI Scenes form figure NDZHF8 9w Homo sepiens cDNA done IMAGE:796444 5 similar to	TR:G1145880 G1145880 TITIN;	Homo sepiens mRNA for KIAA1525 protein, parval cus	Homo sapiens mixiga to ruckatozo prosent, per usa complete cons	Homo sapiens clienty dynem neavy drient 8 (Dyna is) in a chip complete cds	A Hazarez Di ACE1 Homo serviere CDNA done PLACE1004325 5	AUTSD403 FLACE I TUIT CRC 84 Home septens cDNA clone IMAGE 2350009 3' similar to	WINDIN AND SOME OF THE WAR WAS A SUBFAMILY MEMBER 2;	Home sapiens mRNA for KIAA1294 protein, partial cds	Homo sapiens mRNA for KIAA1294 protein, partial cos	Human mRNA for ankyrtn (vartent 2.1)	ne74b12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909963 similar to SW:TSG6_HUMAN P99098 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR;	Homo sepiene neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA	
\- \- \-	Top Hit Detabase	Source	1		I N	EST HUMAN	EST HUMAN	EST HUMAN	7 NT	LN.	Į.	-N	78 NT		EST HUMAN	EST HUMAN	L	LN	EST HUMAN	ESI HOMAN	EST HOMAN	EST_HUMAN	LV.	L/N	Ę	LN.	EST HUMAN	EST_HUMAN	N	Z	LN L	EST HUMAN	ADAINT	1111
	Top Hit Acession	ď		COCS					4758007		8923056 NT	8923056 NT	6382078	4116		-		7657038 NT	134078.1	1.0E-126 BE743922.1	66998.1	1.0E-128 AA460075.1	1.0E-128 AB040958.1	1.0E-126 AB040958.1	1.0E-126 AF257737.1	1.0E-126 AF257737.1	1.0E-126 AU136463.1	1.0E-128 AI806483.1	1 0E-128 AB037715.1	1 0F-126 AB037715.1	X16609.1	4 DE 408 A A 483468 1	14	4/1/VVF
-)n	BLAST E Value		1.0E-125	1.0E-125 AF026029.1	1.0E-125 AW812899.1	1.0E-126 BE074267.1	1.0E-125 BE074267.1	1.0E-126	1.0E-126 X68735.1	1.0E-126	1.0E-126	1.0E-126	1.0E-128	1.0E-126 AA160709.1	1.0E-128 AA160709.1	1.0E-126 X53941.1	1.0E-126	1.0E-126 N34078.1	1.0E-128	1.0E-126 T66998.1	1.0E-128	1.0E-128	1.0E-126	1.0E-128	1.0E-126	1.0E-126	1.0E-128	1 0E-128		1	1		021-⊒0.1
	<u> </u>	Signal		1.74	4.84	1.92	3.58	3.58	1.48	1.45	1.17	1.17	1.48	0.72	7.54	7.54	1.09	1.6	1.74	0.81	0.68	3.22	4.2	4.2	1.02	1.02	0.62	5	0 78	0.78	2.65			0.87
	ORF SEQ	Ö Q		37213	37218	37284	37397	37398	26189	28331	27804	27805	28059		28479	28480	29014	29040		30413		24887				33158		BCFCG	1					35539
	E CHO	NO.		23921	73927	23984	24087	24087	13529	13667	15067	15067	15318	15835	15836	L	<u> </u>	16400	L	17797	18412	49047		1	1	L	L		BLSDZ ST. SOS		20582	1		22346
	Probe	S S S		11259	11285	11377	11486	11488	757	808	2344	2344	2605	3069	3070	3070	3620	3647	4783	5078	5816		0138 8407	6107	7399	7399	7802	}	8		7887		8083	9692

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Homo sepiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), Homo sapiens leukocyte immunogiobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-ILRELATED PROTEIN; contains element MER22 au90e06.y1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE:2782594 5 similar to Hamo sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds IZA2802.11 Sogres_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5* IZA2802.11 Sogres_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5* Homo sapiens delayed rectifier potassium channel subunit isK mRNA, complete cds Homo septens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products 602139138F1 NIH_MGC_46 Home sepiens cDNA clone IMAGE:4298240 5 601149404F1 NIH_MGC_19 Home sepiens cDNA clone IMAGE:3502129 5 801577981F1 NIH_MGC_9 Homo sapiens cDNA clane IMAGE:3926685 5 Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds Homo septens neuroblastome-emplified protein (LOC51594), mRNA Homo sapiens neuroblastoma-amplified profein (LOC51594), mRNA Homo sepiens lost on transformation LOT1 mRNA, complete cds Top Hit Descriptor Homo sapiens mRNA for casein kinase I epsilon, complete cds Homo sapiens mRNA for casein kinase I epsilon, complete ods Homo sapiens DNA for amyloid precursor problen, complete ods Homo sapiens DNA for amyloid precursor protein, complete cds Homo sapiens mRNA for casein kinase I epsilon, complete cds Homo sapiens mRNA for casein kinase i epsilon, complete cds Human macrophage mannose receptor (MRC1) gene, extrn 5 Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA Homo sapiens ubiquitin specific protease 8 (USP8) mRNA Homo saplens ribosomal protein L28 (RPL26) mRNA Homo sepiens chromosoms 21 segment HS21C068 Homo sepiens adlican mRNA, complete ods Human mRNA for cytokeratin 18 Single Exon Probes Expressed in Brain repetitive element; ANZENA NA Database EST HUMAN EST_HUMAN EST HUMAN Tob⊞ EST HUMAN EST_HUMAN EST HUMAN Source È 눋 z ż 뉟 Z z 5903065 NT 4827053 NT 5803065 NT 눋 4506820 NT 7706239 NT 7706239 NT 4506384 NT 6912639 NT Top Hit Acession 1.0E-126 BE261660.1 1.0E-126 BE743922.1 AB024597.1 AB024597.1 1.0E-127 AB024597.1 1.0E-128 BF683175.1 1.0E-127 AB024597.1 1.0E-127 AW 161297.1 AF245505.1 AF114488.1 1.0E-127 AA450131.1 1.0E-127 AF135188.1 1.0E-127 AL163268.2 1.0E-127 AA450131.1 1.0E-127 AF252297.1 1.0E-126 M93196.1 D87676.1 D87675.1 U72621.2 1.0E-127 X12881.1 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-127 BLASTE 1.0E-127 Most Simile 1.0E-127 当(金) 1.0E-127 1.0E-127 1.0E-127 1.0E-127 Value 1.0E-127 4.63 5.47 8 4.71 4.71 3.54 2.44 24 6.02 2.83 1.37 2.73 3.04 7 23.74 4.35 Expression 0.94 0.7 Signal 30413 ORF SEQ 36692 37414 25718 25622 25823 25622 25623 27515 28301 27516 27801 28068 28081 27861 28082 28824 ÖNQ 22503 28926 29592 29993 SEQ ID 24102 12982 23450 17797 12982 12982 12982 13075 13630 14730 15064 15338 443 13004 4780 15325 15338 10968 17198 1492B 17299 16838 16968 17360 1000 10766 11501 12490 SEQ ID 108 168 8 169 287 287 1686 828 2058 881 8 2014 2341 **4098** 2187 3701 4462 45 969 4625 4227 4227

Table 4

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SW:PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA Homo septens similar to heat shock 70kD protein 9B (mortain-2) (H. sapiens) (LOC63184), mRNA Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds Homo septiens similar to heat shock 70kD protein 9B (mortalin-2) (H. septiens) (LOC63184), mRNA Homo sapiens secretory petitiway component Sec31B-1 mRNA, alternatively spliced, complete cds za01a10.r1 Soares melanocyle 2NbHM Homo sapiens cDNA clone iMAGE 291258 5' similar to qm94h09 x1 NCI_CGAP_Lu5 Homo sepiens cDNA clone IMAGE:1896449 3* Homo sepiens Chediak-Higashi syndrome 1 (CHS1), mRNA 601434784F1 NIH_MGC_72 Hamo saplens cDNA clane IMAGE:3919917 6' 601434784F1 NIH_MGC_72 Hamo saplens cDNA clane IMAGE:3919917 5 Homo septiens gene for AF-6, complete cds 601278127F1 NIH_MGC_20 Homo septiens cDNA clone IMAGE:3618822 5* Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA Top Hit Descriptor Homo sapiens mRNA for casein kinase I epelion, complete cds Homo sepiens mRNA for casein Idnase I epailon, complete ods QV3-BN0046-150300-121-h11 BN0046 Homo septens cDNA Homo sepiens Chediak-Higashi syndrome 1 (CHS1), mRNA Homo sepiens Chediek-Higashi syndrome 1 (CHS1), mRNA Human FAU1P pseudogene, trinucleotide repeat regions Human FAU1P pseudogene, trinucleotide repeat regions Homo sepiens mRNA for KIAA1247 protein, partial cds Homo saplens ribosomal protein S2 (RPS2) mRNA Homo sapiens Pendrad syndrome (PDS), mRNA Homo sapiens Pendred syndrome (PDS), mRNA Homo sapiens integrin, beta 8 (ITGB8) mRNA Homo sapiens reelin (RELN) mRNA H.sapiens TCF11 gene, exon 3-6 H. sapiens NOS2 gene, exon 6 Single Exon Probes Expressed in Brain EST_HUMAN Top Hit Databesse EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN Source Ę 4826963 NT 11421914 NT 11427235 NT Ż 4504778 NT 11421595 NT 11421914 N 11427235 NT 눋 11417339 NT 4506718 NT 11437455 NT 눋 Top Hit Acession 4826977 11427235 11417339 AW996292.1 1.0E-127 AF274863.1 1.0E-127 AB024597.1 1.0E-127 AF274863.1 BE895415.1 1.0E-127 AB011399.1 1.0E-127 BE895415.1 1.0E-127 W03547.1 1.0E-127 AB024597.1 .0E-127 AI298932.1 1.0E-128 BE385617.1 1.0E-128 AB033073.1 1.0E-127 X85764.1 X84060.1 1.0E-128 U02523.1 1.0E-127 Most Similar 1.0E-127 1.0E-127 1.0E-127 (Top) Hit BLASTE 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-127 1.0E-128 1.0E-127 1.0E-128 1.0E-128 Value 1.37 5.28 0.89 0.81 1.65 1.65 0.84 4.17 Expression 7.88 0.8 4.17 3.25 3.25 2.25 2.25 3.04 5.5 1.1 1.08 Signer 31329 31428 31813 31979 ORF SEQ 32332 31359 32461 33461 33462 33470 34625 34628 3537 37546 ΒNO 36101 37050 37051 37547 25623 25873 25622 31048 27520 28802 27872 27521 18416 SEQ ID 18445 1884D 18325 20348 1944 18506 19003 20348 20355 22889 23777 Ö 21477 2288 12982 14795 23777 24224 24224 12982 24814 13233 14795 14934 16148 15165 888 SEQ ID 5713 6070 8228 0999 6962 7884 9773 788 8785 9540 8 Ö 7691 8785 10241 11107 11107 11627 12244 12244 11627 12444 447 2063 2063 2208 3389 **2446**

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Top Hit Descriptor	(PBOX1) mRNA	Homo sapiens prospero-beased not recovery (110001); iii. 1	H. saplens gare for more septiment years in the septiment of the latest septiment of the se	80158046811 NIH MGC strangesters CDNA done IMAGE:3020057 5	601 5804 680-1 NITH MICCONTINUE COMMODIAN - dependent (70kD) (PDE1C), mRNA	Trickly September 1 124 Home septems CONA clone IMAGE: 3'	ANTERSAGET NIH MGC 71 Homo sapiens cDNA clone IMAGE:3905794 5'	William emission or restaint ABC transporter (WHITE2), mRNA	Homo earlens mRNA for KIAA0464 protein, partial cds	Umms earliens mRNA for KIAA0454 protein, perfiel ods	AAAAA A NOI OGAD Ewd Homo sepiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338	CHROMOSOME SEGREGATION GENE HOMOLOG CAS.:	Homo explens glutamate receptor, toroutawa, try the last and the second	om68h08.s1 NCI_CGAP_GCA Homo sepasis Curin care in the personal control of the	Homo serviens mRNA for TRABID protein (TRABID gene)	601277828F1 NIH MGC 20 Hamo sapiens cDNA clone IMAGE:3618750 5	EST347340 MAGE resectionces. MAGC Homo septems cDNA	neutralise mouth factor binding protein-2 frumen, placenta, Genomic, 1019 nt, segment 2 of 4]	in the mount factor hinding protein-2 fruman, placenta, Genomic, 1019 nt, segment 2 of 4]	No. 1 himse mRNA contained Zinc finger CZH2 type domains	Homo serviens clutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	Homo sapiens glutathione S-transferase thera 2 (GS I I Z) and glutating is created and contact the same of the sam	genes, complete ods	Homo saparas zinc inigat process (Consessed in 1997)	ZINCE TRICETORY TRICETORY TO THE TRICETORY THE TRICETORY THE TRICETORY TO THE TRICETORY THE TRICETORY THE TRICETORY THE TRICETORY THE TRICETORY THE TRICETORY THE TRICETORY THE TRICETORY THE TRI	ZINC FINGER PROTEIN AZFIU	ZNC FINGER PROJEIN 721 10	Homo septens mkNA for NAA1439 protein, period cos	CMYAS Human cardiac musicle expression library notice salvans convice in the conv	Cardiomyopathy associated gene 5	Cardiomyopathy associated gene 5
Top Hit Databese				UMAN	CINAN		Т	HOMAN			Ž	T HUMAN		H IMAN		T LITTINGN	Т	HOMAN	Z	Z	Z	뒫		۲	Į.	SWISSPROT	SWISSPROT	SWISSPROT	N.		EST HUMAN	EST_HUMAN
Top Hit Acession No.		11426673 NT		E747981.1	E747981.1 EST	88			5523			VA639198.1	11425254 NT	4 COOCO 4	ASCOSOS.	AJ252050.1	3E3844/3.	4W955290.1	337722.1	537722.1	AL096880.1	1.0E-129 AF240786.1		1.0E-129 AF240786.1	11418522 NT	Q14585	Q14585	Q14585	1.0E-129 AB040892.1		1.0E-129 AW755254.1	1.0E-129 AW755254.1
Most Similar (Top) Hit T	Value	1.0E-128	1.0E-128 X69539.1	1.0E-128 BE747981.1	1.0E-128 BE747981.1	1.0E-128	1.0E-128 BF224345.1	1.0E-128 BE614105.1	1.0E-128	1.0E-128 AB007923.1	1.0E-128 AB007923.1	1.0E-128 AA639198.1	1.0E-128		1.0E-128 AA920808.	1.0E-128 AJZ5ZUGU.	1.0E-128 BE384475.	1.0E-128 AW955290	1.0E-129 S37722.1	1.0E-129 S37722.1	1.0E-129 AL096880.	1.0E-129		1.0E-129	1.0E-120	1.0E-129 Q14585	1.0E-129 Q14585	1.0E-129 Q14585	1.0E-129			
Expression	•	6.14	0.7	0.65	0.65	2.58	6.9	0.02	0.67	67.0	0.73	1.63	3.52		3.21	1.35	1.4	7.02	1.33	1.19	2.73	157		1.67	2.78	1.21	1.21	1.21	4		2.26	2.26
ORF SEQ		20086	31147	31013	31814	32082	32516	33080	33471	34276	34277	35903	36541		36550		39689		25839	25830	27154	0745B		27159	L						28611	
	ö	17351	18257	18672	18672	19094	19493	20010	20356	21138	21138	<u> </u>	<u> </u>	<u> </u>			23445	<u> </u>	L	13189	14456	00777	1	14460	i_	1.	L	L	1		16088	ł
Probe SEQ ID	ö	ARAR	2458	88	2883	6324	6831	7327	7692	8446	8448	40027	1080	3	10618	10690	10761	12117	118	4	1713			1717	1838	2125	24.25	3425	216	2	4247	4247

Page 467 of 536 Table 4 Single Exon Probes Expressed in Brain

WO 01/57275

 	T	Τ	Τ	Γ	Τ	Γ		Γ										T		T													
Top Hit Descriptor	Homo saplens KVLQT1 gene	601449740F1 NIH MGC 65 Homo sepiens CDNA clone IMAGE:3853688 3	801449740F1 NIH MGC_85 Homo sepiens cDNA done IMAGE:3853585 5	Homo sepiens KVLQT1 gene	Homo septens similar to ribosomal protein S26 (H. septens) (LOCosoper), Illinoida	Homo seplens WSCR4 gene, exons 3 and 4	Homo sapiens WSCR4 gene, extrns 3 and 4	Homo sapiens mRNA for KIAA0634 protein, partial cds	Home sepiens solute certer family 21 (organic aryon transporter), manuser 9 (SLC21A9), mRNA	Hamo sapiens solute cerrier family 21 (organic anion transpored, inchinal (0.002883)	ae01c01.s1 Strategene schizo brain S11 Homo separas curvo documentations	ar72/07.r.1 Soares NixHMPu S1 Homo septens CUIVA Clorie IMAGE. 101 COS	Homo saplens similar to ribosomal protein S26 (H. saplens) (L.O.Cooper), III. Cooper, III. Coope	AU143115 Y79AA1 Hamo septens CDNA clone Y79AA1001410 5	AU143115 Y79AA1 Homo septens cDNA clone Y78AA1001410 3	VA49005.11 Sources fetal liver splean 1NFLS Home eapleins CUINA CIGITE IN TAMIAS ASIATIOUS=ASIAN;	SP:B48150 B48150 HP-26#HIBERNATION-RELATED FRO IEIN - DIMINION OF THE PROPERTY OF THE SPECIAL PROPERTY OF THE SWINDING HOME SECIENTS CON A GONE DIFFERENTY OF THE SWINDING HOME SECIENTS CON A GONE DIFFERENTY OF THE SWINDING HIBERT PROPERTY OF THE SWINDING	Homo sapiens hypothetical problem (HSPC242), mRNA	Homo sapiens mRNA for KIAA1414 protein, partiel cds	801121995F1 NIH MGC 20 Homo septens cONA clone IMAGE:3345396 5	601121996F1 NIH MGC_20 Homo saplens cDNA clone IMAGE.3315000 0	Human gene for catalese (EC 1.11.1.0) extra 8 maryang 50 months	Home sapiens RET finger protein-like 1 strussmind used with 1 home and 1 protein and 1 protein 1 home and 1 protein and 1 protein 1 prot	1601343016F1 NIT MCC_S 184 Home seniors CDNA clone IMAGE:3685468 5	601343010F1 Nin, MCC, 2017000 Period (RDH) mRNA, complete ods Home sealens retinal dehydrogenese homolog isoform-1 (RDH) mRNA, complete ods	1801343016F1 NIH MGC_53 Homo septens cDNA clone IMAGE:3883488 b	801343016F1 NIH_MGC_53 Hamo septems cDNA clone IMAGE:3683460 5	ULHE-BNO-81/2-08-0-ULM NIH MGC 50 Homo septems curve constitute 1/ mRNA	Human T-call receptor (V athha 22.1, J alpha RPMI4205-variant, C aprim 7)	Т	Г	Π	
Top Hit Detabese Source		IN BLAN	1	101	2 5	E LV	114	12	- LN	TN C8CT	EST HIMAN		TAIL	EST HIMAN	NAM PL		EST HUMAN	EST HUMAN	NI DECC	NIMAN	EST HUMAN	¥	1		EST HUMAN	NAME TO FOUND	EST HUMAN	EST HUMAN	LN LN	FST HUMAN	EST HUMAN	EST HUMAN	
Top Hit Acession No.		J006345.1	1.0E-129 BE869993.1	1.0E-129 BE805953.1	1.0E-129 A.1006345.1	11420830	1.0E-129 AF041056.1	1.0E-129 AF-041056.1	1.0E-128 ABO14554.	114437283		1.0E-129 AA682200.1	1.0E-129 AA623020.1	1142000	1.0E-129 AU143119.1	1.0E-129 AU143113.1	1.0E-129 H83155.1	AL120739.1	×/	1.0E-130 AB037835.1	1.0E-130 BEZ/3194.1	1.0E-130 BLE 013	1.0E-130 AJ010230.1	1.0E-130 BE564219.1	1.0E-130 BE564219.1	1.0E-130 AF240608.1	1.0E-130 BE564219.1	1.0E-130 BE304218.1	1.0E-130 AW 903390.1	1 MB/ / 10.1	1.0E-130 AW 043850.1	1.0E-130 AW 363299.1	
Most Similar (Top) Hit BLAST E	Agida	1.0E-129 AJ006345.1	1.0E-129	1.0E-129 E	10E-129	1.0E-129	1.0E-129/	1.0E-129	1.0E-128/	1.05-128	1.0E-128	1.0E-128	1.0E-129	1.0E-120	1.0E-129	1.0E-129	1.0E-129	1.0E-129	1.0E-130				1	L						-[
Expression Signal		3.73	0.56	0.56	4.15	3.93	2.49	2.49	3.94	0.97	26.0	0.57	4	6.57	1.38	1.38	1.79	2.68	1.3	0.09			3.08	1 17	1.17	1.09							1.07
ORF SEQ EID NO:		31742	32499	32500	32776	32844	33191	33192		35835	35836	36396	37137		37537	37538			25538			77099			28291								30372
SEQ ID		18781	19477	19477	19719	19779	20105	20105	20911	22627	22627	23109	23851	19779	24213	١.	24801	1_	L	1		14407			15648	L	1_	0 15648	5 16865	3 18798			8 17757
Probe SEQ ID		9000	8816	8816	7027	080	7428	7428	8217	92026	8788	10523	11186	11289	11615	11815	2	12483	74	1147	1987	1961	1976	2773	2881	3585	3750	3750	3015	4053	4501	5038	5038

Page 468 of 536 Table 4 Single Exon Probes Expressed in Brain

1/3	57275	- T	-	_			-r		T	7	7		7	т	Т	T		8	4pr	#	7	7	1	<u>-</u>	P	C]	[/\ 	US	01	<u>/00</u>	66 T	7 T	ť
	Top Hit Descriptor	Human germline immunoglobulin lambda light chain pseudogene (VII.1)	CMO-CN0045-170200-225-g03 CN0045 Homo saprens GUNA	CMO-CN0045-170200-225-603 CN0045 Hamo sapiens cUNA	Homo sapiens estrogen-responsive B box protein (EBBP), mrkna	Homo septens solute cerrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLCSA7), mRNA	Homo septens aurora-related kinase 1 (ARK1) mRNA, complete cds	EST368312 MAGE resequences, MAGD Hamo septens cDNA	Hamo sapiens mRNA for KIAA1335 protein, pertial cas	xd36e06.x1 NCL CGAP_0v23 Homo saplens cDNA clone IMAGE:20408/4 3	Homo sapiens contactin 6 (CNTN6), mRNA	Home septiens contactin 6 (CN INB), mrCNA	Homo sapiens hypothetical protein FL/20208 (FL/20208), mr.NA	Homo sepiens hypothetical protein FLJ20208 (FLJ20208), mKNA	Homo sapiens glutamete receptor, metabotropic 5 (GRM3) mRNA	Homo saplens RET finger probein like 1 antisense transcript, partial	258004.17 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:06/590 5 stimiter to 1 K:G222811 G222811 ALPHA 1 CHAIN OF TYPE XI COLLAGEN.;	TARACA M. Source NIHMPU S1 Homo sepiens CDNA clone IMAGE:067590 5' similar to TR:G222811	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;	Homo seplens checipoint suppressor 1 (CHEST), mitiNA	Homo septens hypothetical protein FLJ203/1 (FLJ203/1), minuty	Homo sepiens hypothetical protein FLJ20371 (FLJ20371), mknvA	Homo sepiens DCRR1 mRNA, pertial cds	Homo sepiens DCRR1 mRNA, pente cds	Homo sepiens beta-tubulin mKNA, complete ods	Homo sepiens Cdc42 effector protein 2 (CCP2), mixing	Human heparin cofactor II (HCF2) gene, exons 1 through 3	Homo sapiens RNA-binding protein S1, serine-rich domein (RNINS1), mktva	Homo sapiens mRNA for multidrug resistance protein 3 (ABCAS)	Homo sapiene mRNA for multidrug resistance protein 3 (ABCAS)	HUMS161-08B Human placents polyA+ (I rujwara) Home sapidatis con A cure of the recipe F	HUM516H08B Human placenta polyA+ (Trujwata) Homo saprens curva chore cerv-ordno o	Human ribosoma protein L/ (RFL/) marky, compare cus
	Top Hit Database Source	FA.	EST_HUMAN	EST_HUMAN	F	¥	LN	EST_HUMAN	NT	EST_HUMAN	NT	NT	NT	LN	IN	N	HENT HIMAN		EST HUMAN	F	Z	Į.	Z	N	Z	¥	NI	NT	NT	L	EST HUMAN	EST HUMAN	LZ.
	Top Hit Acession No.		1.0E-130 AW843875.1		11425446	11418777		[1.0E-130 AW103454.1	11432889	11432880	8923197	8923197	4504142			T	0.0E+00 AA228126.1		8923340	8923349			_	02897		6857825					
-	Most Similar (Top) Hit BLAST E Value	1.0E-130 X57825.1	1.0E-130 A	1.0E-130 AW843875.1	1.0E-130	1.0E-130	1.0E-130 AF008551.1	1.0E-130 A	1.0E-130 AB037756.1	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130	1.0E-130 AJ010230.1	7007300	O.OE.	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D833Z7.1	0.0E+00 D83327.1	0.0E+00/	0.0E+00	0.0E+00 M58600.1	0.0E+00	0.0E+00 Y17151.2	0.0E+00 Y17151.2	0.0E+00 D78804.1	0.0E+00 D78804.1	0.0E+00 L16558.1
	Expression Signal	0.55	0.81	0.81	0.75	2.62	0.45	2.39	<u>4</u>	1.25	0.51	0.51	1.72	1.72	2.67	1.58		2	9.	1.02	0.72	0.72	6.7	6.7	17.04	1.19	0.82	4.22	0.78	0.78	3.04	3.04	5.78
-	ORF SEQ ID NO:	32405	32587	32588	32602	32910		34553	34967		36340	36341	37104	37195	37624			C1+4C7	25446	25449	25454	25465			25468						25514	25515	25516
	Exon SEQ ID NO:	19391	19557	19657	19570	10841	21274	21410	21802	22484	23109	23100	23904	23904	24298	15478		12832	12832	12834	12841	12841	}	L	l _		<u>L</u>		1	_	12885	12885	12886
	Probe SEQ ID NO:	6829	6723	6723	6736	7454	8582	8718	9114	9833	10463	10463	11242	11242	11703	12759		₹	4	1	7	7	ଷ	8	25	33	35	39	188	18	88	88	19

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0	1/57275	-	~	<u>-</u>	_	_	_	_	_	-		_	_	_	_		·		4	, ,	—	, ₁	-r ··		P	CI	<u>/L</u>	ļŞO	1/	00	667	
	Top Hit Descriptor	or 48e07.x1 Jile bone marrow strome Homo sepiens cDNA clone HBMSC cr48e07.31	or48607 x1 Jia bone memow stroma Homo sapiens cDNA clone HBMSC cr48e07 3	Human von Willebrand factor pseudocene corresponding to exone 23 through 34	Human von Willebrand factor bseudogene corresponding to entres 23 through 34	Homo sepiens protein tyrosine phosphatase, non-recentor tyre suivertate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosopadase, non-recentor tyre surviving 1 (PTPNS4) mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens amfortde binding protein 1 (amine æddase (copper-containing)) (ABP1), nuclear gene	Homo seriens helenosees as nuclear thousands with HNDDAA TODAA	Homo seriens actin here (ACTR) mRNA	Human polyhomeotic 1 homolog (HPH1) mRNA partiel ods	HA1347 Human fetal liver cDNA library Homo seniens cDNA	Homo sapiens mRNA for KIAA1363 protein, partial cits	Hisaplens noct gene (expn. 2)	16:38b05.x1 NCI_CGAP_UM Homo sepiens cDNA done IMAGE:2230833 3' similar to TR:098551 099551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.	1838b05.x1 NCI_CGAP_UM Homo sapiens cDNA done IMAGE:2230833.3' similar to TR.098551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECY IRSOR	1y01h09.r1 Soares melanocyte 2NbHM Homo septens cDNA clone IMAGE:278017.5	ly01h09.r1 Soares melanocyte 2NbHM Homo eaplens cDNA clone IMAGE:270017.5	Homo sepiens polymenase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	Homo sepiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA	ya83g04.r2 Stratagene fetal spieen (#937205) Homo septiens cDNA clone IMAGE:68310 5	ye83g04.r2 Stratagene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:68310 5	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA	601460375F1 NIH_MGC_66 Hamo septens cDNA clane IMAGE:3863803 5	Homo sepiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA	Homo sapiens serine peimitoy transferase, subunit II gene, complete cds; and unknown genes	601174270F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:3523864 5	601174270F1 NIH_MGC_17 Homo sepiens cDNA dane IMAGE:3529864 5	2d62b05.r1 Sceres_fetal_heart_NbHH19W Homo sepiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);	
	Top Hit Database Source	EST HUMAN	EST HUMAN	N.	۲	Z	Z.	도	F	5	Į.	LN	E	EST HUMAN	N	LN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	Ā	Į,	EST_HUMAN	EST_HUMAN	NT	EST_HUMAN	IN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	
	Top Hit Acession No.	0.0E+00 AW069534.1	0.0E+00 AW069534.1	0.0E+00 M60678.1	0.0E+00 M60676.1	4758977	4758977	4758977	4758977	4501850	450444	5016088		-			0.0E+00 AI623701.1	0.0E+00 AI623701.1			4505938	4505938			4444		4504444			0.0E+00 BE295973.1		
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00 U89277.1	0.0E+00	0.0E+00	0.0E+00 XB1213.1	0.0E+00	0.0E+00	0.0E+00 N36040.1	0.0E+00 N36040.1	0.0E+00	0.0E+00	0.0E+00 T56945.1	0.0E+00 T58945.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 W73973.1	
	Expression Signal	12.55	12.55	1.5	0.91	10.36	10.36	10.18	10.18	0.78	15.25	17.68	23.28	3.51	1.72	1.33	0.89	1.47	1.48	1.48	4.38	4.38	1.29	1.29	8.88	2.1	25.83	+	1.15	0.88	5.4	
	ORF SEQ ID NO:			25524		25538		25536	25537	25544		25553	25558	25562	25563	25566	25572	25572	25573	25574	25586	25587	25593	25594	1	25609		25612	25613	25613	25614	
	Exen SEQ ID NO:		12888	12891	12893	12900	12900	12900	12900	12906	12907	12916	12010	12925	12926	12928	12835	12935	15513	15513	12943	12943	12950	12960	12864	12968	12970	12973	12975	12075	12976	
	Probe SEQ ID NO:	gg 20	29	ಜ	65	ಬ	73	76	92	8	æ	8	8	66	100	105	113	114	115	115	128	128	136	136	9	3	155	158	\$	161	162	

Page 470 of 536 Table 4 Single Exon Probes Expressed in Brain

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	Top Hit Descriptor	QV3-HT0457-140200-088-d04 HT0467 Homo sepiens cDNA	QV3-HT0457-140200-088-d04 HT0457 Homo septems cDNA	Homo sapiens zinc finger protein mRNA, complete cds	Homo septens chromosome 21 segment HS21C002	Homo saciens chromosome 21 segment HS210002	bb24e12.y1 NIH_MGC_14 Homo septems cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631;	bb24e12.y1 NIH_MGC_14 Homo sepiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z GE22631:	Homo sapiens mRNA for KIAA0784 protein, partial cds	Homo septens mRNA for KIAA0784 protein, pertial cds	Human gamma-cytoplasmic actin (ACTGP9) pseudogene	Homo septiens CTCL tumor entigen se14-3 mRNA, complete cds	Homo septens CTCL tumor antigen ser143 mRNA, complete cds	Hamo septens chromosome X MSL3-2 protein mRNA, complete cds	Homo sepiens chromosome X MSL3-2 protein mRNA, complete cds	rpo4f08.x1 NCI_CGAP_UB Homo saplens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN (HUMAN);	tq04f08.x1 NCI_CGAP_Ut3 Home suplens cDNA clone IMAGE:2207847.3' similar to gb;J03191 PROFILIN I (HUMAN);	Homo sapiens DNA mismarch repair protein (MLH3) gene, complete cds	Homo septens ribosomal protein L31 (RPL31) mRNA	Homo septens TADA1 protein mRNA, complets cds	Homo saplens mRNA for KIAA0721 protein, partial cds	Homo sepiens mRNA for KIAA0721 protein, partial cds	Mus musculus testis-epecifio protein, Y-encoded-like (TspW), mRNA	Homo sapiens mRNA for KIAA0758 protein, partial cds	Homo sepiens mRNA for KIAA0758 protein, partial cds	Homo septens NS1-associated protein 1 (NSAP1) mRNA	Homo sepiers chronosome 21 segment HS21C001	Homo saplens chromosome 21 unknown mRNA	H. septens mRNA for interferon alpha/beta receptor (long form)	Homo sapiens chromosome 21 unknown mRNA	Homo septens T-cell lymphome investon and metastasis 1 (TIAM1) mRNA
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	LN FN	Į.	LN L	EST_HUMAN	EST HUMAN	TN	N	N	LZ LX	N	N	IN	EST_HUMAN	EST HUMAN	NT	Ę	۲	NT	IN	IN	NT	L	IN	IN	NT	Z	TN	Ę
	Top Hit Acession No.	0.0E+00 BE162832.1	0.0E+00 BE162832.1	0.0E+00 AF244088.1			0.0E+00 BE018970.1	0.0E+00 BE018970.1		7.1		5.1	0.0E+00 AF273045.1		0.0E+00 AF167174.1	0.0E+00 AI587308.1	0.0E+00 AI587308.1	0.0E+00 AF195658.1	08632			0.0E+00 AB018284.1	78444		0.0E+00 AB018301.1	33805	0.0E+00 AL163201.2	0.0E+00 AFZ31919.1			4507500 N
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D50659.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X89772.1	0.0E+00	0.0E+00
	Expression Signal	0.81	0.81	1.42	29.73	29.73	5.95	5.95	3.05	3.05	67.77	3.74	3.74	4.81	4.81	9.26	9.26	3.08	23.37	4.72	9.19	8.34	3.5	123	1.23	3.97	6.94	3.85	1.71	9.14	1.68
	ORF SEQ ID NO:	25615	25616	25617	25620	25621	25627	25628	26631	25632	25643	25648	25849	25651	25852	25658	25659	25661			25664	25664	25865	25678	25679	25682		25688	25891		25710
	Exon SEQ ID NO:	12977	12977	12978	12981	12361	12988	12988	12963	12963	13002	13007	13007	13009	13009	15537	15637	13019	13021	13022	13026	13028	13027	13041	13041	13042	13044	13049	13051	13059	13071
	Probe SEQ ID NO:	183	<u>1</u>	184	167	167	178	178	181	181	189	\$	호	198	8	205	205	207	80	210	214	215	210	8	8	ឆ	ន	240	242	520	<u>88</u>

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	Top Hit Descriptor	Homo saplens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo saplens hypothetical protein (LOC51250), mRNA	Homo eaplens DCRR1 mRNA, pertial cds	Homo sapiens DCRR1 mRNA, pertial cds	Home satiens DCRR1 mRNA, partial cots	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA	Homo sapiens potassium inwardly-rectifying channel, subfamily J. member 15 (KCNJ15) mRNA	Homo septens potassium invarid v-ectifying channel, subfamily il mamber 15 (KCN 115) mRNA	Homo septens mRNA for KIAA1019 protein, partial cds	Homo septens mRNA for KIAA1019 protein, partial cds	Homo eaplens ribosomei protein S5 (RPS5) mRNA	2x18c06.rt Soares NhHMPu St Home septems cDNA circus IMACE: 753004.F.	Homo sepiens SON DNA binding profein (SON) mRNA	Homo septens SON DNA binding profein (SON) mRNA	Homo sablens intersectin short isoform (TSN) mRNA, complete cols	Homo satiens homonaly uprequiated neu temor-associated kinasa (H.INK) mBNA	Homo saciens homonally upraculated neu timor-associated kinese (HI INK) mRNA	Homo sapiens myelotd/ymphotd or mbed-lineage leukernia (trithorax (Drosophila) homolog); translocated to 4		Homo saplens X-box binding protein 1 (XBP1) mRNA	Human zinc finger protein zfp31 (zf31) mRNA, partial cds	Homo septens chromosome 21 unknown mRNA	Homo sepiens chromosome 21 unknown mRNA	Homo septems chromosome 21 unidonown mRNA	Homo septens T-cell fymphome invasion and motastasis 1 (TIAM1) mRNA	Homo septens GA-binding protein transcription fector, alpha subtunit (60kD) (GABPA) mRNA	Human mRNA for KIAA0184 gene, partial cds	Human mRNA for KIAA0184 gene, pertial ods	Homo seplens T-cell (ymphoma inyasion and metastases, 1 (TIAM1) mRNA	AU134963 PLACE1 Homo septems cDNA cione PI ACE1000800 5		one IMAGE:2018457 3' similar to gb:X54199	RC2-CT0320L300100-018-000 CT0320 Home sentem conta	VALOU BERTE OFFICE OFFI
9.0	Top Hit Database Source	Z	L'N	LN.	N L	N.	EST_HUMAN	1	NT	N	Z.	LN	EST HUMAN	Ę	IN	N	LN	K		NT	NT	NT	NT	NT	TN	NT	NT	LN T	Ę	¥	T HUMAN	Ā	EST HUMAN	Т	٦
	Top Hit Acession No.	4507500 NT	7708028 NT	0.0E+00 D83327.1	0.0E+00 D83327.1	0.0E+00 D83327.1	0.0E+00 AW845283.1	4557029 NT	4557029 NT	0.0E+00 AB028942.1	0.0E+00 AB028942.1	4506728 NT	0.0E+00 AA480002.1	07152	4507152 NT	0.0E+00 AF114488.1	7857213 NT	7857213 NT		5174574 NT	4827057 NT		0.0E+00 AF231919.1		0.0E+00 AF231919.1	4507500 NT	4503854 NT			4507500 NT	0.0E+00 AU134963.1			0.0E+00 AW754180.1	
	Most Similer (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00 U71600.1	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00 D80006.1	0.0E+00 D80008.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	
	Expression Signal	1.68	3.07	1.19	3.28	3.28	0.78	6 .65	6.65	4.97	4.63	4.23	3.76	18.93	16.53	2.33	4.97	6.23		266	1.71	1.45	242	242	3.84	233	0.94	4.1	1.9	1.89	1.07	8.31	1.54	1.83	
	ORF SEQ ID NO:	25711	25713		25728				25735	772/44	25745			25746	25746	25750	25759	25759		25771	25775	25780	25784	25785	25786	25788	25792	25793	25793	25795	25806	25849	25850	25813	
	Exen SEQ ID NO:	13071	13073	13083	13084	13084	13085	13093	13083	13103	13104	15540	13105	13108	13106	13110	13122	13122		13136	13139	13142	13146	13146	15541	13148	13151	13152	13152	13154	13163	13203	13204	13170	
	Probe SEQ ID NO:	283	285	278	277	277	278	287	287	202	298	887	300	301	302	306	319	320	1	332	338	341	88	8g	347	8	352	383	354	356	367	378	378	383	

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Top Hit Descriptor	Homo sepiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo seplens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fo binding protein (FC(GAMMA)BP) mRNA	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	Homo sepiens (gG Fc binding protein (FC(GAMMA)BP) mRNA	Homo septens IgG Fo binding protein (FC(GAMMA)BP) mKNA	H. seplens gene for RNA pol II targest authurit, exprise	H. seplens gene for RNA pol II largest subunit, excha 23-29	H. septens gene for KNA pol II largest suburit, exons 20-29	H. seplens gene for RNA pol II largest eubunit, exons 23-23	Homo eapiens ribosomal protein (L19 (RPL19) mRNA	yg09e02.r1 Soares infant brain 1NIB Homo sapiens GUNA cione inwiscus iouz. o	Homo sapiens phosphoribosylgiyoinamide formyltransfersse, phosphoribosylgiyoinamide synureusse, The shoet calculation indicates synifications (GART) mRNA	United and the state of the sta	Inditio espicies in the control of the control espicies of the control espicie	Home septens miking for MAN TOTA protecting per use case.	Home sapiens SON LAYA Bread process (SON) Instance	Homo septens SON LINA binding protein (SON) minna	Mus musculus truncated soon protein (sort) minny, curitated cus	Homo sappens interfered garmina receptor 1 (11)	IES127054 Cerebellum II Homo septens County of end	801111020111N MIS WEST TO THIS SERVICE AND THE WAS THE	Homo sapiens 5-hydracydyparanae (seronami) receptor 15 (1117.15) innach	Homo sepiens 5-hydraxydybarnine (serocanin) receptor 15 (n.i.k.i.b.) illinum	Homo septems Keratin 18 (KK118) micrvA	Homo seplens keratin 18 (KRT18) mRNA	Homo sapiens chronosome 21 segment HS21C046	Homo sapiens chromosome 21 segment HS210046	Hamo sepiens chromosome 21 segment HS21C045	Homo sapiens mRNA for KIAA1209 protein, partial cds	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 6	801274951F1 NIH_MGC_20 Homo sapiens cDNA cione IMAGE:3615/36 9
Top Hit Detabese Source	Z	LN	Z	LX	LN LN	ĮN	NT	Ę	Ę	Z	N _T	TN	NT	EST_HUMAN	1	Z	Z	Ł	¥	N	Þ	. 1		EST HUMAN	¥	۲	INT	TN	<u>N</u>	LN	NT	LN.	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	4503680 NT	4503680 NT	TN 0896094	4503680 NT	TN 0898084	4503680	4503680 NT	4503880 NT	74870.1	<i>(</i> 74870.1	<7487 0.1	1	4506608 NT			1N 4785354	4506728 N	0.0E+00 AB028942.1	4507152 NT	4507152 NT	0.0E+00 AF193607.1	4557879 NT	0.0E+00 AA324282.1	0.0E+00 BE254447.1	4504532 NT	4504532 NT	4657887	4857887 NT	AL163246.2	AL163246.2	0.0E+00 AL163246.2	0.0E+00 AB033035.1	0.0E+00 AU132898.1	0.0E+00 BE385144.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00 X74870.1	0.0E+00	0.0E+00 R17795.1	!	0.0E+00	0.00.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00					
Expression Signal	8	2.49	2.40	1 17	30	1,30	277	0.84	1.35	1.35	1.07	1.07	28.13	1.5		1.31	3.18	3.93	5.45	5.45		1.99	2.01	0.97	3.15	3.15	1.23	123						
ORF SEQ ID NO:	25816									25825	25824			25435		25851		25852	25853	L					25879	25880								
Exon SEQ ID NO:	43470	13172	44472	42474	13175	13175	13176	13177	13178	13178	13178	13178	13182	12822			13206	13207	13208	L	L	13219	13224	13225	L	13241	L	丄	L	Ļ	L	1	L	L
Probe SEQ 10 NO:	200	3 6	207	3 8	380	380	380	39-1	392	392	393	383	397	411		419	420	421	422	422	423	433	438	430	455	455	481	\$	¥2.	472	477	484	8	491

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Top Hit Descriptor	PMO-DT0065-130400-002-c06 DT0065 Homo sepiens cDNA	Novel human gene mapping to chomosome 1	Homo saplens PC326 protein (PC326), mRNA	IL2-FT0159-070800-120-F07 FT0159 Homo sepiens cDNA	Homo sepiens chromosome 21 segment HS21C010	QV2-BT0635-160400-142-h05 BT0635 Homo septens cDNA	601764858F1 NIH_MGC_53 Homo septens cDNA clone IMAGE:3896998 5	Home saplens mRNA for KIAA1476 protein, partial cds	Homo sapiens transcription elongation factor B (Sill), polypeptide 1-like (1 CEB1L) micha	Homo saplens guanine nucleofide binding protein (G protein), alpha 11 (Gq dass) (GNA11) mKNA	Home saplens guanine nucleotide birding protein (G protein), alpha 11 (Gd class) (GW11) mixivs	Home saplens entitle (LOC54443), mRNA	Homo sapiens anillin (LOC54443), mRNA	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat	regions	UI-H-BI1-ecb-h-04-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone IMAGE:2713951 37	Homo sepiens RGH1 gene, retrovirus-like element	Homo sapiens ublquinol-cytochrome c reductase, Rieske Iron-sulfur polypoptide 1 (UQCRFS1), nuclear gene percentan mitro-handral protein mRNA	Grace production and production of the control of t	FOURTH ADDITION OF INTERNATIONAL PARTY SAME IN A CHARLE IN A CONTRACT OF	MOUSZZOZY FINITY MOCZY TRAIN SEPTEMBER WAS ARRESTED TO THE TRAIN SEPTEMBER MONTH SEPTEMBER FILIDATOR (FILIDATOR) MRNA	Home services hypothetical protein FL/20701 (FL/20701), mRNA	Homo saplens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA	Homo septens Smad- and Olf-Interacting zinc finger protein mRNA, partial cds	Homo saplens Smad- and Olf-Interacting zinc finger protein mRNA, partial cds	Homo sapiens NOD1 protein (NOD1) gene, exprs 1, 2, and 3	Homo septens low density tipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRF2), mKNA	Homo sepiens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens low density lipoprotein-related protein 2 (LRF2), mKNA	Homo sapiens low density lipoprotein-related protein 2 (LRVZ), mrxvA	260-67, r1 Soeres testis JNH Hamp sapiens CUNA clone IMAGE: 720/52 5	Homo agriens Kichiz gene, retromus-like element
Top Hit Database Source	EST HUMAN	NT	5 NT	EST_HUMAN	LN	EST_HUMAN	EST HUMAN	TN	TN	K	NT	NT	FN F		뒫	EST_HUMAN	LN	i i		Z	HOWEN TOWN	- F2	L	LN	TN	Z	NT	NT	님	Ę	N 8	EST HUMAN	토
Top Hit Acession No.	0.0E+00 AW938825.1	0.0E+00 AL117233.1	8923955	0.0E+00 BF373403.1		0.0E+00 BE081527.1	0.0E+00 BF028005.1	0.0E+00 AB040909.1	6006030 NT	4504036 NT	4504036 NT	8923831 NT	8923831		0.0E+00 AF003528.1	0.0E+00 AW135324.1			21/4/42		0.0E+00 BF104898.1	OSCSOST NI	TNI PSEINT	0.0E+00 AF221712.1			6806918 NT	6806918 NT	6806918 NT	68069	6806918	-	0.0E+00 D11078.1
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0€+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00		0.0=+00	0.0E+00 J04086.1	0.0E+00	0.0=+00	00+30.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00		0.0E+00
Expression Signal	1.11	1.33	127	0.77	5.37	1.29	1.14	1.68	27.68	4.33	4.33	26'0	0.97		5.82	1.89	8		263	7	1.83	0.98	0.80	1.15	1.15	3.18	12	3.83	3.83	0.92	0.92	1.35	10.1
ORF SEQ ID NO:	25911				25924	25628	25934	25941	25944	25945	25946	25948				25958			25982				RESECT OF					26022	26023	26024	26025	26034	26038
Exon SEQ ID NO:	15543	13278	13279	13283	13290	15544	13302	13308	13311	13312	13312	13314	13314		13318	١.	13336						133/0	13378	13378	13387	L	Ĺ.	13391	13392	13392	13399	13403
Probe SEQ ID NO:	492	2	495	499	88	513	518	624	527	528	628	53	530		535	543	553		572	585	88	980	20 2	8 8	8	800	612	613	613	914	614	620	624

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:415567 5' similer to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (H1MAN).	Zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to abb:A21187 AI PHA-2-MACROCS OR! II N DEFC: IDECT (19 14 A ST)	Hamo septens novel SH2-containing profein 3 (NSP3) mRNA	Homo sapiens glutamate receptor, ionofronic, N-methyl D-essentate 28 (CRIN2B) DNA	Homo saplens CCAAT-box-binding transcription factor (CBE2) mRNA	Human neutral amino acid transporter (ASCT1) cane, excn 8	Homo sapiens sodium/calcium exchanger isotom NaCs3 (NCX1) mRNA complete calc	Homo sapiens sodium/calcium exchanger isoform NeCa3 (NCX1) mRNA, complete crts	Homo saplens protein kinase. X-linked (PRKX) mRNA	Homo sapiens protein kinase, X-linked (PRKX) mRNA	Human endocenous retrovirus pHE 1 (FRVp)	Homo sablens high-mobility oranin (prophistone characterist) hatter a (1997)	Homo seriens mRNA for KIAA 1080 meters and individually protein (CIMC1) mKNA	Transcendent in the A LOS protein, parties of	morno saprens similar to rat integral membrane ghycoprotein POM121 (POM121L1), mRNA	IDPSGU1.81 NCI_CGAP_Ent.1 Homo sepiers dDNA done IMAGE:1129633 3' similar to gb:X57352	Human von Willebrand fechnologie avons 23 through 24	Human von Willebrand factor cense evens 23 though 34	HOMO SEDIENS TIVE TOWNSHIP ASSOCIATION OF A LITERAL AND A	Homo sapiens ALR-like profesh mRNA nertial Ale	Homo sapiens ALR-like probein mRNA pertial cds	Homo sapiens hypothetical protein FLJ21634 (FLJ21634) mRNA	TCAAP100779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo	September 2014 Figure 1 CANTO / 2	Homo sapiene MHC class I antique (LITA C) IIINNA, FLANCI alleba, complete cds	Homo services choride chemies (CA (ACA) months, much complete cas	Human classification activates behalved access to a complete so a complete construction activates behalved access to a complete construction activates behalved access to a complete construction access to a comp	Human plasmington activator intelliged acres 2 to 9	Homo saniens zinc finger brokein 24.2 (7NIC242) DNIA	Homo seciens mRNA for represent mortal cal-	801445647F1 NIH_MGC_65 Homo saplens CDNA clone IMAGE;3849803 5'
gle Exon Pro	Top Hit Defabase Source	EST_HUMAN	EST HUMAN	LN	LN PA	N	NT	IN	LN	F	TN	LN	Z	Į			EST HUMAN	N	IN	5	¥	NT	F	EST HIMAN	Т							EST_HUMAN
Sin	Top Hit Acession No.	0.0E+00 W78811.1	0.0E+00 W78811.1	4885526 NT	F009009 NT	5031624 NT			0.0E+00 AF108389.1	4826947 NT	4826947 NT		4504424	0.0E+00 AB029012.1	7468	200	0.0E+00 AA614537.1			5032192 NT			11545800 NT		Γ					6912749		П
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0€+00	0.0E+00	0.0E+00 U05235.1	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00 X57147.1	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00 M60675.1	0.0E+00 M80675.1	0.0E+00	0.0E+00 AF264750.1	0.0E+00 AF264750.1	0.0E+00	0.0E+00 BE241577 1	0.0E+00 AF226990.2	0.0E+00 AF228990.2	0.0E+00 AF170492.1	0.0E+00 J03784.1	0.0E+00 J03784.1	0.0E+00	0.0E+00 D30612.1	0.0E+00 BE869735.1
	Expression Signal	0.78	0.76	4.99	2.88	1.17	2.53	1.07	1.07	4.98	4.98	1.15	10.4	4.49	243		9.24	4.34	4:34	1.71	4.95	4.95	12.29	2.12	1.07	1.07	2.41	1.07	1.07	1.38	1.86	3.01
	ORF SEQ ID NO:	26041	26042		26054	28057	2000-1	26064	28086	20070	28071		20084	26088	28101		20115	26119	26120	26129	26135	26136	26139	26146	28170	26171	26172	20175	26176	26177	26179	26180
	Exen SEQ ID NO:	13407		_	_ i		13422	13428	13428	25	13431	13047	13453 E\$453	13448	13458		13468	13471	13471	13481	13486	13486	2388 888	13463	13512	13512	13513	13516	13518	13519	15551	13521
	Probe SEQ ID NO:	829	83	83	88	8	£	ğ	4 8	g	853	ĝ	788	672	681		983	969	88	ğ	712	712	744	719	739	739	740	743	743	746	748	740

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Table 4

Single Exon Probes Expressed in Brain	Top Hit Descriptor Top Hit Descriptor	Т	HOMAN				Intrinsin micros for KLAA0184 gene, peritel cds				78 NT Home enforcement for NAAdulio partial cds								OINT Homo septers 1-cell humbonne investor and matter (1904) (GABPA), mRNA			NT Homo september mRNA for KIAA And a constitution of CLCDAS) gene, complete cds					NT Homo septens mRNA for KIAA000 mortal and an analysis and an		T HUMAN	Т	LOMAN				NT Homo sapiens hormonally upregulated neu tumor-especiated kinasa (HINK) mRNA
Sing	Top Hit Acessian No.	0.40045.4		0.05-00 AB044300 4	9.1	100 DE 10					5174478	4507500 NT	7657213 NT	7857213 NT	4557686 NT	0.0E+00 AF108830.1	T	503854	4507500 NT	4507500 NT		-	_	7152	0.0E+00 AB028942.1 N	4506728 NT	Υ.	_	-	-		7867213 NT	7657213 NT	7657213 NT	7867213 NT
	Most Similar (Top) Hit BLAST E Value	00000	30.0	O OF FOO	200	0.01	0.0F+00 Decode	0.0E+00 X807724	0.0E+00 AB02071	0.0E+00 AB02071	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF108830	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF027153.	0.0E+00 AB028942	0.0E+00 AB028942	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB020717.	0.0E+00 AB020717	0.0E+00 AA533272	0.0E+00 AA533272	0.0E+00 BF677894.	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	3.54	70	207	284	1 2 2	100	213	5.97	5.97	9.88	11.63	1.96	4.28	2.81	1.39	1.39	1.58	2.09	2.09	1.32	4.82	4.62	9.56	4.34	0.8	22	2.2	2.46	2.45	9.44	1.94	1.94	3.31	3.31
	ORF SEQ ID NO:	26183	28184	26192	26198	26208	26209	28213	28217	26218	26222		26242	26243	26245	26251	26252	26257	26262	26263		26274	26275	26276	26277	26278	26281	26282	26283	26284		26285	26286	26287	26288
	SEQ ID NO:	13524	L	L	L	L	13547		13556	13556	13560	13561	13577	13578	13580	13585	13585	13290	13583	13593	13600	13604	3884	13605	3808	200	13611	13611	13612	13612	13613	13617	13617	13618	13618
	Probe SEQ ID NO:	752	753	761	704	775	775	780	784	784	788	8	88	8	8	814	814	819	22	22	8	ğ	2	835		3	\$	2	2	875	ट्स	847	\$	858	88

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NA | EVA
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|------------|-------------------------------|---------------------|--|----------------------|--|--|--|--|---|--|--|--|---|---
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Top Hit Describtor	in the complete cost and unknown gene	Homo septens 14422 utggate gene, compensor and unknown gene	HOMO SECTIONS IN THE CONTRACT STATE OF THE CONTRACT OF THE CON	Homo sepiens 14q32 Jaggedz gere, conlines cus, and sepiens 14q32 Jaggedz gere, conlines cus, and sepiens sepiens 14q32 Jaggedz gere, conlines cus, and sepiens	Homo saplens DKFZP666W0122 protein (DKFZP589W0122), ilinuitin	Homo sapiens inner membrane protein, mitochandrial (mitofilin) (IMM I.), mitorage 21 amiliar to	and Ann 1 Stratagene fetal retine 937202 Home sapiens cDNA clone IMAGE 808230 5 SITTERED	SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8: SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8: FETEA104 WATM Homo saplens cDNA clone 51/124 similer to DNA-DIRECTED RNA POLYMERASE II	Comment See and Pro with BLASTX or p) (adjuncted See and Pro with BLASTX or p) ESTATION WATMI Homo suplems done 51/24 similar to DNA-DIRECTED RNA POLYMERASE II	(alignment Ser and Pro with BLASTx or p)	Homo septens hypothetical protection (1997) (HSPA9B) mRNA	Homo septems need smooth (June 1997) (CDH6) mRNA	Homo sepiens cecnsin o, n-cara remit (common) (CDH6) mRNA	Homo septens ceditarini, n. valimini, n. val	(Homo septems reported protein P. 120695 (FL)20695), mRNA	Indus sapiens rightunderer processing (TUBA8 gene)	Home septens hypothetical protein FLJ20080 (FLJ20080), mRNA	Home senions attyletion repair, alkB homolog (ABH), mRNA	Homo sapiens Deeth associated protein 3 (DAP3) mRNA	MR0-BN0115-200300-003-t08 BN0115 Homo septens CDNA	Homo sapiens potaselum channel, suctemily K, member 8 (Norths), minder	Homo sapiens potassium channel, subfamily K, member 8 (Novine), innum	Homo sapiens protein kinase, X-finked (FTKKA) mrvky	Horro sapiens protein kinase, X-linked (PRIXA) mirava	Homo septens riboscomes protein 52.8 (T. 52.12) in the septents riboscomes protein 197.00 men.	Home explans hypothetical protein Fuzzusus (Fuzzusus), illings	Homo septens DNA for Human P2XM, complete cds	Homo saplens DNA for Human P2XM, complete ods	Homo sepiens similar to rat integral membrane glycoprotein Fow Later (Fow Later) How Annual Later (Fow	Homo seplens similar to rat integral membrane glycoprotein Powi 21 (Powi 212), managed to the property of the	Homo saplens Npw38 binding protein NpwBP (LOC51728), mrsvv	H.sapiens ART4 gene	
Top Hit Database Source			Z	Į.	12	12		EST_HUMAN	EST_HUMAN	EST HUMAN	NT	NT	2 NT	F	Ę	¥	LN .	Z	TN T	FST HUMAN	<u> </u>	Z	¥	N	NT.	TN.	LZ.	Z	TN 6	NT	LNIG	LN	
Top Hit Acession No.				T	7007	100100/	9803114				802293	4758569	4826672	4826672 NT	8923624 NT	2362	0.0E+00 AJ245022 1	8923087 N I	5174384 NI	0.0E+00 4/3011/	T708434 NT	TN8134 NT	TN17408047	4826947 NT	4506712 NT	TN 0923290	0.0E+00	AB002050 1	U.OE TO ABOUT JASTARS INT	TR67468 NT	T708500 NT	0.0E-000 VD5828 1	Valores.
Most Similar (Top) Hit To BLAST E	Value	0.0E+00 AF111170.3	0 0F+00 AF111170.3	0.0E-00 AE111103	0.00	0.0E+00	0.0E+00	0.0E+00 AA458680.1	0.0E+00 N43182.1	0.0E+00 N43182.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00		0.05+00				1				0.0=+00	\perp		
Expression Signal		1.83	23	27	3.70	3.06	2.5	1.43	1.9	0 +	86.6	2.40	1 80	8	3.63	3,63	119.02	1.19	3.52					200									3 0.87
ORF SEQ ED NO:		28416		20410	28417	28420	26424		26428		27407	20445							28471														79 26638
Exon SEQ ID	ö	42755	3	13755	13756	13750	13763	i	L	<u> </u>	1	\perp	_1	13802	1	1	上	L	L	13818							3 13870		13875	13876	_		23 13879
Probe SEQ ID	ë		\$	895	966	88	1003	1004	1007		9	1010	1025	1043	2 3	<u> </u>	1048	255	1052	1080	1074	1097	1097	1110	1110	1111	1113	1118	1118	1119	1110	1122	1123

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139 0.0E+00 200E+00 200E+00 17000010 17 Horio septions glutamate decentrolytes (1 km in GNU) (3AD1), transcript vertent GAD25, mRNA 200E+00 200E+00 2705070 NT Horio septions glutamate decentrolytes (1 km in GNU) (3AD1), transcript vertent GAD25, mRNA 200E+00 200E+00 2705070 NT Horio septions glutamate decentrolytes (1 km in GNU) (3AD1), transcript vertent GAD25, mRNA 200E+00
0.76 0.0E+00 4557887 NT 4.54 0.0E+00 AF034996.1 NT 1.52 0.0E+00 R922593 NT NT 1.77 0.0E+00 AF284750.1 NT 1.53 0.0E+00 AF284750.1 NT NT 1.53 0.0E+00 AF284750.1 NT NT 2.33 0.0E+00 AF284750.1 NT NT 2.33 0.0E+00 AF284750.1 NT NT 2.33 0.0E+00 AF284750.1 NT NT 2.34 0.0E+00 AF284750.1 NT NT 2.35 0.0E+00 AF284750.1 NT NT 2.35 0.0E+00 AF284750.1 NT NT 2.35 0.0E+00 AF28478.1 NT NT 2.07 0.0E+00 AF0840940.1 NT NT 2.04 0.0E+00 AF0840940.1 NT NT 2.04 0.0E+00 AF0840840.1 NT NT 2.04 0.0E+00 AF084084.1 NT NT 2.04 0.0E+00 AF084084.1 NT
1.63 0.0E+00 AF264750.1 NT 1.63 0.0E+00 AF264750.1 NT 2.33 0.0E+00 AF106718.1 NT 2.359 0.0E+00 AF308479.1 NT 2.359 0.0E+00 AF084479.1 NT 2.07 0.0E+00 AB040840.1 NT 2.07 0.0E+00 AB040840.1 NT 2.04 0.0E+00 AB040840.1 NT 2.04 0.0E+00 AF08418.1 NT 2.04 0.0E+00 AF30840.1 NT 2.04 0.0E+00 AF30840.1 NT 2.04 0.0E+00 AF30840.1 NT 2.04 0.0E+00 AF30840.1 NT 2.04 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.78 0.0E+00 AF30804.1 NT 3.77 0.0E+00 AF30804.1 NT 3.77 0.0E+00 AF30804.1 NT
2.07 0.0E+00 AB040840.1 NT 2.07 0.0E+00 AB040840.1 NT 2.04 0.0E+00 5174748 NT 2.04 0.0E+00 5174748 NT 2.04 0.0E+00 5174748 NT 2.04 0.0E+00 767629 NT 1.63 0.0E+00 7657529 NT 1.63 0.0E+00 7657529 NT 2.03 0.0E+00 7657529 NT 2.03 0.0E+00 7657529 NT 2.03 0.0E+00 7657529 NT 2.03 0.0E+00 7657529 NT 2.03 0.0E+00 7657529 NT 2.03 0.0E+00 7657529 NT 2.03 0.0E+00 7657529 NT 2.03 0.0E+00 7657629 NT 2
3.78 0.0E+00 AF089106.1 1.63 0.0E+00 7857529 NT 1.63 0.0E+00 7857529 NT 2.03 0.0E+00 5803148 NT 0.89 0.0E+00 4508004 NT 1.12 0.0E+00 5803146 NT 0.72 0.0E+00 4508004 NT
0.72

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens mRNA for KIAA0577 protein, complete cds	Homo sepiens KiAA0170 gene product (KIAA0170), mRNA	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	Homo sepiens period (Drosophila) homolog 3 (PER3), mRNA	Homo sapiens period (Drosophile) homolog 3 (PER3), mRNA	Human endogenous retrovirus HERV-K10	Homo sepiens mRNA for Femilial Cylindromatosis cyld gene	Homo septens perdal TTN gene for titin	9g38b08x1 Sogres besits NHT Homo sapiens cDNA done IMAGE:1837427 3' similar to WP:T27A1.5 CE14213;	RAN, member RAS cnoopene family-forno sapiens RAN, member RAS cnoonen family (RAN) mRNA	Homo sepiens proprotein convertase subtilisin/kadin type 2 (PCSK2) mRNA	Homo saplens proprotein convertase subtilishin/kexon twoe 2 (PCSK2) mRNA	Homo septens KIAA1114 protein (KIAA1114), mRNA	Homo sepiens KIAA1114 protein (KIAA1114), mRNA	Homo sepiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements	Homo septens alpha1-6fucosyfransferase (alpha1-6FucT) gene, exon 7	Homo seplens titin (TTN) mRNA	Homo septens titin (TTN) mRNA	Human nebulin mRNA, partial cds	Human nebulin mRNA, partial cds	Novel human gene on chromosome 20	Novel human gene mepping to chomosome 1	Human mRNA for KIAA0240 gene, partial cds	Homo sepiens calcimeurin binding protein 1 (KIAA0330), mRNA	Homo saplens KIAA0170 gene product (KIAA0170), mRNA	Homo sepiens KIAA0170 gene product (KIAA0170), mRNA	Human von Willebrand factor pseudogene corresponding to excres 23 through 34	Human von Willebrand factor pseudogene corresponding to excrts 23 through 34	Homo sepiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA	EST371757 MAGE resequences, MAGF Homo septens cDNA	as34e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE.815116.5	Cercopithecus aethlops cyclophilin A mRNA, complete cds
gie Exon Pro	Top Hit Databese Source	N	N	N	L	N _T	LN LN	FX	TN	EST_HUMAN	Į	Z	LN FN	LN	Į	Z	N	LN L	Z	NT	NT	TN	L	NT	NT	NT	١	Ę	Z	ᅜ	EST_HUMAN	EST_HUMAN	Þ
Cio	Top Hit Acession No.	0.0E+00 AB011149.1	7881965 NT	7681965 NT	8567387 NT	8567387 NT	M14123.1	0.0E+00 AJ250014.1	4.1277892.1	A[208756.1	6042206 NT	4505848 NT	4505648 NT	TV05585 NT	7705585 NT	-	-	4507720 NT	4507720 NT			.1	-		6912457 NT	7861965 NT	7861965 NT			7706434 NT	1.	_	-
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M14123.1	0.0E+00	0.0E+00 AJ277892	0.0E+00 AI208756	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AJ238093	0.0E+00 AF038280	0.0E+00	0.0E+00	0.0E+00 U35837.1	0.0E+00 U35637.1	0.0E+00 AL132999	0.0E+00 AL137784	0.0E+00 D87077.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M60676.1	0.0E+00 M60676.1	0.0E+00	0.0E+00 AW959687	0.0E+00 AA481172	0.0E+00 AF023860
	Expression Signal	4.71	2.04	6.88	3.01	3.01	1.82	1.38	3.39	1.59	13.21	9	5	4.08	4.08	4.59	3.02	6.39	5.39	17.93	17.93	2.50	1.82	1.73	4.53	1.65	1.55	0.97	0.97	1.37	121	1.76	40.82
	ORF SEQ ID NO:		26721	22.132	26723	28724			26817	26821	26822	26833	26834	28837	26838	28839	26852	28863	26864	26868	26869	22876	28877	28882	28885	25887	26888	26893	20894	26932	28949	20850	26953
	Exan SEQ ID NO:		14049	14050		14051		[14140	14143	14144	14163	14153	14155	14155	14157	14168	14178	14178	14183	14183	14183	14194	14198	14201	14203	14203	14207	14207	14246	14283	14264	14269
	Probe SEQ ID NO:	1299	1300	1301	1302	1302	1314	1387	1383	1396	1397	1408	1406	1408	1408	1410	1420	1431	1431	1436	1436	448	1447	1461	1454	1458	1456	1 8 1	1460	1500	1518	1517	1522

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Single Exon Probes Expressed in Brain

E	Homo saplens mRNA for KIAA1809 protein, partial cds Homo saplens mRNA for KIAA1809 protein, partial cds Homo saplens mRNA for KIAA1809 protein, partial cds
Ingle Exon Plift In Database Source	토토
t Acess No. No. 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.	F F-
Control Cont	0.0E+00 AB046829.
Signal Signal Signal Signal Signal Signal 124 124 124 124 124 1272 211 211 211 127 11.72 1	77
ORF SEQ. ID NO: 26854 26857 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 26858 27007 27007 27004 27014 27015 27015 27015 27015 27018 27018 27018 27018 27018 27018 27018 27018 27018 27018 27018 27018 27018 27020 27020 27021	27051
Expn SEQ ID NO: 14289 14271 14277 14277 14277 14277 14277 14277 14277 14277 14277 14300 14300 14300 14323 14323 14323 14323 14323 14323 14323 14335 14335 1435 14	14361
	1614

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Top Hit Descriptor	MR0-HT0166-191199-004-b11 HT0168 Homo serviens cDNA	MRC-HT0166-191199-004-b11 HT0166 Hamo saplens cDNA	wg81b07x1 Soeres_NSF_F8_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE:2371477 3' similar to TR:062788 Q62788 CYS2HIS2 ZINC FINGER PROTEIN	Homo saplens hematopoletic-derived zinc finger protein (HD-ZNF1) mRNA	Homo sapiens T-cell receptor gamma V1 gene region	Human zino-finger protein 7 (ZFP7) mRNA, complete cds	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds	Homo saplens keratin 18 (KRT18) mRNA	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA	hu11405.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:31962813' similer to TR:095147 095147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE:	hu11d05x1 NCI_CGAP_Lu24 Homo espiens cDNA clone IMAGE:3186281 3' similar to TR:095147 095147 WRP-1 LIKE PROTEIN TYROSINE PHOSPHATASE	Homo septens gamme-eminobutyric ecid (GABA) A receptor, gamme 2 (GABRG2) mRNA	VOSSOB. IT Sources breast 3NbHBst Homo sapiens CDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HI IMAN).	yo59e08.rf Soares breest 3NbH8st Homo sepiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMY, TRANSPEPTIDASE 5 PREC; IRSOR (HI MAN).	H.sapiens H2B/h gene	H.sapiens H2B/h gene	Homo saplens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA	Homo saplens WNT16 protein (WNT16) mRNA, complete cds	Homo saplens FOXJ2 fortheed factor (LOC55810), mRNA	Homo saplens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds	TCR zeta [human, Genomic/mRNA, 385 nt, segment 1 of 8]	Homo saplens NOD2 protein (NOD2), mRNA	Homo saplens SMCY (SMCY) gene, complete cds	Homo sapiens ribosomal protein S2 (RPS2) mRNA	Homo saplens E1A binding protein p300 (EP300) mRNA	Homo saplens E1A binding protein p300 (EP300) mRNA	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds	2d68g09.r1 Soeres_fetal_heart_NbHH19W Homo saplens cDNA clone IMAGE:345664 51
Top Hit Database Source	EST HUMAN A	EST_HUMAN N				E E	도			EST HUMAN IN	EST HUMAN IN		EST HUMAN G		Т	I		H											EST_HUMAN Zd
Top Hit Acession No.	0.0E+00 BE144364.1	0.0E+00 BE144364.1	0.0E+00 AI768104.1	4758513 NT	4-			4557887 NT	7857065 NT	4.1	BE222374.1	4557610					5031748 NT	AF169963.1	8923841 NT	1826973	2.1		11545911 NT	1.1	4506718 NT	4557556 NT	4557556		
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF05717	0.0E+00	0.0E+00 M29580.1	0.0E+00	0.0E+00	0.0E+00 BE22237	0.0E+00	0.0E+00	0.0E+00 H30132.1	0.0E+00 H30132.1	0.0E+00 Z80780.1	0.0E+00 Z80780.1	0.0E+00		0.0E+00	0.0E+00	0.0E+00 AB02654;	0.0E+00 S94400.1	0.0E+00	0.0E+00 AF27384	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U63963.1	0.0E+00 W 76571.1
Expression Signal	1.25	1.25	1.68	1.2	2.61	1.78	1.78	1.35	1.6	1.12	1.12	3.24	3.18	3.18	1.32	1.32	13.71	1.11	3.53	1.11	4.08	2.19	1.16	1.83	98.9	3.37	3.37	1.42	12
ORF SEQ ID NO:	27095	27096	27100	10172	27102	27106	27107	27109	27110	27113	27114	27116	27119	27120	27122	27123		27133	27136	27145	27162		27167	27181		27228	27220	27232	
Exen SEQ ID NO:		14405	14409	14410			14414	14416	14417	14420	14420	14421	14424	14424	14426	14426	14429	14437	14138	14445	14461	14453	15577	14481	15578	14523	14523	14525	14528
Probe SEQ ID NO:	1659	1659	1663	1664	1865	1669	1669	1871	1672	1675	1675	1677	1680	1680	1682	1682	1685	1983	<u>8</u>	1702	1708	13.0	1725	1730	1778	1782	1782	1784	1787

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	Top Hit Deskriptor	Lows earliers nuclear autosmiticanic sperm protein (histone-binding) (NASP) mRNA	The state of the s	Figure Industries process representations		Homo sapiens activeting transcription factor 4 (tex-responsive enhancer element B67) (ATF4) mRNA	Homo saplens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA	Homo saplens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA	mo sapiens protein tyrosine prospinatase, receptor 1/20 m. P. J.	Homo saplens Retine derived Pro-contain factor-1 (INPT-1), many	Homo septers notification of comments and september of the comments of the com	Homb septence in the Control of the KIAA1152 protein Dartial Cds	ATTO SERVICE OF THE PROPERTY O	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Homo septens potassium voltage-gated channel, Sheb-related subfamily, member 1 (KCNB1) mRNA	Human retinal degeneration atom (NLOS) gene, exert i	Human regrass degende about 1904 (1905) gains and antiens cONA clone IMAGE:2722333 3	ULH-BIT-BIT-A-07-2-01:31 NOT COAP Sub3 Homo septens CDNA done IMAGE:2722333 3	PANA 7018 AT 1 MGC 20 Homo septerts CDNA clone IMAGE:3547 239 5	1472164F1 NIH MGC 20 Homo septems cDNA done IMAGE:3547239 5	RC2-BN0128-200300-012-b04 BN0126 Homo seplens cDNA	Homo sepjens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	Homo sepiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	Homo saciens DNA polymentate zeta catalytic subunit (REV3) mRNA, complete ods	Himan transcitutaminase mRNA, complete cds	Human transcultaminase mRNA, complete cds	Home saplens transforming growth factor, beta 3 (TGFB3), mRNA	Homo saciens transforming growth factor, beta 3 (TGFB3), mRNA	Homo sapiens death receptor 6 (DR6), mRNA	
-	Top Hit Database Source				Ĭ.												П	7	EST HUMAN	7	7									
	Top Hit Acession No.		505332			4502284 NT	4502264 NT	4502264 NT	4506328 NT	9005855 NT	205855	_	0.0E+00 AB032978.1	4826783 NT	4826783 NT		0.0E+00 U07147.1	-	_\	١		0.0E+00 BE006242.1	4506384 N		0.0E+00 AF1574/6.1	0.0E+00 M98478.1	M984/8.7		TN 904/064	000/00/
	Most Similar (Top) Hit BLAST E		0.0E+00	0.0E+00 U14967.1	0.0E+00 AB002331.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U07147.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.00	0.0E+00	0.0E+00	0.0E+00	۱					0.06+00
	Expression Signal		2.74	5.68	2.79	4.07	4.07	4.07	183	5.82	5.82	1.12	1.12	4.35	4.35	5.47	5.47	1.48	1.46	3.49	3.40	0.83	2.16	2.16						1.42
	ORF SEQ ID NO:	_	27238	27251	27254	27255	27256	77.07.0	27.266	27278	27277		27288	\				<u> </u>	27297					27363		27372				3 27383
	SEQ ID		15579	1	1_		-	1 _	1.		1_	1_	L	l	l	١.	L		<u>L</u>	14606		7 14624	3 14653	1	14881	5 15582	5 15582	14666		3 14668
	SEQ ID		1788	Ę	1802	7.00	187	Ş	3 5	1874	1828	1836	1836	1840		1840	5 6	1844	184	1868	1888	1887	1916	1916	1924	1925	1925	1930	1930	1933

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	Top Hit Descriptor	Homo saciens glutathone S-transferase frota 2 (GSTT2) and glutathlone S-transferase treta 1 (GSTT1) genes, complete cds	Human topolsomerase pseudogene 1	Homo sepiens histidine ammonia-lyase (HAL) mRNA	Homo sapiens histidine ammonla-lyase (HAL) mRNA	Hamo sapiens chromosome 21 segment HS21C052	Homo saplens nebulin (NEB), mRNA	Homo sapiens nebulin (NEB), mRNA	Hamo sapions activin, alpha 4 (ACTN4) mRNA	Homo sapiens actirin, alpha 4 (ACTN4) mRNA	Home sepiens mRNA for KIAA0790 protein, pertial cds	Homo sapiens mRNA for KIAA0790 protein, pertial cds	Human TFEB protein mRNA, partial ods	Human TFEB protein mRNA, partial cds	X69b01.x1 NCI_CGAP_Pan1 Homo saplens cDNA clone IMAGE:26799133'	M69h01.X1 NCI_CGAP_Pen1 Homo sepiens cDNA clone IMAGE:2679913.3	Homo sapiens calcineurin binding probein 1 (KiAA0330), mRNA	Homo sepiens celcineurin binding protein 1 (KIAA0330), mRNA	Homo sepiens KIAA0408 gene product (KIAA0408), mRNA	Homo sepiens mRNA for KIAA0577 protein, complete cds	H.seplens genes for semenogeth I and semenogeth !!	H.sapiens genes for semenogelin I and semenogelin II	Homo sepiens mRNA for KIAA1513 protein, pertial cds	Homo sepiens SMCY (SMCY) gene, complete ods	Homo sepiens SMCY (SMCY) gene, complete cds	Homo septions TP53TG3a (TP53TG3a), mRNA	AU140831 PLACE4 Homo septens cDNA done PLACE4000321 6	Homo sapiens KIAA1114 protein (KIAA1114), mRNA	Homo saplens KIA4114 protein (KIA4114), mRNA	7822E10 Chromosome 7 Fetal Brain cDNA Library Homo saplens cDNA clone 7822E10	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA	Homo sapiens phosphodiesterase 6A, cGMP-epecific, rod, alpha (PDE6A), mRNA	HSC0IC021 normalized infant brain cDNA Hamo saplens cDNA clone c-0ic02
	Top Hit Detebase Source	<u> </u>	Ę	Ę	Ł	TN	L	NT	TN	NT	NT	IN	N _T	N	EST_HUMAN	EST HUMAN	LNT	NT	ᅜ	NT	NT	LN.	IN	IN	LN	TN	EST_HUMAN	LN	LN	EST_HUMAN	EST HUMAN	LN LN	N ₁	EST_HUMAN
25	Top Hit Acession No.	0.0E+00.AF240788.1		4809282 NT	4809282 NT	0.0E+00 AL163252.2	8400716 NT	8400716 NT	4826638 NT	4829638 NT	0.0E+00 AB018333.1	0.0E+00 AB018333.1		0.0E+00 M33782.1	0.0E+00 AW193024.1	0.0E+00 AW193024.1	6912457 NT	6012457 NT	7662095 NT	0.0E+00 AB011149.1		247558.1	0.0E+00 AB040946.1	0.0E+00 AF273841.1	0.0E+00 AF273841.1	7708742 NT	0.0E+00 AU140831.1	7705565 NT	7706585 NT	0.0E+00 AA077589.1		657468	4585863 NT	0.0E+00 Z42399.1
	Most Similar (Top) Hit BLAST E Value	0.05+00	0.0E+00 M55832.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M33782.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Z47556.1	0.0E+00 Z47558.1	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signel	427	1.35	2	7.	1.15	1.09	1.09	2.49	2.49	1.36	1.36	89.	.88	1.57	1.57	5.96	5.96	2	1.10	1.58	1.58	3.75	1.02	1.02	1.04	4.13	1.55	1.55	2.04	204	2.41	1.91	16.0
	ORF SEQ ID NO:			27396	27397		27410	27411	27412	27413	27427	27428			27434	27436	27436			27440							27511			27513				27517
	Exan SEQ ID NO:	14870	14875	14884	14684	14695	14697	14697	14608	14698	14709	Ĺ	14715	14715	14717	14717	14718	_	<u> </u>	1_	L					l	14785	L.	L	1_	1			14792
	Probe SEQ ID NO:	1035	1940	1949	1949	1959	1961	1961	1962	1982	1973	1973	1979	1979	1981	1981	1982	1982	1984	1985	1986	1986	1993	2014	814	2046	2052	2053	2053	2055	2055	2057	2059	2080

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Ongo Lyon: Copos Lybrassoc III Dialil	Top Hit Descriptor	qv90f08.x1 NCL_CGAP_Ut2 Homo septens cDNA clone IMAGE:1988871.3' similar to contains. Alu repetitive element,	601485146F1 NIH, MGC 69 Hamo saplens cDNA clone IMAGE:3887747 5	601902604F1 NIH_MGC 19 Hamo sepiens cDNA clone IMAGE:4135320 5	801902604F1 NIH_MGC_19 Hano septens cDNA clone IMAGE:4135320 5	RC3-CT0413-270700-022-d10 CT0413 Homo sepiens cDNA	RC3-CT0413-270700-022-d10 CT0413 Homo sepiens cDNA	Human plasma membrane calcium ATPase Isoform 2 (APT2B2) mRNA, comjete cds	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, comjete cds	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA	QV1-GN0065-140800-318-c10 GN0065 Homo septens cDNA	Homo sapiens X-linked juvenile retinoschists protein (XLRS1) gene, excn 6 and complete cds	601672065F1 NIH_MGC_20 Hano septens cDNA clone IMAGE:3954785 5	PMO-BT0547-210300-004-F04 BT0547 Homo septens cDNA	Homo saplens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	IL3-CT0219-271099-022-G10 CT0219 Homo septens cDNA	Homo sepiens metabotropic glutamate receptor 1 alpha (mGkuR1alpha) mRNA, complete cds	QV-BT065-020399-092 BT095 Homo sapiens cDNA	QV-BT065-020399-092 BT065 Homo sepiens cDNA	Homo sepiens potassium large conductance calclum-activated channel, subfamily M, beta member 3-like (KCNMRs) mRNA	Human DNA-binding protein mRNA. 3'end	601122338F1 NIH MGC 20 Hamo septens cDNA dane IMAGE:3348688 51	AV738288 CB Homo septens cDNA clone CBNBDE08 5'	AV738288 CB Homo septens cONA clane CBNBDE08 6'	0032e01.s1 NCI_CGAP_Lu5 Hamo septens cDNA clane IMAGE:1567898 3'	602014829F1 NCI_CGAP_Bm64 Homo septens cDNA clone IMAGE:4150734 5'	801572186T1 NIH_MGC_55 Hamo septens cDNA clone IMAGE:38390123'	CM1-TN0141-250900-439-b09 TN0141 Homo suplems cDNA	CM1-TN0141-250900-439-b08 TN0141 Homo septens cDNA	601900261F1 NIH_MGC_19 Homo septens cDNA clone IMAGE:4129622 5	bb84602.71 NIH_MGC_10 Hamo sapiens cDNA done IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN;	
אום ראחוויד נטו	Top Hit Database Source	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	TN	NT	LN	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN		N	EST_HUMAN	IN	EST_HUMAN	EST HUMAN	Ŀ	Z	T HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST HUMAN	EST_HUMAN	П		EST_HUMAN	
	Top Hit Acession No.	0.0E+00 AI244247.1	0.0E+00 BE877225.1	0.0E+00 BF315325.1	0.0E+00 BF315325.1	0.0E+00 BE697125.1	0.0E+00 BE697125.1	00620.1	.00620.1	4758489 NT	0.0E+00 BE767964.1	0.0E+00 AF018963.1	0.0E+00 BF027662.1	0.0E+00 BE072624.1		0.0E+00 AF240786.1	0.0E+00 AW752708.1		AI904640.1	A1904640.1	TM C2C287	14787.1	-	0.0E+00 AV738288.1	0.0E+00 AV738288.1	VA931691.1	3F344434.1	3E748800.1	7.	Ļ		-	
	Most Similer (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 L00620.1	0.0E+00 L00620.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	1	0.0E+00.	0.0E+00/	0.0E+00 L76627.1	0.0E+00 AI904840.	0.0E+00 AI904640.	00+100	0.0E+00 L14787.1	0.0E+00 BE274898	0.0E+00	0.0E+00	0.0E+00 AA931691	0.0E+00 BF344434	0.0E+00 BE748800	0.0E+00 BF377897	0.0E+00 BF377897	0.0E+00 BF313617	0.0E+00 BE018750.	
	Expression Signal	1.78	3.46	1.48	1.48	3.07	3.07	3.71	3.71	1.36	2.08	1.59	3.78	1.03		1.08	1.3	1.47	6:39	6.39	105	12	1.05	7.59	7.59	4.4	5.68	1214	3.55	3.55	2.04	1.83	
	ORF SEQ ID NO:		27526	27528		27532	27533	27544	27545	27549			27572	27573		27574	27576	27577	27579	27580			27844	27647	27648	27850	27654	27855	27859	27660	27865	27668	
	Exan SEQ ID NO:	14794	14799			14804	14804	14812	14812	14817	14838	14839		14842	,	14844	14847	J		14850	14883	14908	14912	14914	14014	14916	14920	14921	14925	14925	15588	14831	
	Probe SEQ ID NO:	2062	2067	2069	2069	2072	2072	2080	2080	2085	2107	2108	2110	2111	- 6	2113	2116	2117	2119	2119	2153	2179	2183	2185	2185	2487	2191	2192	2196	2196	220	2203	

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	Top Hit Descriptor	2k53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:480540 3' strailer to db.X85857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);	2633c07.s1 Sceres_pregnent_uterus_NbHPU Homo septens cDNA clone IMACE:1486540 3 similer to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);	Homo sapiens chromosome 21 segment HS21C004	Homo sapiens chromosome 21 segment HSZ1C004	Homo sapiens KiAA0952 protein (KIAA0952), mKNA	Homo espiens KIAA0852 protein (KIAA0852), mixiva	Human beta-prime-adaptin (BAMZZ) gene, excit to	Homo saplens E1A binding protein page (Enace) minute	Homo sapiens KJAA0952 protein (KLAA0952), mrkwa	601433525F1 NIH MGC /Z Homo septens curva cione invacation of	601495208F1 NIH MGC_70 Home septems CUINA GIGHE IMAGE: 3097437 5	801495208F1 NIH MIGC_70 Homo sapiens CLINA cione invasor: 3097457 3	Homo sapiens mRNA for KIAA1363 protein, partial cds	Homo sapiens differentially expressed in PLCP (mouse nomadag) a (DETO), III NAVA	Homo sapiens differentially appreased in PLICE (mouse inmoved) of ULL OF HINNOR	0209007.XI Sogres retail INST Speed Title of Inditional September Chita Control INACE 750740 5	ZV/8a11,TI Sogres bital fattes NDCTIFO BY HORIO SQUARE BOOK AND BITAL IN THE STATE OF THE STATE	ZV/8a11.r1 Scares total tetus indicates with control salvers to the control of th	60/20/1840FT NCI_CLEMF_DITION FINANCIAL CONTROLL	Figure Septials podessial character NZ. Linears, complete con	Home septents first of Authors to process, permised and	Linear Separate in the control of th	THOUS SACHE INVITED ON INCHINATION SACHES ON A CHORE INVIDENCE 3295370 3' SHTHIST TO TR: 094939 094939	KIAA0857 PROTEIN;	Homo sepiens phosphorylase kinase alpha subunit (PHKA2) gene, exon 32	ty57c08.x1 NCI_CGAP_Utz Hamo septens dDNA clane IMAGE:2283182 3'	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Homo seplens KIAA0952 protein (KIAA0952), mKNA	Homo saplens sperm specific antigen 2 (301-82), minute	Homo saplens specific artigen 2 (SSFAZ), mrthA	Hamo sapiens KIAAUZTB gene product (NIAAUZTO), miruka
	Top Hit Detabase Source	EST_HUMAN	EST_HUMAN	NT	NT	Į,	Ę	Ļ,	L	Z	EST HUMAN	EST HUMAN	EST HUMAN	NT	NT	FN 84	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	Z	Z	Ž.	Z	EST_HUMAN	N	EST_HUMAN	TN	Z	78 NT	78 NT	LX
	Top Hit Acession No.	0.0E+00 AA042813.1	0.0E+00 AA042813.1	0.0E+00 AL163204.2	0.0E+00 AL163204.2	7862401 NT	7682401	J36264.1	4557556 NT	7662401 NT	0.0E+00 BE895281.1	0.0E+00 BE905563.1	0.0E+00 BE905563.1	0.0E+00 AB037784.1	11545748 NT	5	0.0E+00 AI078404.1	0.0E+00 AA429001.1	0.0E+00 AA429001.1	0.0E+00 BF347039.1	L02840.1	0.0E+00 AB020717.1	0.0E+00 AB020/1/.1	6325466 NI	0.0E+00 BE676095.1	0.0E+00 AF044571.1	0.0E+00 AI625542.1	7862401 NT	7662401 NT	5803178	5803178	7662007 NT
	Most Similar (Top) Hit BLAST E	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U36264.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00				0.0E+00		0.0E+00			L		0.0E+00			0.0E+00
	Expression Signal	1.55	1.56	3.37	3.37	2.3	2.3	1.37	5.71	2.03	1.71	1.27	1.27	2.35	4.02	4.02	1.87	2.33						1.30	117				1.88	1.95		1.24
	ORF SEQ ID NO:	27869	27870	27678	27679	27680	27681		27704	60112	27717	27720	27721			27790	27761	27763		27768	27772			27775	277780					27789		27783
	SEQ ID NO:	14932	14932	14940	14940	14941	14041	14946	14964	14071	14078	14981	14981	14983	Ī	ĺ_	15025	<u>.</u>	15027	15029	15034	15035		15036	45042	1	L	上	1.	1	L	15058
	Probe SEQ ID NO:	7304	2204	2212	2212	2213	2213	2218	2236	2243	2250	2253	2253	2258	2289	2280	2300	2302	2302	2304	2309	2310	2310	2311	2347	233	23.24	2325	2325	2328	2328	2334

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Table 4
Single Exon Probes Exonse

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Single Exon Probes Expressed in Brain	Top Hit Descriptor		Homo sapiens KIAA0218 gene product (KIAA0218), mRNA	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA	AU 13 14Z N LANS Home suppens CDNA clone NT2RP3002064 5'	001300843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5	Homo earlone VIA Angul - U.Z104 SN0033 Homo sepiens cDNA	Home services in November (KIAA0244), mRNA	Home services have e-principlinate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA	indring septems necessary-prosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA	4 (CYP3A4) and cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide	polypeptide 5 (CYP3A5) gene, partial cas	AU118082 HEMBA1 Home serviews CONA down LIENDASCOCCO CI	AU118082 HEMBA Home series CONG CONTROL INVESSE 5	A1148082 HEARBAT LINES APPRIES CLIVIA GOVE HEMBA1002839 5	Company of the Salvette Calva done HEMBA1002839 5	Tright september (FLZ0081 (FLZ0081), mRNA	MINUS / U-90800-029-412 BN0070 Homo sapiens cDNA	ACTIBOD, HEMBAT Home septens about done HEMBA1006155 5'	000002x1 Source_NhHMPu_S1 Home septens cDNA clone IMAGE:1660683 3' similar to TR:008962	Home and the state of the state	ANA ASSESSE A HILL AND THE TOTAL PLUZORS (FLUZORS), MRNA	WELTHINGS SOME AND THE THOUSENESS OF THE SOUR SOME SOURCE	A BRODERSO HALL SOUND THAT I NOUZT HOMO sepiens cDNA	Homo explored in the control of the	Homo eacher is grudentiated receiptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA	months gare for choice/stokinh type-A receptor, complete cds	Home supports gare for challed stokinin type-A receptor, complete cals	From septembring and an appendix of the septembring and a septembr	Home Court I Not Court From Sapiens cONA clone IMAGE:4153870 5	Troin september (1908 XII, alpha 1 (COL12A1), mRNA	Constant busses 2000 422-h11 MT0033 Homo seplens cDNA	CMIC-M I UUSS-150800-428-h11 MT0033 Homo sapiens cDNA	numan d protein-coupled receptor (GPR1) gene, complete cds	Robe street All 1900 (GPR1) gene, complete cds	OUZ18455811 NIH_MGC_42 Homo sepieris cDNA clone IMAGE:4300383 3'
gle Exon Pro	Top Hit Detabese Source	1	- N	RI LIMAN	TOWNER TO THE	EST HIMAN		į	Ę				EST HUMAN	Т	Т		T CLIMAN	Т	7	NAME: HERE		HIMAN	EST HIMAN	Т	NUMBER OF THE PROPERTY OF THE				Т	5720777 NT	Т	Т	NAMOL -		T LE PARKE	7
Sin	Top Hit Acession No.	TACCOOL	1002001	A11341421 ES	0 0F+00 BE704026 4	0.0E+00/AW867076 1	7882017 NT	4758497 NT	4758497 NT					0.0E+00 AU118082.1		800	0.0E+00 BF814424 1	T	1		8923820	5.1	2	1	8008003	85808.1			3452741	57.20777 N	831003 1				-	
	Most Similar (Top) Hit BLAST E Value	0.05400	20110	0.0E+00 AI 11311	0 0F+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 P	0.0F+00.0		0.0E+00 A1042035	0.0E+00	0.0E+00 BE80560	0.0E+00 BE83783	0.0E+00 AB00562	0.0E+00	0.0E+00 D85606.1	0.0E+00 DR5808 1	0.0E+00 AF106275	0.0E+00 BF345274	0.0E+00	0.0E+00/BER31003 4	0.0F+00 RE831003 4	0.0F+001113888 4	0.0E+00 (113668 1	0.0E+00 BF569144	
	Expression Signal	124	3.2	239	4.31	1.51	2.89	2.03	2.03		1	9.25	7.98	7.98	7.98	96.0	0.91	1.06		3.74	96.0	4.44	-	0.98	4.5	2.09	2.09	191	122	4.45	1.24	124	0.83	0.93	2.08	
	ORF SEQ ID NO:	27794	27807	27811		27812	27813	27814	27815				27817	27818	27819	27820		27872			27873		27878		27892	27896	27897	27906	27911	27919	27922	27023	27927	27928	27929	
	Exon SEQ ID NO:	15058	١.		15075				15078		18070	8/05/	1800	15081	15081	15082	16099	15136		15137	15138	15141	15145	15154	15157	15160	15160	15168	15172	15179	15183	15183	15188	15188	15189	
	Probe SEQ ID NO:	2334	2348	2352	2353	2354	2355	2356	2356		7357	388	8	2369	2359	2360	2377	2415		2416	2417	2420	2424	2433	2437	2441	2441	2449	2454	2461	2465	2485	2470	2470	2471	
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		T	T	T	Τ	Т	T	Τ	Τ	Τ	Τ	Τ	Τ	T	T	Τ	Τ	Τ	Ť	T	T				Π	Ţ		T	T	T)66 	٦	
Top Hit Descriptor	handhod x1 NCJ CGAP Kid12 Homo saplens cDNA clone IMAGE:2872759 3'	III-HF-BP00-als-0-07-0-ULT NIH MGC_51 Homo saplens cDNA clone IMAGE:30/2/80.5	Homo satiens protein kinase, AMP-ectivated, alpha 2 catalytic subunit (PRKAA2) mRNA	Homo seciens protein Idnase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) midNA	RC3-ST0197-300300-018-004 ST0197 Homo saplens cDNA	AN 5625530F1 NIH MGC 7 Homo sapiens cONA clone IMAGE:3946518 5	Homo seplens death receptor 6 (DR6), mRNA	UI-H-BI4-goz-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA olone IMAGE:3086535 3	Homo sepiens mRNA for membrane transport protein (XK gene)	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mKNA	601503356F1 NIH MGC_70 Homo septens cDNA clone IMAGE:3803148 3	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), III CA	Homo sepiens hypothetical protein FLJ20388 (FLJ20386), mRNA	Hirman Sector (Sector) mRNA, complete cds	801508211F1 NIH MGC 71 Homo septens cDNA clone IMAGE:3909868 6	And 189241F1 NIH MGC 69 Hamp septens cDNA clone IMAGE: 3891371 5	801489241F1 NIH MGC 89 Home septens cDNA clone IMAGE:3891371 5	Homo saptens adlican mRNA, complete cds	601064738F1 NIH MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5	AU143277 Y79AA1 Homo septems cDNA clone Y79AA1001673 5	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5	601105312F1 NIH_MGC_15 Homo seplens aDNA clone IMAGE:2387855 5	601105312F1 NIH MGC_15 Homo sapiens cDNA done IMAGE: 2967833 3	7027112.X1 NCL CGAP GC8 Homo sapiens dDNA clone IMAGE: 3' similar to 1 K. Cuuz-to Couz-to	HYPOTHETICAL 9.3 KD PROTEIN;	FOUND SECTION MICE 17 Home sapiens CDNA clone IMAGE:3529159 5	Uncompensation in KIAA1415 protein, perties cds	Homo seriens mRNA for KIAA1415 protein, pertial cds	UI-H-BW1-4mp-f-12-0-UI.s1 NCI_CGAP_Sub7 Hamo septens cDNA clane IMAGE:30/0631 3	602152653F1 NIH MGC_81 Homo saplens cDNA clone IMAGE:4283612 6	601869073F1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:4111411 5	601869073F1 NIH MGC 17 Homo sapiens cONA clone IMAGE:4111411 6	
Top Hit Database Source	NAME OF THE	TOT TOWN	NAMOL ISH			TOTAL TOTAL		EST HIMAN	LN	L	EST HUMAN	-			Net LIMAN	TOWN IN TOWN	EST LIMAN	101	NAME OF TAXABLE	EST HIMAN	EST HIMAN	EST HIMAN	EST HUMAN	2 - 12	EST_HUMAN	LN	EST HUMAN	N	NAMIN TOUR	NAM III FOR	EST HIMAN	EST HIMAN	E01-11011
Top Hit Accesion · No.		0.0E+00 AW 466922.1	0.0E+00 AW501010.1	5453965	5453965	0.0E+00 AW813853.7	0.0E+00 BE795542.1	765/038	0.0E+0015F-308464.1	£453874	0.0E+00	1007001	/02/400	892334	0.0E+00/U93239.1	0.0E+00 BE886450.1	0.0E+00 BE875511.1	0.0E+00 BE8/5511.1	0.0E+00 AF-2455U5.1	0.0E+00 BE536921.1	0.0E+00 AU1452/1.1	0.0E+00 AU1432/ /. I	0.0E+00 BE282080.1	0.0E+00 BE282080.1	0.0E+00 BF223041.1	0.0E+00 AF245505.1	0.0E+00 BE296613.1	0.0E+00 AB037836.1	0.0E+00 AB037836.1	0.0E+00 BF313630.1	0.0E+00 BF6/2818.1	0.0E+00 BF-204131.1	0.0E+00 BF204131.1
2 = W	Vartue	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00.0	0.0E+00	000	0.0E+00		0.05+00	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0=+00	0.0E+00	0.00	0.0=+00												
Expression Signel		3.34	2.99	0.91	0.91	1.66	5.22	1.4	1.48	1.83	328	1.3	1.96	201	221	1.44	5.18	6.16	1.19	1.2		7		1.8	1.07	7.94	2.22	2.13		2.47			1.83
ORF SEQ ID NO:		27940	27941	27958	277959		27971	27383		27974		27977		27979		27984	27989							28015	28018					е	3 28065	8 28069	8 28070
Exan SEQ ID	<u>.</u>	15200	15202	15215	15215	16226	15231	14668	15232	15234	15236	15238	15239	L	L	15246	上	15249	15251	15269	15275	15275		15278	15277		١.	1 -	1_	7 15319	1 15323	5 15328	5 16328
1 0	 Ž	2482	2484	2498	2498	2509	2514	2515	2516	2518	2520	2522	2523	2524	2525	2530	2534	2634	2536	2554	2661	2561	2562	2562	2563	2566	2680	2606	2808	2807	2811	2815	2615

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Top Hit Descriptor	th19b08.x1 NCI_CGAP_Brn25 Horro sepiens cDNA done IMAGE:2168055 3' similar to gb:L20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);	Homo sapiens TATA box binding protein (TBP) associated tactor, NNA polymeraso II, 1, 2012 (TNI 27) mRNA	COS	JONE IMAGE: 3944304 5	Home IMAGE:3051389 5	clone IMAGE:3939222 6	drogenese 1 (IMPDH1) mRNA	Homo septents from (illustrate from the property) alpha Dodgectosidese A (GLA), L44 like ribosomal protein	O.C. ICAAD) and a man 4	Z (GUCKIB) gains, axaii i	A complete orle	T2RP3000779 5	T28P3000779 5	NA CONA	NA clone IMAGE:3316089 3'	Adom IMAGE:3628923 5	A clare IMAGE:3610267 5'	2012/00/3/1 Min motor for the firm (mathests to liver in mouse) Il Homo sapiens cDNA 5' end similar to ribosomal		clone IMAGE:3943591 5	WOW JONG	1) gama complete cds	view like 1 complete cds	Ann MAGE 3945983 5	A clone IMAGE:3689564 5	3VE09 5'	(KIAA0757) mRNA	(KIAA0757) mRNA	J20477). mRNA	
	IN19608.X1 NCL_CGAP_BRIZ5 Horno septem CALCIUM-TRANSPORTING ATPASE PLA	Homo sapiens TATA box binding protein (1E mRNA	Homo sapiens mRNA for KIAA1438 protein, perual cds	601590108F1 NIH MGC 7 Homo sapiens CUNA done inward: 3944204 5	601500108F1 NICH MCC / Truin separate CONA close IMAGE:3051389 5	601143/22F1 NIH MGC_19 Hollio series con concern MAGE:3939222 6	1 MPDH1) mRNA	HOMO SEPTERS INIT (IIIOSIIIO II MICHIGANICALINAI III	Homo septems bruid is (yes) or mace (prish) (L44L) and FTP3 (FTP3) genes, complete cds	Homo saplens guarylate cyclase activating protein 2 (GUCA ID) gene, awn i	AU133385 N 2KP4 Homo sapiens contraction in E. C. Consider of	Human bullous pemphigoid ahugan (br.AGI) minut, compete con	AU130403 N IZRES Hamo suprens color care N IZ Color	Т	Т	Т	601208/14FT NIT MCC 18 HOUR SAME COLOR COMP INA GE 3610267 5	CT409444 LCC calline (matestasis to IV	protein L29	601589825F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 3	Human beta-prime-adaptin (BAMZ2) gene, exon o	Homo sepiens neureguin 1 (NKG1), ransonprivenent Smills, illingto	Homo sapiens skeletal muscle Lim-protein (Triti.) year, complete cds	Homo sapiens nezak mikwa la Gir-bilaing processing 1 compression 1 compr	8018918911 NIFL MGC / HOLLD SEPTEMBER CANA CLOSE IMAGE 3689564 5	6013354657 I NIT MCC 39 I MIN SEPTEMBRY FOR 51	AV /2104/ T15 From strange associated PD1 (KIAA0757) mRNA	Union segrents specification and associated PD1 (KIAA0757) mRNA	Homo septens sperimency morten El 20477 (FL 20477), mRNA	TOTIO SEPTEMBE INFORMATION PROPERTY.
Top Hit Detabese Source	EST_HUMAN	FN FN	NT	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LZ.	, LN	K	EST_HUMAN	NT		EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	TN	TN	¥	Z	EST HUMAN		EST HUMAN	N.	<u> </u>	Z
Top Hit Acession No.	0.0E+00 AI571737.1	5032150 NT	0.0E+00 AB037859.1	0.0E+00 BE795445.1	0.0E+00 BE795445.1	0.0E+00 BE293328.1	0.0E+00 BE792472.1	4504686 NT	J78027.1	0.0E+00 AF173227.1	0.0E+00 AU133385.1	0.0E+00 M69225.1	0.0E+00 AU130403.1	_		_	0.0E+00 BE383185.1	0.0E+00 BE531263.1	0 0E+00 AA318723.1	0.0E+00 BE794884.1	0.0E+00 U36253.1	7089517 NT	0.0E+00 AF110763.1	0.0E+00 AB051828.1	0.0E+00 BE796376.1	0.0E+00 BE563433.1	AV72164		5174488INT	892344
Most Similar (Top) Hit BLAST E Value	0.00+000	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U78027.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00+100	0.0E+00	0.0E+00	0.0E+00		0.0E+00	00+∃0'0					0.0E+00
Expression Signal	2.08	2.19	4.95	1.02	1.02	2.55	4.92	1.51	12.1	6.55	1.22	1.08	2.22	222	1.71	1.25	4.37	2.57	76.7	5.57	3.83		1.78	1.27	7.77	3.48				121
ORF SEQ ID NO:	28072	28073	28077	28078	28079	28080		28096		28103				28110	28112	28115				28160						28191		28194		28196
Exen SEQ ID NO:	15920	16330	15333	15334	15334	15337	15344	15352	15361	1	1_	1	15371	16371	1_	L	L	15378		15432	1	1	1	1_	1	<u> </u>	1_	15453	15463	15454
Probe SEQ ID NO:	8	2 6	2624	2822	2822	2625	2632	2841	7 8 8	2652	2858	2838	7887	2661	2063	2888	2867	2668		2/20	27.2	2733	2734	2736	2742	2745	2746	2748	2748	2749

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Table 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo saplens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds	AV651068 GLC Homo septens cDNA done GLCCLD073'	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA	CM1-TN0141-250800-439-b08 TN0141 Homo sepiens cDNA	Homo sepiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA	Homo sapiens carebellar degeneration-related protein (34kD) (CDR1) mRNA	801580903F1 NIH MGC 9 Hamo saplens cDNA clone IMAGE: 3929472 5:	Homo sepiens chromosome 21 segment HS21C001	UI-H-BW1-amm-e07-0-UI:s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 31	Homo septens chandratin suffate proteoghycen 4 (metanome-associated) (CSPG4) mRNA	Homo sepiens anglopoletin-3 (ANG-3), mRNA	Homo seplens englopoletin-3 (ANG-3), mRNA	602085579F1 NIH MGC 83 Homo saplens cDNA clone IMAGE-4249915 5'	Homo sapiens protein tyrosine phosphatase, receipt twe. T (PTPRT), mRNA	AV725534 HTC Homo sepiens cDNA clone HTCCCA03 6	AV725634 HTC Homo sepiens cDNA clone HTCCCA03 5	au55d04.y1 Schineider fetal brain 00004 Homo sepiens cDNA chane IMAGE:2518863 5 straiter to SW:R13A HUMAN P40429 60S RIBOSOMAL PROTEIN L13A	602071957F1 NCI CGAP Brief7 Homo septens cDNA clone IMAGE 4274879 51	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5	AU131494 NT2RP3 Homo septens, cDNA, done, NT2RP3002672,5	AU131494 NT2RP3 Hamo sepiens CDNA dane NT2RP3002672 5'	600944794F1 NIH_MGC_17 Homo saptens cDNA clone IMAGE:2960806 5	600944794F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:2960806 5	głycoprobin D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]	Homo saplens BTRCP2 mRNA for F-box and WD-repeats protein Isoform C. complete orls	Homo sapiens ALR-like protein mRNA, partial cds	Homo sepiens ALR-like protein mRNA, partial cds	Homo sepiens cytochrome P450, subfamily I (dioxin-inducible), potypeptide 1 (glaucoma 3, primary Infantile) (CYP1B1) mRNA	Homo sepiens cytochrome P450, subfamily I (diodn-inducible), potypeptide 1 (glaucoma 3, primary infantile) (CYP181) mRNA	H.saplens serine hydroxymethyltransferase pseudogene	
T gle Exon Prot	Top Hit Database Source	N	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN T	IN	EST_HUMAN	NT	EST_HUMAN	M	NT	NT	EST HUMAN	LN FN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	M	Į.	Į.	F				
Sin	Top Hit Acession No.	8923441 NT	0.0E+00 AF290195.1	0.0E+00 AV651068.1	3F377897.1	0.0E+00 BF377897.1	4757983 NT	4757963 NT	0.0E+00 BE747193.1	0.0E+00 AL163201.2	0.0E+00 BF514110.1	4503098 NT	7705275 NT	7705275 NT	0.0E+00 BF677694.1	7427522 NT	0.0E+00 AV725534.1	0.0E+00 AV725534.1	1879163.1		E872768.1	1			1.1					4503202 NT	4503202 NT		
٠	Most Similar (Top) Hit BLAST E. Value	0.0E+00	0.0E+00/	0.0E+00	0.0E+00 BF377897	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI879163.1	0.0E+00 BF530661.1	0.0E+00 BE872768.1	0.0E+00 AU131494.	0.0E+00 AU131494.	0.0E+00 B	0.0E+00 BE300344.1	0.0E+00 S76830.1	0.0E+00 AB033281.1	0.0E+00 AF264750.1	0.0E+00 AF284750.1	0.0E+00	0.0E+00	0.0E+00 X85980.1	
	Expression Signal	1.21	2.5	13.89	3.13	3.13	33.8	33.8	2.58	1.15	3.36	0.89	. 2.1	2.1	4.67	1.75	13.56	13.56	7.61	5.41	5.55	1.6	1.6	20.25	20.25	4.22	4.35	8.39	8.39	3.52	3.52	3.52	
	ORF SEQ ID NO:	28197	28198			28200	28203	28204	28209		28219		28227	28228	28229	28237	28239	28240		28245	28246	28247	28248	28249	28250	25634		26144	26145	26436	26437	28258	
	Exen SEQ ID NO:	15454		15456	15457	15457	15461	15461	15465	15478	16477	15483	15489	15489	15490	15498	15499	15499	15501	15504	15505	15507	15507	15508	15508	12995	15515	13491	13491	13776	13776	15608	
	Probe SEQ ID NO:	2749	2750	2751	2752	2752	2756	2756	2760	277.1	2772	2778	2784	2784	2785	2791	2794	2794	2796	2789	2800	580	2802	2803	2803	5808	2812	2818	2818	2822	2822	2840	

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Top Hit Deterberse Top Hit Descriptor	Source	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds	Homo sepiens mRNA for KIAA1527 protein, partial cds	Homo saplens chromosome 21 segment HS21C001	Humen eodium chennel mRNA	Human AHNAK nucleoprotein mRNA, 6' end	EST_HUMAN PMO-HT0342-281299-003-e02 HT0343 Homo septems cDNA	EST_HUMAN PMO-HT0343-281299-003-e02 HT0343 Homo septems cDNA	H.septens kt3 gene for HLH type transcription factor	Homo sepiens chromosome 21 segment HS21C068	Homo sepiens zinc finger protein 221 (ZNF221), mRNA	Homo sepiens zinc finger protein 221 (ZNF221), mRNA	Homo sepiens zinc finger protein 221 (ZNF221), mRNA	Homo sepiens gammine-cytoplasmic actin (ACTGP3) pseudocene	Homo sepiens gennme-cytoplesmic actin (ACTGP3) pseudogene	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	H. sepiens mRNA for nuclear DNA helicase (I	Homo expiens protocedherin alpha C1 (PCDH-alpha-C1) mRNA, complete ods	Homo sapiens sukeryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sepiers serine/threonine kinase 9 (STK9) mRNA	EST_HUMAN DKFZp586G0621_r1 596 (synonym: hute1) Homo sapiens cDNA clone DKFZp589G0621	Homo septens KIAA0054 gene product Helicass (KIAA0054), mRNA	Homo sepiens KIAA0054 gene product, Helicase (KIAA0054), mRNA			EST_HUMAN QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA		<u> </u>	Homo sepiens iHIb5 gene for hair keratin, exons 1 to 9	Homo sapiens EphA4 (EPHA4) mRNA	Homo sepiens cukenyodic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	h18407x1 NCI_CGAP_Bm25 Homo sepiens cDNA clone IMAGE:2167981 3' similer to TR:016247 EST_HUMAN 016247 F44E7.2 PROTEIN.;
Top Hit Acession	Ž	0.0E+00 AF068624.1	0.0E+00 AB040990.1	0.0E+00 AL163201.2	0.0E+00 M91803.1	0.0E+00 M80902.1	0.0E+00 BE154504.1	0.0E+00 BE154504.1	0.0E+00 X73428.1	0.0E+00 AL163268.2	7019584 NT	7019584 NT	7019584 NT	0.0E+00 D50657.1	0.0E+00 D50657.1	0.0E+00 AL096857.1	0.0E+00 Y10658.1	0.0E+00 AF152303.1	4503470 NT	4503470 NT	4507280 NT	0.0E+00 AL047599.1	7861883 NT	7661883 NT	4503098 NT	0.0E+00 BE081896.1	0.0E+00 BE081896.1	0.0E+00 AL163206.2	0.0E+00 AL163206.2	Y19210.1	4768279 NT	4503470 NT	0.0E+00 AI661002.1
Most Similar (Top) Hit BIAST F	Value	0.0E+00	0.0E+00			0.0E+00					0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y19210.1	0.0E+00	0.0E+00	0.0E+00
Expression		1.34	1.22	2.81	263	1.94	1.29	1.29	1.18	2.59	1.03	1.03	1.03	18.48	18.48	1.69	7.2	1.42	47.87	47.87	236	1.06	0.97	26.0	2.96	5.46	5.46	2.08	2.09	4.18	1.33	20.94	1.91
ORF SEQ					28285		28269	28270			28272	28273	28274	28277	28278	28281			28282	28283	28292	28296	28297	28298		28300	28301	28312	28313		28321	28322	28323
Exon SEQ ID	ö				15620	15822	15625	15625	15827	15628	15629	15629	15629	15633	15633	15636	15637	15638	15639	15639	15649	15652	15853	15653	15654	15857	15857	15664	15064	15671	15673	15674	15675
Probe SEQ ID	ö	2841	2843	2849	2862	2854	7857	2857	2859	2860	2861	2861	2861	2888	2866	2869	2870	2871	2872	2872	2882	2885	2888	2886	7887	88	2800	2897	2897	2805	2907	28082	2900

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70	1/5/2/5		—	<u> </u>	- <u>-</u>	_	_	_	7	_	T e	T₩	т-		_	<u>.</u>		· .	7	#		_	PC	T	/U	S0	1/	000	56'	7 -
igle Extensive Expressed in Brain	Top Hit Descriptor	br18d07.x1 NCI_CGAP_Brn25 Homo septens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN	ZINC FINGER PROTEIN 132	Homo seplens protocadharin gamma C4 (PCDH-gamma-C4) mRNA gymniada Afr	Homo saplens mRNA for KIAA1267 protein pertial cds	Homo sepiens mRNA for KIAA1267 protein, perties ods	Homo septens mRNA for KIAA 1508 profein partial cds	Homo saplens mRNA for KIAA1508 protein, partial cds	Homo saplens KIAA0100 gene product (KIAA0100), mRNA	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA	Homo septens myeloid/fymphoid or mbæd-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MILT4) mRNA	7n40b03.x1 NCI_CGAP_Lu24 Hamo sepiens cDNA clone IMAGE:3567028 3' similer to TR:Q9VLN1 Q9VLN1 CG17283 PROTEN.	7n40d03.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3567028 3' similer to TR:Q9VLN1 Q9VLN1 CG17283 PROTEIN	Homo seplens melenome emidoen family B. 4/WAGERA) mBNA	Homo saciens melanoma entiden, family B. 4 (MAGERA) mRNA	Homo septens neuredn III (NRXN3) mRNA	H. sapiens mRNA for M phase phosphoprotein 10	Homo sepiens mRNA for KIAA1208 protein, partial cds	H.saplens NFH gene, exon 4	H.sapiens NFH gene, exon 4	Homo sepiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 8	of 43f09.x1 Sceres_bedis_NHT Hamo septens cDNA clone IMAGE:1752809 3'	Homo saplens prospero-related homeobox 1 (PROX1) mRNA	Homo saplens mRNA for PKU-alpha, partial cds	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA	Homo sapiens calcium channel, voltage-dependent, gamma suburat 3 (CACNG3), mRNA	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA	Homo sapiens mRNA for KIAA1431 protein, partial cds	Human displacement protein (CCAAT) mRNA
gie Exoli Pio	Top Hit Dertabase Source	EST HUMAN	SWISSPROT	ΝŢ	μ	NT L	Ę	Ŋ	N.	Z	둗	Į.	EST HUMAN	EST HUMAN	Ę	١	Ŋ	Į.	ΤN	Ę		ī	T HUMAN							- L
	Top Hit Acession No.	0.0E+00 AI561002.1	P52740	38.1			0.0E+00 AB040941.1	0.0E+00 AB040941.1	7861903	7881903	5174574	5174574	_	0.0E+00 BF110702.1	05084				4.1						0.0E+00 AB004884.1	7662273	29755	0.0E+00 5729755 N		
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 P52740	0.0E+00,			0.0E+00,	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 E	0.0E+00 E	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X98494.1	0.0E+00	0.0E+00 X15309.1	0.0E+00 X15309.1	0.0E+00	0.0E+00 AI149880.1	0.0E+00	0.0E+00 A	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00 M74099.1
	Expression Signal	1.91	1.63	2.01	1.92	1.92	4.58	4.58	3.58	3.58	3.21	3.21	1.18	1.18	215	2.15	1.69	0.98	2.38	5.56	5.58	7.87	1.13	1.12	2.86	1.52	3.75	3.76	+	1.17
	ORF SEQ ID NO:	28324	28326	728327		28340	28341	28342	28345	28346	28347	28348	28352	28353	28364	28365	28370		28373	28374	283/5	28376	78307	16007	28282	28404	28406	28407	28412	28439
	Exan SEQ ID NO:	15875	15677					_		15698	15699	15899	15703	15703	15712	15712	15719	15720	15723	15724	13/24	07/01	15/39	2 2	15/4/	/6/61	15/39	15750	15/63	15791
	Probe SEQ ID NO:	2909	2911	2912	2928	2928	2829	2828	2032	2832	2933	2933	2938	2938	2948	2946	2953	2054	2967	8082	8 8	8 6	288	300	2 2	8 8	238	88	2	3020

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	Top Hit Descriptor	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA	ae67b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMA(Æ:9/1133 3	Homo sapiens angiostath binding protein 1 mRNA, complete cds	Homo sapiens anglostatin binding protein 1 mRNA, complete cds	Homo sepiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA	Homo saplens titin (TTN) mRNA	Human connextn 43 processed pseudogene	Homo sapiens HLA cless III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 Z1- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B i	(Bf), and complement component C2 (C2) genes,>	Homo sapiens very large G-protein coupled receptor-! (VLGKI) mixiNA, complete cus	Homo saplens KIAA0440 protein (KIAA0440), mRNA	Homo sapiens KiAA0440 protein (KiAA0440), mRNA	Homo sepiens A kinase (PRKA) anchor protein 1 (AKAP1), mikina	Homo septens A kinase (PRKA) anchor protein 1 (AKAP1), mKNA	Homo saplens SWI-SINF complex protein p2/0 mixina, partial cos	Homo sapiens hypothetical protein rLLZ20695 (rLLZ20695), mr. NA	Homo sapiens death receptor 6 (UK6), mKNA	outselos st NCI_CGAP_512 Homo septens culturador incomo o	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA	#58f08.x2 NCI_CGAP_Pan1 Home septens cund corre invace	Homo sepiens telomerase reverse transcriptase (TERT) gene, exons 1-6	Homo septems telomenase reverse transcriptase (TERT) gene, exons 1-6	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mKNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mKNA	Homo sapiens caspese 8, apoptosis-related cysteine protesse (CASPS) mirona	Homo sapiens caspase 8, apoptoeis-related cysteine protease (CASPS) mrthA	Homo sepiens pyrin (MEFV) gene, complete cds	Homo sapiens mRNA for KIAA1507 protein, partial cds	601464995F1 NIH MGC 67 Hamp sapiens CLINA clane IMACE.3868246 b	wb10f04.x1 NCI_CGAP_GC6 Homo septens cDNA clone iMAGE::3302/19.3 similar to in:ustraza ustraza ZINC FINGER PROTEIN.;	AU123664 NT2RM2 Homo sapiens cDNA done NT2RM2000735 5	
	Top Hit Database Source		T HUMAN		F					LN	LN								EST_HUMAN		EST HUMAN	Т	L					NT		EST_HUMAN			
	Top Hit Acession No.	TN 58055 NT	0 0F+00 AA774783.1			4557590 NT	4507720 NT	M65189.1		0.0E+00 AF019413.1	0.0E+00 AF055084.1	7862125 NT	7862125 NT	4502014	4502014 NT	0.0E+00 AF265208.1	8923624 NT	7857038 NT	0.0E+00 AA994842.1	4885312 NT	0.05400.41580204.1	0.0E+00 AF128803.1	0.0E+00 AF128893.1	7857213	7867213 NT	4502582	4502582 NT	0.0E+00 AF111163.1	0.0E+00 AB040940.1	0.0E+00 BE779039.1	0.0E+00 A(632569.1	0.0E+00 AU123664.1	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	00E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M65189.1		0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	00000	00+400	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	
	Expression Signal	0.85	307	5.43	5.43	1.36	-	5.8		1.28	3.86	11.	1.11	2.09	2.09	2.25	1.17	122	1.09	1.18	4 00	68.7	233	122	1.22	127	1.27	9.77	1.28	0.84	0.72	4.44	
	ORF SEQ ID NO:	28637			28647	28653	28861			28068		28672	28673				28696		28710			201728											
	SEQ ID	15083	4 FORE	15003	1_	L	1	L	1	16018	1_	L	16023	1	L		1	ļ.	L	L		100/0				_	1_	L			l		
	Probe SEQ ID NO:	2220	2000	3230	3230	3262	37.48	3255		3256	3258	3284	338	3280	3280	3285	3286	3297	3300	3309		3378	22.25	3327	3327	3329	3320	3333	3335	3342	3352	3391	

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Table 4
Single Exon Probes Exonesco

1/5/2/5					- s8				(V 2)					73634	73634		Ī	-					PC	CT	U:	SO:	1/0	06
Top Hit Descriptor	Hamo sapiens offschov recentor femily 10 subfamily Commend (Consocial)	Home extens ofference of the second of the s	Home series as action (1971) and the series are actions as a series of the series as a ser	The second secon	Homo sapiens T-type calctum channel alpha t subunit Alpha till-a isoform (CACNA til) mRNA, complete cds	IMRTI-SNUUSS-100400-001-c08 SN0033 Home sapiens cONA	Home earlier KIA 6005	Homo sariens harded filement of the control of the	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mens	Home earliest strategy was 184	Homo septents swarder muscle Link-protein 1 (FHL1) gene, complete cds.	Becteriophage P replication region including repA, parA, and parB genes and incA, incB, and incC	Homo conjene and all the c	WP14d10.x1 NCI_CGAP_Lu19 Honor aspirers dDNA done IMAGE:2484819 3' similar to TR:073634 073634, NFI IBA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NEL BA1 CELI A NUICEO NA NUICEO NA NEL BA1 CELI A NUICEO NUICEO NUICEO	wp144102 NGL CAAP LL19 Home septens dDNA clone IMAGE:2464819 3' similar to TR:073634 073634	MEDICAL CELL ADMESION MOLECULE.	Homo saplene v.f.ce FB (militios and)	Homo services whee EB I must be described with an object to make the model (FOS), mRNA	Human endoamats retradus LEDV 240	Human MDS1A (AMI 1947)S1 fision) mbNA	Homo saplens hypothetics and A Possess	Homo sablens hypothetical moteln (A Engales)	IOTTO Sections cell-line KG1 transmington and the control of the cell-line KG1 transmington and the cell-line KG1 transmington and the cell-line KG1 transmington and the cell-line kG1 transmi	Homo septens cell-fine KG1 transcriptional regulation (1972)	Hamo sepiens chromosome 21 infraver mBNA	01143853F1 NIH MGC 15 Home sealers Chala described	601143853F1 NIH MGC 15 Home advants CONA CIONE IMAGE:3051373 5	Homo sablens noteseitim voltene natural and in 1919
Top Hit Detabese Source	N IN	Į.			- N	ES HOMAN			<u> </u>	F		<u> </u>		HOT HIMAN	TOT UTWAN	NAMOL D										EST HUMAN	Т	
Top Hit Acession No.	7363436 NT	7363436 NT	TV06239 NT		O OF TOO AWARATOR 4	2454	7862401	4502398 NT	5803067 NT	0.0E+00 AF110783.1	37038		7427522				52332	6552332 NT	14123.1 NT		9558718 NT	8			-231922.1 NT		Γ	28795
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	000	200	00+400	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 K02380.4	0.0E+00	0.0E+00 Alg35159.1	0.0E+00 AR35159 4	0.0E+00 AJ278120 1	0.0E+00	0.0E+00	0.0E+00 M14123.1	0.0E+00 U43293.1	0.0E+00	0.0E+00	0.0E+00 AF045452.1	0.0E+00 AF045452.1	0.0E+00 AF231922 1	0.0E+00 BE304791.1	0.0E+00 BE304791.1	0.0E+00
Expression Signal	0.95	0.95	1.36	57.	000	1.88	1.56	1.34	5.37	1.75	2.4	5.47	1.5	3.54	3.54	2.48	1.82	1.82	1.31	5.4	1.18	1.18	1.84	1.84	1.12	2.21	2.21	0.92
ORF SEQ ID NO:	28807	28808	28810	28811		28824	28825	28826	28827	28179	28840	28844	28846	28853	28854	28859	28868	28869	28874	28880	28884	28885	28890	28801	28898	28905	28908	28909
Exan SEQ ID NO:	16156	16156	16159	16160	16164	16175	16175	16178	16178	15441	16191	16194	16196	16204	16204	16208	16215	16215	16220	16228	- - - - - - - - - - - - - - - - - - -	16231	16235	18235	10241	16252	16252	16255
Probe SEQ ID NO:	888	88	340	3402	3406	3418	3418	3410	3421	3430	3435	3438	3440	3448	3448	3452	3459	3459	\$ \$	3470	3476	3475	34/9	丄		-1	_ [3499

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Single Exon Probes Expressed in Brain	. Top Hit Descriptor	te05g12x1 Soares_NH-IMPu_S1 Homo sapiens cDNA done IMAGE:2088742 3' similar to TR-Condon	U00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN;	Human endogenous retroviral DNA (4-1), complete retroviral segment	AV 701869 ALIB Homo septems aDNA done ADBDAH08 5'	Homo sapiens semenogelin II (SEMG2) mRNA	namo sapiens hamologous yeast 44.2 protein mRNA, complete cds	Novel ruman gene mapping to chamosome X	nomo septens minna for KIAA1476 protein, pertial cds	Homo septens sal (Drosophile)-like 1 (SALL1), mRNA	ox77c11x1 Sogres_NhHMPu_S1 Homo septems cDNA clone IMAGF-1667356 9, similar to WD-TARD 1	CE13742;	Homo sapiens butyrophilin, subtamily 3, member A3 (BTN3A3), mRNA	QV0-CT0225-230300-169-e01 CT0225 Homo sepiens cDNA	Homo saplens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cots	602084563F1 NIH_MGC_83 Homo seplens cDNA clone IMAGE.4248508 5	QV0-D 1 0047-170200-123-g01 DT0047 Homo sepiens cDNA	002132486F1 NIH_MGC_81 Homo septens cDNA clone IMAGE:4293645 5'	002102486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:42g3645 5'	High 24 C. C. C. C. C. C. C. C. C. C. C. C. C.	HIGAGOL AND TO COLUMN SECTION SECTIONS CON COME IMAGE: 2979024 3'	forms explicit Courses JNR_ 1 GBC S1 Homo sapiens cDNA clone IMAGE:2979024 31	Home services in the art suitable (glucosemine) 3-0-suifotransferase 1 (HS3ST1) mRNA	Home series in the Authority of the product (KIAA0806), mRNA	House septents mailing 1 (Optizable syndrome) (MID1) mRNA	Trains explores mixing (Optizoladia syndrome) (MID1) mRNA	Home separate microva for G protein-coupled inward rectifier potassium channel, complete cds	Tromo septeras glycor aldenyde-3-phosphate dehydrogenase (GAPD), mRNA	Trains expens WAVEZ mitNA for WASP-family protein, complete cds	Tramo septents SH2-containing protein Nsp2 mRNA, complete cds	Light September 2012-containing protein Nsp2 mRNA, complete cds	Hours experts of concecne 21 segment HS21C004	MR2-CT0222-281080-055-05 CT0222 U	COLORS COLORS COLORS CONA
gle Exon Pro	Top Hit Detabase Source	HOU HOU	TO HOMAN	ECT UTALAN	NAMOL 121	I N	IN I	-N			T	EST HUMAN	ヿ	HOMAN	Т		Т	Т	Newpor	T WINGAN	Т												HUMAN	٦
Sin	Top Hit Acession No.	A1384007 4	M10078 1	0.0E+00 AV701960 4	4806904	0 0F+00 AF078869 4	T		10/0	FIN 042/240	7.00	1.7081501	Weenst 4					,	1928087	0.0E+00/AW6646931	Γ	826763	7662319 NT	4557752 NT	4557752 NT	• 1	1680401	3028542 4 NT		T				
	Most Similar (Top) Hit BLAST E Value	0.05+00 4138400	0.0E+00 M10978	0.0E+00	0.00	000+00	0.0E+00	0.0E+00	00+100	00-1-00	90.0	O OF TOO AIUSTSU	O OF TOO AWARDS	0 000	0.05.00	0.0E+00 BF6/6393	O OF TOO BEATTOR	0.0F+00 RE672054	0.0E+00	0.0E+00	0.0E+00 AW66460	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D87327.1	0.0E+00	0.0E+00 AB028542	0.0E+00 AF124250	0.0E+00 AF124250 1	0.0E+00 AL 163204	0.0E+00 AL 163204	0.0E+00 AW851714	
	Expression Signal	0.89	1.11	1.28	0.85	1.74	1.49	121	1.37	1.37	8	2	4.17	0 78	8 48	900	0.74	0.74	96.0	1.08	1.08	1.42	0.83	0.82	0.82	2.67	33.2	2.6	3.38	3.38	1.85	1.85	1.62	
	ORF SEQ ID NO:	28914	28917	28940	28941		28945	28948	28963	28964		28967		-	28976	28988	28996	28997		28989	29000	29004	29007	29015	29016	29030		29049	29051	29052	29061	28062	29065	
	Exam SEQ ID NO:	16260	16263	16285	16286				16316	16316	16317	16319	16324	16331	16332	16343	16356	16356	16357	16359	16359	16362	16364	16374	16374	16391	16395	16411	16413	16413	16421	16421	18424	
	Probe SEQ ID NO:	3504	3507	3529	3530	3531	3539	3542	3561	3561	3562	3564	3569	3578	3577	3589	3603	3603	3604	3000	3808	808	3611	883	3624	3638	3842	3668	3660	3880	3968	3000	3671	
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ORF SEQ Expression (Top) Hit Top Hit Accession Database ID NO: Signel Value	A SOCIAL	29067 1.53 0.0E+00 5729928 NT	29069 1.81 0.0E+00 AB018339.1 NT	29071 1.1 0.0E+00 AB020717.1 NT	29072 1.1 0.0E+00 AB020717.1 NT	28074 22.21 0.0E+00 7882237 NT	29075 22.21 0.0E+00 7682237 NT	20084 4.35 0.0E+00 AW298134.1 EST HUMAN	29085 4.35 0.0E+00 AW 298134.1 ESI_HUMAN	20105 1.08 0.0E+00 AA483659.1 EST_HUMAN	29109 1.14 0.0E+00 AB020710	29111 3.31 0.0E+00 7657468 NT	29120 0.82 0.0E+00 AB037835.1 NT	29130 4.9 0.0E+00 7662183 NT	29133 4.29 0.0E+00 4506718 NT	29138 1.08 0.0E+00 7857085 N I	0.0E+00 /00/005 N I	0.71 0.0E+00 AF195658.1 N	AF179/33.1	29187 2.3 0.0E+00 7867488 NI	29188 2.3 0.0E+00 765/405 NI	20183 1.24 0.0E+00 4/38011 11	29194 1.01 U.UE-400 101511111111111111111111111111111111	29197 1.01 0.05-00 A137 083.1	1.97 0.0E+00 Ar 132480.1		10.39 0.0E+00 S78685.1 NT Homo septiens ATP-sensitive invertily rectnying N-criticing subusility (NCO2020), mRNA	222 0.0E+00 7710148NT	29204 6.03 0.0E+00 7882183	29207 1.23 0.0E+00 AF069601.2 NT	29208 1.23 0.0E+00 AF069601.2 INT	28213 0.97 0.0E+00 AB001523.1 NI	29214 0.97 0.0E+00 AB001523.1 NT
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SEQ ID	<u> </u>	18426	L	1_	16430	_	1	1_	16445	10107		\perp	┸	L	1_	_		┖	1	1								_	1	1		1_	1_
Probe SEQ ID	<u>.</u>	2673	2875	3677	3877	3679	3679	3692	3602		3714	37.75	3730	37.42	3745	3751	3751	8	3802	3804	380	3908	3809	3812	3813	3814	3818	8 8	3018	3020	3824	3829	3828

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Single Exon Probes Expressed in Brain	Top Hit Descriptor		Homo sapiens transfert receptor potential channel 5 (TRPC5), mRNA	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA	Human zinc finger protein ZNF134 mRNA, complete cds	Homo sapiens intersectin short Isoform (ITSN) mRNA, complete cots	Inomo septens potessium voltage-galed channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Indino septems familiar memba retardation protein 2 (FMR2) gene, exon 11	Homo earliene SCSS-Interacting protein 1 (SRRP129), mRNA	widthouse authinpriyan gane, parted cas widthouse ICGAP_Lym12 Home sapiens cDNA clone IMAGE:2411065 3' similar to TR:043340	University of the second of th	num separate moverne protein S8 (RPS8), mRNA	DN ZPHYMV413_T1 434 (Synonym: htes3) Homo saplens cDNA clone DKFZp434N0413 5'	Homo serviews AP4 removes a submit of the serviews of the serviews AP4 removes the serviews AP4 removes a submit to the serviews AP4 removes a submit to the serviews and the serviews are submit to the serviews and the serviews are submit to the serviews and the serviews are submit to the serviews are submit to the service and the service are submit to the service and the service are submit to the service and the service are submit to the service and the service are submit to the service and the service are submit to the service are	Homo services all the services of the services	Homo employee makes and the control of the control	Homo contacts LIDD/17 L	Home carlens prescults.	Homo equipme star face to the following the face of th	RCZ-HTDRAM-1708M-014	MXRA5 Human matrix tissue expression library Home septens cDNA clone Incyte 1996725 similar to MXRA5. Matrix remodeling associated name is	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996728 similar to MXRA5	Meauty remodelling essectated gene 5	normo septeris in-pote protein FBISB (FBISB) mRNA, perties cds	UNT-EN-MING-U/-U-U.ST NCI_CGAP_Sub5 Homo sapiens cDNA clone IN/AGE:2736949 3'	DIAZ TONA 10040X AX LOS TONES CON CON MAGE 3608800 5'	Homo seriese Mineral Control of the	601103827F1 NILL LLOO 7 LL	601193827F1 NIH MGC 7 Home septent clone IMAGE:3537774 5	Humen G2 protein mRNA, pertial cds
igle Exon Pro	Top Hit Database Source		ž!	Z	2	ż	Z L	I I	E L		ECT LIBRAR	N LOWER	EST HIMAN	PACIFIC IN	Į						T HUMAN		T	LO LO	7	EST HIMAN	7		T HUMAN	T	\Box
รัง	Top Hit Acession No.	20100	1N 5272FB0	45031/8/IN	- 1 3	121467	0.0E+00 AF114488.1	AF012845 1 NT	4750474 NIT		AIR64727 4	TN/C450674	AI 040338 1	8005887 NT	6005887 NT	4504138 NT	4505078 NT	2.1	4506758	4585642INT	5.1	0.0E+00 AW888221.1		Ī				245			
	Most Similar (Top) Hit BLAST E Value	007200	0.05-00	0.00	0.05.00	0.05	0.0	0.0F+00 AF01284	00+100	0.0E+00 AF09911	0.0E+00 AIR6472	0.0E+00	0.0E+00 At 04033	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF14941	0.0E+00	0.0E+00	0.0E+00 BF35529	0.0E+00 A	0 05+00	0.0E+00 AF129533 1	0.0E+00	0.0E+00 BE378602 1	0.0E+001A	0.0E+00	0.0E+00 BE264998.1	0.0E+00 BE264998.	0.0E+00 U10991.1
	Expression Signal	1 12	8 48	8 18	4	1	2 88	1.05	1.43	0.74	2.16	424	1.35	1.28	1.28	3.22	1.82	1.18	1.2	1.47	1.18	1.05	1.05	1.82	-	2.81	0.92	249	0.98	0.98	1.42
	ORF SEQ ID NO:	28218	28222	38233	29228	7000	82282	29232	20233	29235	29244	29248	29251	29256	29257	29259		29263	29273	29277	29286	20288	29289	29295	20208	28303	28311	20312	29313	28314	20330
	SEQ ID NO:	16582			16588	1	1	16595	16598	16598	16606	16609	16612	16617	16817	18619	16621	16625	10034	10638	16646	16648	16648	16654	16657	16862	16870	16672	16673	16673	18702
	Probe SEQ ID NO:	3831	3835	3835	3837	3838	3841	3844	3845	3847	3856	3859	3862	3867	3867	3889	3871	3875	3884	3888	3898	3898	3898	3904	3907	3912	3920	3922			3952

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Probe SEO ID	Econ SEQ ID		Expression	Most Similar (Top) Hit	Top Hit Acession No.	Top Hit Database	Top Hit Descriptor
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4045	┸	29418	1.32		0.0E+00 AB002314.2	Į.	Homo saylans chromosome 21 segment HS21 C003
4046	<u>l</u> _	29419			0.0E+00 AL163203.2	Z	Homo emigra transcription factor 1-like (MYT1-f) mRNA, complete cds
4047	L	22 29420			0.0E+00 AF036943.1	Z	Homo caniens mRNA for race-2 (race gene)
4048	16793	13 29421		١	0.0E+00 AJZ77Z76.1	Z	Homo septems mRNA for rape-2 (rape gene)
4048	8 16793	29422		١	AJ27727	Z	Home series ratinoblastome-binding protein 4 (RBBP4) mRNA
4054	16789			١		Z L	Home seriens retinoblestome binding protein 4 (RBBP4) mRNA
4054	18789		6.29			- N	Home seriens G protein-coupled receptor 21 (GPR21), mRNA
4069	16813				3 4885306 IN	I N	Home seniors mRNA for KIAA0287 gene, pertiel ods
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4074	L		5.87		11419287 NI	Z	From September 1111 (September 1111) From Architecture 1 which has similarities to BAT2 genes
4075	١.		1.94		0.0E+00 AL096857.1	LN!	Nova numer micro (CCRR) mRNA, complete cds
4080	Ĺ	28453			AF16552	į į	Truth september of the
409	1_					N	Lumb sealers motern kinese, X-linked (PRKX) mRNA
4091	13867	87 26526				N.	Home series by throughlin subfamily 3, member A2 (BTN3A2), mRNA
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	Top Hit Descriptor	Homo sepiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA	Homo sapiens mRNA for KIAA0895 protein, partial cds	wto4d04.x1 NCI_CGAP_GC8 Hamp septiens cDNA clone IMAGE:2313873 3	wu04d04.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2313973 3	MR1-HT0707-100500-001-e02 HT0707 Hamp septems cUNA	WR1-HT0707-100500-001-a02 HT0707 Homo sapiers cDNA	601120778F1 NIH_MGC_20 Hamo sapiens cunA ciane IMAGE: 2207030 3	Homo sepiens mRNA for KIAA1125 protein, pertie ods	Homo saplens mRNA for KJAA1125 protesn, partial cds	Homo saplens nuclear receptor coectivator 3 (NCCA3), mixiva	be51f04x1 NIH_MGC_10 Hamo septens aDNA done IMAGE:2800055 3 similar to SW:1FIK_DOVIN Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR;	UI-HF-BM0-edx-c-02-0-UI.rt NIH_MGC_38 Homo septens cDNA clone IMAGE:3063147 6	Homo septiens hypothetical protein FL/10498 (FL/10498), mKNA	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg Jelly, sea uronin	homolog)-like (PKOREJ) mRNA	zu88h07.s1 Scenee_testis_NHT Homo saplens cDNA cione IMAGE:/4319/ 3 similar to contains Atd. repetitive element.contains element MER35 repetitive element;	2168H07.81 Sogres testis. NHT Homo septems cDNA clone INAGE:743197 3' similar to contains Atu	repetitive element contains element MER35 repetitive element;	Homo saplens chromosome 21 segment HSZ1C103	Human apolipoprotein B-100 mRNA, complete cds	PM2-DT0023-080300-004-a08 D10023 Homo expiens CUNA	Homo saplens myelodyspiesta syndrome 1 (MUST) minny	Homo septens myelodyspieste syndroms i (MLC) i mruna	Homo sapiens F-box protein Fbi4 (Fbi.4) mixtva, pertein cas	qd23f06,xf Sogres_placerta_8t06weeks_ZNDf1r3t03W Homo septens quina cigne invalce. If 2407 a 3	SITILE DUCATION WILLY COURT OF THE COURT OF	Human CSFAS (Criss) gene, par use control and control	Home sapiens proprogen convertable submissionade type z (robnz) minus	Home septens proben ranges C, nu (Pranch), minary	Homo Spiens protein masse C, itu (Tracca), ilinara	
	Top Hit Database Source	N	TN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Z.	L	NT.	EST HUMAN	EST_HUMAN	NT NT	NT		Ā	EST HUMAN		EST HUMAN	F	IN	EST_HUMAN	Ę	L'N	Ę		EST HUMAN	L.	L	Į,	L	2
5	Top Hit Acession No.	4503854 NT	1]	1	.1	.1	.1	.1	5729725 NT	0.0E+00 AW675599.1		8	8922468 NT		5174632 NT	0.05+00 44401438-1		0.0E+00 AA401438.1			9.1	4826827	4826827 NT	AF174590.1				4505646 NT	6563384 NT	6563384	רירשטרט
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 AI982597.	0.0E+00 AI982597.	0.0E+00 BE184856.	0.0E+00 BE184856	0.0E+00 BE274217	0.0E+00 AB032951	0.0E+00 AB032951	0.0E+00	0.05+00	0.0E+00.4	0.0E+00	0.0E+00		. 0.0E+00	400+300		0.0E+00/	0.0E+00 AL163303	0.0E+00 J02610.1	0.0E+00 AW93688	0.0E+00	0.0E+00	0.0E+00 AF174590		0.0E+00 AI189844	0.0E+00 U14520.1	0.0E+00	0.0E+00	0.0E+00	1.19201U100+30.0
	Expression Signal	1.08	0.89	4.93	4.83	0.82	0.82	2.34	0.99	0.99	224	5.50	1.14	1.28	1.26		2.8	000	100	8.97	1.01	4.08	0.83	0.74	0.74	1.4.7		2.52	4.32	1.35	0.78	0.78	1.58
	ORF SEQ ID NO:	29470	29476	29482	L		29486		29495		29498	<u> </u>	29511		29515				/2023	29538		29606		29633	28634	22636				29650			29684
	Ban SEQ ID NO:	16842	16850	16855	L	L	L		L	L	L	<u> </u>	\perp	1	1	1	16893	<u> </u>	10805	16909	L	1	1_	L.	L	L		17010	17012	17024	17030	Ш	17036
	Probe SEQ ID NO:	4099	4107	4112	4112	4115	4115	4120	4128	4126	4128	8677	4140	4142	4142		4151		4108	4169	4205	4240	4255	4261	4261	4283		4270	4273	4285	4294	4291	4297

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	Top Hit Descriptor	Human G2 protein mRNA, partial cds	Homo sapiens COMPLEMENT COMPONENT C14 RECEPTOR (C1QR), mRNA	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, afternative spilice products,	pertial cds	H.saplens H2B/h gene	H.saplens H2B/h gene	xg68e10x1 NCI_CGAP_Ut4 Homo septens cDNA done IMAGE;2633514 3' stmiler to 1 R:P97365 P97365 ZINC FINGER PROTEIN 64;	H. saplens H4/d gene for H4 histone	H.sapiens H4/d gene for H4 histone	Homo sapiens KIAA0300 gene product (KIAA0390), mRNA	Homo seplens KIAA0390 gene product (KIAA0390), mRNA	Homo saplens caudal type fromeo box transcription factor 4 (CDX4), mRNA	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo saplens myosin regulatory light chain interacting protein (MIK), mkNA	Homo sapiens membrane-bound antinopeptidase P (XNPEP2) gene, compilere cos	Homo sapiens ACTN2 gene for alpha-Actinin 2, exan 10	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10	Homo sapiens HPS1 gene, Intron 5	seq1329 b4HB3MA Cot8-HAP-Ft Homo septens CUNA clone b4HB3MA-CUIS-HAF-FLCOUS	seq1329 b4HB3MA Cof8-HAP-Ft Hamo septens cDNA done b4HB3MA-CO I 8-HAP-Ft203 3	Human endogencus retrovirus HERV-K10	xx28e08.x1 NCL_CGAP_Eso2 Homo septens cDNA done IMAGE:25894463 striitar to SW:AHINK_HUMAN Q09668 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK;	Homo sepiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA	wc56b02.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2322803 3' similar to contains MER22.b2 PTR5 repetitive element;	Homo sapiens chromosome 21 segment HS21C007	PM1-HT0305-101198-002-d03 HT0305 Homo sapiens cDNA	Homo saplens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo saplens mRNA for putative ankyrin-repeat containing protein (ORF1)	Homo saplens G protein-coupled receptor 50 (GPR50) mRNA	Homo sapiens serine-threonine protein kinase (MINBH) mknA, camprete cas
	Top Hit Detabase Source	NT	¥	N		NT	NT	LN	EST_HUMAN	NT	LN	L	TN	۲N	NT	٦	NT	TN	NT	LN P	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	LN.	EST_HUMAN	Z.	EST HUMAN	F	LZ	NT	L
	Top Hit Acession No.		6912281 NT	2					33.1			7662091 NT	7662091 NT	4885126 NT	0.0E+00 AJ271736.1	7019456 NT	0.0E+00 AF195953.1	1		1	F10233.1	F10233.1	M14123.1	0.0E+00 AW084964.1	051619	0.0E+00 Ale96898.1	2	0.1	1	0.0E+00 AJZ78120.1	4758467 NT	0.0E+00 AF108830.1
-	Most Similar (Top) Hit BLAST E Value	0.0E+00 U10991.1	0.00	0.0E+00 AF153047		0.0E+00 L14581.1	0.0E+00 ZB0780.1	0.0E+00 Z80780.1	0.0E+00/	0.0E+00 X60483.1	0.0E+00 X60483.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00 T10233.1	0.0E+00 T10233.1	0.0E+00 M14123.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AL 163207	0.0E+00	0.0E+00	0.0E+00		
	Expression Signal	1.58	831	1.16		4.17	2.88	2.88	0.94	1.42	1.42	8.62	8.62	12.59	1.14	0.98	6.5	1.25	125	1.81	1.43	1.43	67.0	5.68	1.57	0.83	8 82	3.17	1,89	1.99	1.29	2.88
	ORF SEQ ID NO:	29865				20702					29718		Ŀ			29766		29778	L		29814			29828		20834		20835				29846
	SEQ ID	17038	1704B	17008		17076	17080	17080	l	L	L	L		1	1	17137	17145	L	L	1_{-}	17189	17189	L	11	1_	1	1	1	1	1	丄	17219
	Probe SEQ ID NO:	7007	4307	4377		4837	4341	4341	4342	4348	4348	4353	4353	4366	4367	4400	4408	4414	4414	4436	4453	4453	4456	4468	4488	4470	4472	4475	4481	4484	4483	4484

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, evon	Homo sapiens pyrin (MEFV) gene, complete cds	Homo septens pyrin (MEFV) gene, complete ods	Homo septems zinc finger protein 195 (ZNF195), mRNA	Homo saplens syncytin precursor, mRNA, complete cds	Homo sepiens protocedherin gamma C3 (PCDH-gamme-C3) mRNA, complete cds	Homo sepiens zinc finger protein 211 (ZNF211), mRNA	Homo sepiens eukaryotic transletion elongation factor 1 alpha 1 (EEF1A1) mRNA	Homo sepiens low density apoprotein receptor-related protein 6 (LRP6) mRNA, and translated products	Homo sepiens chandratin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	Homo explens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA	Homo sepiens iduranate sulphate sulphatese (IDS) gene complete cds	Homo sepiens KIAA0390 gene product (KIAA0390), mRNA	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA	Hamo seplens PTEN (PTEN) gene, excris 3 through 5	Homo septens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)	Homo sepiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex).	2018g08.s1 Strategene fetal retine 937202 Homo septeme cDNA clone IMAGE Gnostal 3	Homo septens odz (odd Ozhan-m, Drosophila) homolog 1 (ODZ1), mRNA	Homo sepiens chromosome 21 segment HS21C084	y92b01.s1 Source_pineel_gland_N3HPG Homo sepiens cDNA clone IMAGE:231721 3'	y92b01.st Soares_pineel_gland_N3HPG Homo sepiens cDNA clone IMAGE:2317213'	Homo sepiens cyclophilin-related protein (NKTR) gene, complete cds	Homo sapiens chromosome 21 segment HS21C100	Homo sapiens gene for netriuredo protein, pertial ods	Homo sepiens learatin 18 (KRT18) mRNA	Homo sapiens keratin 18 (KRT18) mRNA	Homo sapiens inwandly-rectifying potassium channel Kir2.1 (KCNU2) gens, exon 2 and complete cds	Homo sapiens invardiviacitifying potassium chennel Kr2 1 (KCN I2) name servi 2 and complete Ad	and modified the result is a second of the s
gle Exon Pro	Top Hit Detrabase Source	FZ	N	IN	IN	N	NT	TN TN	LN T	Ę	¥	ĮΣ	Ę	¥	Σ	NT	뒫	¥	EST HUMAN	N.	5	EST_HUMAN	EST_HUMAN	IN	뉟	Į.	Ę	T	ħ	Ĭ	
Sin	Top Hit Acesslon No.	S78684.1	-	0.0E+00 AF111163.1	FN 5265000	0.0E+00 AF208161.1	0.0E+00 AF152337.1	5454175 NT	4503470 NT	4505016 NT	4503098 NT	4502558 NT	135485.1	7662091 NT	7662091 NT		_			7657410 NT	0.0E+00 AL163284.2						4557887 NT	4557887 NT			
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF143314.	0.0E+00 AJ245418.	0.0E+00 AJ245418.1	0.0E+00 AA174072.	0.0E+00	0.0E+00	0.0E+00 H92741.1	0.0E+00 H92741.1	0.0E+00 AF184110.	0.0E+00 AL163300.2	0.0E+00 AB037521.1	0.0E+00	0.0E+00	0.0E+00 AF153819.1	0.0E+00 AF153819.1	
ı	Expression Signal	1.26	1.06	1.06	2.56	6.16	4.31	1.32	15.47	0.79	1.61	2.03	2.38	12.72	12.72	96:0	10.33	10.33	1.68	1.46	3.16	1.04	1.04	2.8	4.94	1.66	1.53	1.53	1.52	1.52	
	ORF SEQ ID NO:	23858		09862	29870		29882	29886	29894	29900	28903	29908		29910	29911	29925	20028	29929				20947	29948	28949	28850		29958	28859	29960	29961	
	S	17229		17230					17280		17271	17275	17279	17281	17281	17298	17301	17301	17316	17318	17320	17321	17321	17322	17323	17324	17331	17331	17332	17332	
	Probe SEQ ID NO:	4483	4494	4494	4502	4507	4512	4515	4525	4532	4536	4540	4544	4546	4546	4563	4566	4566	4581	4583	4585	4586	4588	4587	4588	4589	4596	4596	4597	4597	

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ORF SEQ Expression (Top) Hit Acession Detabase ID NO: Signal BLASTE No. Source	29962 1.5 0.0E+00/AF167441.1 NT Mus musculus E-cacherin binding protein E7 mRNA, complete cds	1 22 0.0E+00 AB028970.1 NT	1.22 0.0E+00 AB028970.1 NT	5.25 0.0E+00 Y18890.1 NT	1.08 0.0E+00 AA418246.1 EST_HUMAN	2.27 0.0E+00 AF089841.1 NT	0.0E+00 AL163278.2 NT	1.06 0.0E+00 AL163278.2 NT	Z	NT NT		6453812 NT	6453812	0.0E+00 T58945.1 EST_HUMAN	0.0E+00 T56945.1 EST HUMAN	0.0E+00 BE278730.1 ESI_HUMAN	0.0E+00 U56651.1 NT	0.0E+00 M80902.1 N1	2.23 0.0E+00 M60197.1 INT	2.23 0.0E+00 M89197.1 N	AF184110.1	30042 2.02 0.0E+00 7662181 NT Homo sabiens N.A.A.U.S.O. gene product (N.C.A.D.C.), niii ush	2005 0 0E+00 U07563.1 INT Human proto-oncogene tyrosine-protein kinase (ABL) gene, excn 1a and excns 2-10, complete cds		30050 0.97 0.0E+00 S71448.1 NT		30051 0.97 0.0E+00 S71448.1 NT	1.45 0.0E+00 X58467.1 NT	30065 1.05 0.0E+00 7304922 NT	30066 1.05 0.0E+00 7304922[NT	30073 1.4 0.0E+00 AF026801.1 INT	
	28862	20070	20071	29979	29987		28998	29900	30000	30001	30002	30005	30006	25593	25594		30020	30033	30036	30037	30040	30042	30040	2000	30050		30051		30065	30068	30073	30078
Probe Exam ORF SEQ ID SEQ ID ID NO: NO:	4508 17333	L	1	L	1_	<u> </u>	1	L	L	4630 17365	4631 17366	4635 17370	L	L	L	4639 17373	4600 17394	4865 17399	4668 17402	4668 17402	4871 17405	4873 17407	47444	4000	4881 17415	\perp	4681 17415	1_	1	1		L

Page 503 of 536 Table 4 Single Exon Probes Expressed in Brain

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Top Hit Descriptor	Homo sepiens proteinx0008 (AD013), mRNA	UIH-BI3-4W-C-04-0-UI.s1 NG CGAP SUBS Hario saprats control con	Homo saplens HSPC024-tso mRNA, complete ods	Hirman connects 43 processed pseudogene	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)	genes, complete cds	M.fasckouleris mRNA for metalloprotesserike, distribution promitives	Homo sapiens Williams-Beuren syndrome deletion transcript e (W.D.C.C.C.)	Mus musculus zinc finger transcription record in a co., compression of the conference of the conferenc	Homo sepiens fragile X mental retardation 2 (FMFX) mission	Homo sapiens actin, alpha, cardiac muscle (ACLO), mrvvA	ZING FINGER PROTEIN 132	Homo serviens hypothetical protein FLJ20073 (FLJ20073), mRNA	Horner sentens KIAA0187 gene product (KIAA0187), mRNA	traine Traine and the come 1-2; T-cell receptor eights (1cr-eights) gene, occurs 1-2; T-cell receptor eights (1cr-eights) gene, J1-	J61 segments; and Tor-C-alpha gene, exons 14	Human Tor-C-delta gene, seons 1-4, Tor-V-delta gene, exons 1-2, T-cell receptor alpha (1 or-sapra) gene, 31-	J61 segments; and Tor-C-cipha gene, exons 1-4	H.saplens MeCP-2 gene	H.sapiens MeCP-2 gene	Homo saplens difromosome 21 segment host two	Homo sapiens TATA box binding protein (TBP) essociated factor, Kilva pulying associa, i. p. 2000 (11)	mRNA	H. septiens MICA gene	Homo sapiens zinc iniger process (no see 12)	Home septems minor or include present in the property of the p	Mus musculus ciris in the properties of collect collect collect collection (MGEAG), mRNA	Homo sapiens marin grante and research in 18 and 19	Homo sapiens desmoptant (1, p. 1), (1), (2), (1), (1), (1), (1), (2), (1), (1), (1), (1), (1), (1), (1), (1	Home saplens zno-finger Drive-bitaing process (1991)	Homo sapiens mind datas i region	Hone sapiens opide receptor, detail (OTNO) in the	Homo sapiens spires variant Arvarisco minum, parameter des	Homo sapiens COLTATO gain in activity conserva
Top Hit Database Source	٦	FOT HIMAN	TIME	֓֡֜֝֓֜֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓		Ę	F	Z	LZ.	N	Į.	SWISSPROT	1	Z I	Z	H	Ž	Ę	Ę	F	Z		Z	NT			LN	LN.	LN	NT	N _T	SINT	NT	Ę
Top Hit Acession No.	7019320	Ī						9.1		03766		2	000000	0005788	7681979	7	1.18040	194081.1			0 05 100 AI 183280.2	10000	5032150	(92841.1	4585642	0.0E+00 AB014533.1	6677848	5174580	4758199	7705548	0.0E+00 AF055086.1	4505508 NT	0.0E+00 AF091711.1	0.0E+00 D63562.1
Most Similar (Top) Hit To BLAST E	005+00	200	0.0E+00 AW 444651	0.0E+00 AF083242.1	0.0E+00 M65189.1	0 0F+00 AF240786.1	0 0F+00 X87205.1	0 0F+00 AF084479.1	0 0E+00 AF097418.1	005+00	00110	0.00.00	0.0=+00.0	0.0E+00	0.0E+00	i i	0.0E+00 M94081.1	0.0E+00 M94081.1	A DELLON XOAROR 1	0.0F+00 X94628.1	1		0.00+00			0.0E+00/	0.0E+00		00±±00		L		١_	
Expression Signal	78 0	5	1.88	1.82	228	ç	2000	444	90	26.	10.0	13.5/	-	5.7	76.0		1.84	18				7.90	117				224							1.07
ORF SEQ ID NO:	12000	300/	30103											30159	30163		30164	4000		3016/		30171	90476										30199	
Exan SEQ ID NO:		17444	17487	17472	17482	1	\perp	-1.	_1	\perp	_ \		17532	17536	17540		17541		- 1		_1	5 17546		1/334	Ŀ	1_	1		1	1	1	7/0/1		1
Probe SEQ ID NO:		4712	4735	4740	4750		4790	4 19	4796	4797	4798	4800	4801	4805	4809		4810		4810	4812	4812	4815		4823	4832	7833		100	3	050	3	4 642	104	4045

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01/5	7275	1	9	Ţ	_	T		1		Ţ	T	T	T	T	T	T	T	31 See	" "		-	_	PO	T/I		1/9	006	67	-
Top Hit	Top Hit Descriptor	Homo sapiens farnesy/ diphosphate synthase (farnesy/ pyrophosphate synthetase, dimethydallytranstransferase, geranytranstransferase (FDPS) mRNA	Homo sapiens statytransferase 8 (alpha-N-acetyineuraminate: alpha-2,8-statytransferase, GD3 synthase) (SIAT8) mRNA	Homo septems mRNA for KIAA0287 cene peritel ode	Homo sapiens mRNA for KIAA0287 dene, partial cris	Homo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, combien cds)	Homo septens chromosoms 21 segment HS240084	ULH-BI3-aM-f-02-0-UI:81 NOI CGAP Sub5 Homo sapiens cDNA close IMACE 20050601 21	Homo sapiens hypothetical protein FL11190 (FL11190) mRNA	Homo sapiens beaded filament structural protein 1. filensin (BFSP1) mRNA	Human ribosomal protein [2] mRNA complete cyle	601303729F1 NIH_MGC 21 Hamo sepiens obta done IMAGF-3638118 F	Homo septens desmoplakin (DPI) (DSP) mRNA	Homo sepiens KIAA0862 protein (KIAA0952), mRNA	Homo sepiens mRNA for KIAA1043 protein, partial cds	Homo saplens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo saplens hypothetical protein FLJ20477 (FLJ20477), mRNA	no14g09.s1 NCI_CGAP_Phe1 Homo sepiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;	no14g08.s1 NCI_CGAP_Phe1 Homo septens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN :	hor4g08.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140	Home services USDC44 - DNA	Home engine LODOs 44 - Ditte	Homo sariens DNA mismatch made	H. septems mRNA similar to D29763 mouse mRNA for seizure-related gene product 6. Shares domains with	BMPs, Tolloid, Sushi repeat proteins	Homo sapiens EG-AP ublquitin-protein ligase (UBE3A) gene, exon 3	Mus musculus michael for aczonin, short spiloed variant (acz gene)	Homo seciens chromosome 21 segment HS21Cno	
Top Hit	Detabase Source	84 NT	F	LN	N FN	¥	TN	EST_HUMAN	5	<u></u>	LY.	EST HUMAN	5	1	L	Ŀ	L	EST_HUMAN	EST_HUMAN	FAT LIMAN	T								
Too Hit Acession	No.	4503684	4508952 NT	0.0E+00 AB006625.1		0.0E+00 AB026898.1			8922926 NT	4502398 NT	114967.1	0.0E+00 BE408863.1	4758199 NT	7682401 NT	0.0E+00 AB028966.1	8923441 NT	8023441 NT	0.0E+00 AA601248.1								010/03.1			
Most Similar (Top) Hit	BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00 U14967.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00 AA801248.1	0.0E+00 AA601246 1	0.0E+00 AF181483.1	0.0E+00 AF181483 1	0.0E+00 AF195658.1	00.10	O DE +ON AED1670E 4	0.0E-00 A-010/0	0.0E+00 Y19186.1	0.0E+00 AL163209.2	
Expression	Signal	1.68	1.03	3.09	3.09	0.85	1.45	1.02	1.61	1.09	4.60	2.95	3.18	1.15	1.01	234	234	0.81	0.81	0.81	1.11	1.11	0.71	300	1 2	1.5	1.5	1.26	
ORF SEQ	ID NO:	30212	29852	30224	30225	30232	30243	30248	30251	30255			30268	30271	302/4	30283	30284	30291	30292	30288	30296	30296	25661		30312	30313	30314		
E E	N O	17589			17802	17612	17626	17633	1/83/	17840	17843	17852	1/930	17681	8	*/0/-	1/0/4	17083	17883	17683	17888	17686	13019	17800	1738	17700	17709	17717	
Probe	NO.	4890	4865	4875	4875	4885	4899	909	3	4912	4015	4924	978	£	2 2	1	1	4958	4958	4958	4961	4961	4973	4978	4985	4086	4996	4894	

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Raffus norvegicus multidomain presynaptic cytomatrix protein Piccolo mRNA, complete cds, long splice Raffus norvegicus multidomain presynaptic cytomatrix protein Piccolo mRNA, complete cds, long splice Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA Homo sapiens potassium inwardiy-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA zn03g10,r1 Stratagene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:546402 5 zn03g10.r1 Stratagene hNT neuron (#637233) Homo saplens cDNA clone IMAGE:546402 5 Homo saplens deleted in bladder cancer chromosome region candidate 1 (DBCCR1), mRNA Homo sapiens glutamete receptor, ionotropic, N-methyl D-asparate 2A (GRIN2A) mRNA Homo saplens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRINZA) mRNA Homo sapiens PR domein containing 1, with ZNF domein (PRDM1) mRNA Bacillus amyoliquefaciens sacB gene for levensucrase (EC 2.4.1.10) Homo sepiens vescular endothelial cadherin 2 mRNA, complete cds Homo sapiens vascular endothetial cadherin 2 mRNA, complete cds Homo sapiens germmma-cytoplasmic actin (ACTGP3) pseudogene Top Hit Descriptor Homo sapiens ecotropic viral integration site 24 (EVI2A), mRNA Homo seplens ecotropic viral integration site 2A (EVI2A), mRNA Mus musculus mRNA for leucine-rich repeat protein, partial cds Homo sapiens toll-like receptor 7 (TLR7) mRNA, complete cds Homo sepiens microtubule essociated protein 2 (MAP2) mRNA EST367889 MAGE resequences, MAGD Homo eaplens oDNA Human endogenous retrovirus-K, LTR U5 and gag gene Homo sepiens mRNA for KIAA0559 protein, partial cds Homo sepiens mRNA for KIAA1513 protein, partial ods Homo saplens chromosome 21 segment HS21C081 Homo sepiens 4F2 light chain (LOC51597), mRNA Homo sepiens 4F2 light chain (LOC51597), mRNA Homo sapiens HEF like Protein (HEFL), mRNA Homo sapiens putative GPR37 gene, exen 2 Homo sepiens putative GPR37 gene, excn 2 Homo sepiens gebebr1 receptor gene, exen 6 Homo sepiens titin (TTN) mRNA Homo sapiens titin (TTN) mRNA Single Exon Probes Expressed in Brain variant verient EST_HUMAN **EST HUMAN** Top Hit Database Source EST_HUMAN 4507720 NT 눋 눋 <u>눈</u> Ę 7857074 NT Ę 11421001 NT 4557362|NT 눋 눋 눋 ż È 7708245 NT Ę Ę 눋 5005002 NT Ę 눋 4507720 Top Hit Acession 7857074 8923822 7706245 8923822 7657008 4505096 6006002 0.0E+00 AA084272.1 0.0E+00|AF240635.1 0.0E+00 AF240635.1 AB011131.1 0.0E+00 AL163281.2 0.0E+00 AA084272. 0.0E+00 AF227534.1 AW855819.1 0.0E+00 AF245702.1 0.0E+00 AB040946.1 0.0E+00 AF227534.1 0.0E+00 AJ010179.1 0.0E+00 D50657.1 Y12477.1 0.0E+00 Y12477.1 0.0E+00 D49802.1 Y08032.1 0.0E+00 0.0E+00 0.0E+00 0.0E+00 **Most Similar** 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 1980年 0.0E+00 0.0E+00 0.0E+00 0.000 BLASTE 0.0E+00 0.0E+00 0.0E+00 0.0E+00 Value 0.97 0.95 0.95 1.1 14.05 0.97 0.78 268 1.14 Expression 1.07 5 86 2 0.00 6.53 5 Signal 30375 ORF SEQ 29553 30359 30376 30380 30388 30415 30327 30381 30387 30389 30392 30391 30394 30418 30445 30449 ÖNQ 30450 30452 30447 30451 SEQ ID 17724 16924 16924 17768 17747 17764 17769 17775 17761 17798 Щ В 17798 17800 17800 17828 17807 17816 17833 17834 ÿ 17829 17830 17834 17835 17837 17844 5012 5028 5042 5045 SEQ ID 5001 5012 5049 5050 **489** 500 5052 5058 8009 5079 5056 5079 5088 5081 5110 5116 5118 5119 5081 5111 5117

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Table 4 Single Exon Probes Expressed in Brain	. Top Hit Descriptor	Homo saciens mRNA for Nucleosome Assembly Protein 1-like 3 complete and	Homo seciens mRNA for neuraxin Jaloha mohian complete Ade	Homo sepiens mRNA for KIAA1112 protein partial case	Hunan sodium channel mRNA	Homo saciens ring finger probein 15 (RNF15) mRNA	Homo sepiens acontrase (ACO2) gene, nuclear gene encoding mitochandrial protein even 15	Homo sapiens keratin 12 (KR 12) dene. complete cals	Homo saplens keratin 12 (KRT12) gene, complete cds	W006g08.xf NCI CGAP Kid12 Home semisers cDNA close INA CE:2484004 91	Homo septems protocedherin stoha 13 (PCDHA13) mRNA	RC3-GN0078-310800-013-b03 (3N0078 Horm seniors c/NA	Homo eaplens polycystic kidney disease-like 2 broken (PKD) 2) mRNA American	Homo seriens polytystic kidney dissessable 2 profess (N. 100-10) mbus	H. saders immunodebuiln heavy chain gene veriable ration	Hassiens imminoriolo in beautobale sava tarabale savat	7410008x1 NCI CAAP CI 1 Home contains ANA stone 1440 E-2004 ca.	ht98e02.x1 NCI_CGAP_Lu24 Homo septents CONA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN BA3804 UNDATURETION DO ATTEN MARKET AND ATTEN MARKET STATES OF SIMILAR TO SW:Y054_HUMAN	1901589422F1 NIH MGC 7 Hams sentens china class that CE and 2004	601389422F1 NIH MGC 7 Homo saniens c'ONA clone IMAGE: 3043804 E	ed04e04.x1 Soares_placerta_8tx0wee(s_2NbHP8tx0W Homo sapiens cDNA done IMAGE:1722702.3*	Homo sablens eosinophi percelogas (EPP) cana asm 7	Homo sabiens Sp4 transcribition factor (SP4) mRNA	602118928F1 NIH MGC 56 Homo seniens china close MACE:4226254 F	AU13408 OVARCI Home septems CDNA close OVARCIONA SU	AU134406 OVARC1 Home serviens of NA clore OVARC1001684 5	601061489F1 NIH MGC 10 Homo serdens CDNA chine IMAGE: 447830 FF	601105891F1 NIH MGC 15 Homo sardens cDNA cleare IMAGE: 2088310 5	602071372F1 NCI CGAP Bm64 Homo sapiens oDNA clara IMAGE-4214272 51	602071372F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272 5	Homo saplens Bloom syndrome (BLM) mRNA	Homo saplens mRNA for KIAA0466 protein, partial cds
ale Exon Pro	Top Hit Detabese Source	L	NT	Į.	IN	۲	TN	IN	NT	EST HUMAN	1.	EST HUMAN	F	Į.	Z	Ę	EST HUMAN	TOT LIMAN	EST HUMAN	EST HUMAN	EST HUMAN	F	5	EST HUMAN	EST HUMAN		EST HUMAN	Π	Г	EST HUMAN		MT
Sin	Top Hit Acession No.	0.0E+00 AB027013.1	0.0E+00 AB035358.1	0.0E+00 AB029040.1	M91803.1	5454013 NT	0.0E+00 AF093093.1	0.0E+00 AF137286.1	0.0E+00 AF137286.1	0.0E+00 AI934954.1	58579	0.0E+00 BE931080.1	Γ	Γ					T				11421038 NT		Γ						4557364 NT	
	Most Similar (Top) Hit BLAST E Value	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00 M91803.1	0.0E+00	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X56163.1	0.0E+00 X56163.1	0.0E+00 BE675498	0.00	0.0E+00B	0.0E+00 B	0.0E+00 A1189142.1	0.0E+00 M29908.1	0.0E+00	0.0E+00 BF005962.1	0.0E+00 AU134408.1	0.0E+00 AU134408.1	0.0E+00 BE538857.1	0.0E+00 BE292784.1	0.0E+00 BF526328.1	0.0E+00 BF526328.1	0.0E+00	0.0E+00 AB007935.1
	Expression Signal	5.57	1.19	1.18	1.08	1.37	3.44	2.52	2.52	1.29	1.77	3.81	ဇ	ဇ	1.66	1.66	6.56	1.75	1.83	1.83	0.81	6.17	4.68	7.18	0.73	0.73	1	1.07	1.60	1.80	1.82	0.91
	ORF SEQ ID NO:	30473	30477	30481		30484		30495	30496	30623	30626	30639	30643	30644	30652	30653	30763	30764		30766	30787	30770	30780		30791	30792	30799	30826	30831	30832	32513	30858
	SEQ ID NO:	17857	17861	L	17871					18000	18003	18017	18021	18021	18027	18027	18104	18105	18106	18106	18107	18111	25066	18132	18133	18133	18138	18147	18151	18151	1949	18171
	Prabe SEQ ID NO:	5139	5150	5151	5154	5155	5162	5172	5172	5192	5185	5209	5213	5213	5220	5220	6239	5300	6301	5301	5302	5306	5310	5329	5330	5330	5336	53	5348	8348	5367	6370

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Single Exon Probes Expressed in Brain	Top Htt Descriptor	Homo sapiens mRNA for KIAA0468 protein, pertiel ods	Homo septens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds	Human gene for dihydrolipcamide succinyltransferase, complete cds (excn 1-15)	Human gene for dihydrolipoamide succinyltransferase, complete ods (exon 1-15)	Homo sapiens offschory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA	H.sapiens mRNA for myosin	HUM418D05B Clontech human fatal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5	HUM418D05B Cloritech human fetal brain polyA+ mRNA (#6535) Home sapiens cDNA clone GEN-418D05	ig.	602042322F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5'	602042322F1 NCI_CGAP_Bm67 Homo sepiens cDNA dane IMAGE:4179988 5	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA	601150252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502909 5'	MR0-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA	601105291F1 NIH_MGC_15 Hamo sapiens aDNA clane IMAGE.2987903 5'	601105291F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE.2987903 5	Homo sapiens offactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA	Homo septens offectory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA	Homo sapiens very long-chein acyl-CoA synthetese homolog 1 mRNA, complete ods	Homo seplens very long-chein acyl-CoA synthetese homolog 1 mRNA, complete cds	Homo sepiens Surf-5 and Surf-8 genes	Homo sepiens Surf-5 and Surf-6 genes	qf94g10.x1 Soares_placenta_8b9 wedts_ 2NbHP8tc9W Homo sapiens_cDNA_ctone IMAGE:1757730.3' similar to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR;	EST02238 Fetal brain, Stratagene (catt936206) Homo sapiens oDNA clone HFBCA448	UI-HF-BL0-sdh-d-02-0-UI.n1 NIH_MGC_37 Hamo sapiens cDNA done IMAGE:3061658 51	H. sapiens isoform 1 gene for L-type calctum channel, exch 14 adrid 15	PM3-CT0263-091299-007-h05 CT0263 Homo sepiens cDNA	PM3-CT0263-091299-007-H05 CT0263 Hamo sapiens cDNA	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA	Human beta-prime-adaptin (BAM22) gene, exon 13
gle Exon Prob	Top Hit Database Source	IN		F	LZ.	Z		LN LN	EST HUMAN	Г		EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	•		EST_HUMAN			F	NT.		٦	EST HUMAN	Г	EST_HUMAN	LN			T_HUMAN	N _T
Sin	Top Hit Acession No.	0.0E+00 AB007935.1	0.0E+00 AF257737.1	0.0E+00 AF257737.1	728535.1	728535.1	11420819 NT	238133.1	D61564.1		J61584.1	3F529831.1	0.0E+00 BF529931.1	0.0E+00 BF313139.1	4392	3E260777.1	0.0E+00 AW867316.1	0.0E+00 BE292889.1	3E292889.1	11420819 NT	11420819 NT	0.0E+00 AF064254.1	0.0E+00 AF064254.1	0.0E+00 AJ224639.1		0.0E+00 AI198515.1	A85719.1	W 405472.1		0.0E+00 AW361877.1		177.1	J36261.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D28535.	0.0E+00 D26535.	0.0E+00	0.0E+00 Z38133.	0.0E+00 D61564		0.0E+00 D61584.	0.0E+00 BF52993	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE26077	0.0E+00	0.0E+00	0.0E+00 BE29288	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00 M85719.	0.0E+00 AW4054	0.0E+00 Z26269.1	0.0E+00/	0.0E+00	0.0E+00	0.0E+00 U36261.
	Expression Signal	0.91	4.85	4.85	1.06	1.06	1.88	0.81	0.78		0.78	2.55	2.55	2.92	4.37	1.15	3.51	2.33	2.33	1.51	1.51	4.35	4.35	295	2.95	0.61	6.98	4.83	1.25	1.94	1.94	1.94	2.55
	ORF SEQ ID NO:	30859	30863	30864	30878	30879	30906	30912	30836		30937	30941	30942	30946	31132	31171		31196	31197	31219	31220	31228	31229	31239	31240	31271	31277	31286	31296	31306	31307	31308	31315
	Exan SEQ ID NO:	18171	18174	18174	18187	18187	18201	18206	18225		18225	18228	18228	18233	18244	18276	18285	18298	18298	18319	18319	18326	18326	18333	18333	18363	18367	18374	18386	18396	18396	18396	18401
	Probe SEQ ID NO:	6370	5374	5374	5387	5387	5401	5407	5428		5426	5429	5429	5434	5445	5477	5486	2200	2200	5521	5521	5528	6528	5535	5535	5566	3570	222	2590	5601	5601	5601	5605

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	Top Hit Descriptor	Library sanders mRNA for KJAA1641 protein, partial cds	Luma sarians KVL0T1 gene	Home services (VI OT1 defre	7	7	Т	Т	Т	Τ	Т	ods Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete		Т	T	T	1	Т	Т	T	Г	1	\neg		- 1	Т	Τ	-	
	Top Hit Database Source		\ <u>\</u>	Z		ESI HOMAN	NAM IL FOR	TION TO	EST HIMA	40048478 NT		뉟	LN TOT	ESITION	NAME OF TOTAL	ESI TOM	EST HUMAN	COT HIMAN	101	FST HUMAN	EST HUMAN		EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN		EST HUMAN	
8 -	Top Hit Acession No.			J006345.1			11416B01 N	E7911/3.1	SPECIAL DISCOURT	10048479	NA COLONIA	196961.1	J86961.1	0.0E+00 BF338835.1	0.0E+00 AF142621.1	0.0E+00 BE273983.1	0.0E+00 BE503098.1	0.0E+00 BF569905.1	0.0E+00 AA454642.1	0.0E+00 AFZ1/288.1	0.0E+00 BEG261+1.1	DESCRIPTION OF THE PROPERTY OF	0.0E+00 BE673986.1	0.0E+00 BE673986.1	0.0E+00 AW276760.1	0.0E+00 BF031742.1	BF031742.1	0.0E+00 AW470848.1	121
	출독띠	A MILIE	0.0E+00 AB046861.	0.0E+00 AJ006345.1	0.0E+00 AJ006345.1	0.0E+00 AI207616.1	0.0E+00	0.0E+00 BE7911/3.	9.0	0.0E+00 BE300062.	0.01	0.0E+00 UB6961.1	0.0E+00 U86061.1	0.0E+00	0.0E+00	0.0	0.0E+00	0.0E+00	0.06.+00	0.0E+00	0.00+00	0.05+00				H	$_{\perp}$		
	Expression (Signel F	-	1.03	1.58	1.58	1.19	6.23	121	1.13	6.69	1.67	4.05	4.05	2.28	1.03	3.06	0.88	1.87	1.21	2.38		227	0.55	0.55	1.14	1.16	1.16	0.58	
	ORF SEQ E		31344	31404	31405	31416	31430	31433	31444	31445	31446	31447	31448				31486		L			31535	31552	31553					31599
	<u> </u>	 S	18431	18/85	18485	1	1	18514	18523	18524	18525	18526	18526	1	L	1_	<u> </u>	1_	L		3 18602	8 18807	19620	1	1 _	L	1_	59 18646	72 18659
	-	ö Z	9000	2000	200	20093	11.13	2777	5731	5732	5733	6734	6774	5752	5758	5757	877.8	2/13	6778	5811	5813	5818	5831	1887	3 8	2630	5847	6859	5872

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Single Exon Probes Expressed in Brain

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Top Hit Descriptor	Human anion exchanger (AE1) gene, exons 1-20	601587971F1 NIH MGC 7 Homo septems cDNA cione IMAGE 3842329 5	801587971F1 NIH MGC 7 Hamo sapiens cDNA clone IMAGE:3942329 51	q50b11.xf NCI_OGAP_Brn25 Homo septens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT;	q60b11.x1 NCI_CGAP_Brn25 Homo saptens cDNA clone IMAGE:1859001 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT:	MR0-HT0923-220800-102-b05 HT0923 Homo septiens cDNA	Homo septiens peptide transporter 3 (LOC51286), mRNA	Human mRNA for alpha mannoeldase II leozyme, complete cds	IL3-HT0062-010999-014-A04 HT0062 Homo sapiens cDNA	7e02c12x1 NG_CGAP_Lu24 Home septens cDNA clone IMAGE:3281302.3' similar to SW:Y176_HUMAN Q14881 HYPOTHETICAL PROTEIN KIA6178:	Homo sepiens KIAA0285 gene product (KIAA0285), mRNA	AV650020 GLC Homo septems cDNA clone GLCCAD09 3'	UI-HF-BL0-accg-12-0-UI.s1 NIH MGC 37 Hamp sepiens cDNA clone IMAGE:3058751 3'	N27b03.11 Soeres placenta Nb24P Homo septens cDNA clone IMAGE:149833.57	Human gane for the light and heavy chains of myelopercoddase	aa14e07.r1 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:813252 5	1257408.X1 NCI_OGAP_Ov35 Homo sepiens cDNA done INAQE:2282887.3' similer to SW:NTCS_HUMAN P53789 SODIUM-AND CHI. ORIDE-DEPENDENT ORFATINE TRANSPORTER 2	601305368F1 NIH MGC 39 Hamo sepiens cDNA clane IMAGE:3639816 5	601306368F1 NIH_MGC 39 Hamo septens oDNA clone IMAGE:3639818 5	MR0-BT0264-221199-002-111 BT0264 Homo saplens cDNA	MR0-BT0284-221199-002-f11 BT0284 Homo sepiens cDNA	Homo espiene Acheele-Scute handogue 2 (ASCL2) gene, complete cds	AU119245 HEMBA1 Hamo sepiens cDNA clone HEMBA1005360 5'	AU119245 HEMBA1 Hamo seplens cDNA clone HEMBA1005360 5	601468712F1 NIH_MGC_67 Hano septens cDNA done IMAGE:3871809 5	H. sapiens germline immunoglobulin heavy chain, watable region, (13-2)	W825607.x1 NCI_CGAP_GC6 Hamo septens cDNA clane IMAGE:2498220 3'	601105344F1 NIH_MGC_15 Homo saplens cDNA done IMAGE:2887883 5	601105344F1 NIH_MGC_15 Hamo septens cDNA clane IMAGE:2867963 5
Top Hit Database Source	N.	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN		N.	EST_HUMAN	EST HUMAN	l l	EST HUMAN	Т	EST HUMAN	Π	L HUMAN	EST HUMAN	Т	Т	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	TN		П	EST_HUMAN
Top Hit Acession No.	L35830.1	0.0E+00 BE797385.1	0.0E+00 BE797385.1	0.0E+00 AI198025.1	0.0E+00 Al198025.1	0.0E+00 BF357123.1	11435830 NT	J55849.1	0.0E+00 AW178142.1	0.0E+00 BE674544.1	7882039 NT	0.0E+00 AV650020.1	0.0E+00 AW575598.1	101255.1		5.1	0.0E+00 Al612841.1	0.0E+00 BE735980.1	0.0E+00 BE735990.1	0.0E+00 AW748596.1	0.0E+00 AW748598.1		0.0E+00 AU119245.1	0.0E+00 AU119245.1	3.1				0.0E+00 BE283153.1
Most Similar (Top) Hit BLAST E Value	0.0E+00 L35830.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D55649.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00 H01255.1	0.0E+00 X15377.1	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00 U77629.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X92217.1	0.0E+00 AI989483.1	0.0E+00	0.0E+00 E
Expression Signal	1.53	1.22	1.22	0.57	0.67	0.85	1.08	0.65	1.03	0.66	1.33	8.59	3.13	6.26	1.6	0.65	6.	4.71	4.71	0.86	98.0	9.0	15.59	15.59	0.8	1.12	1.52	6.91	6.91
ORF SEQ ID NO:	31897	31903	31004	31919	31920	31921	31931	31939	31961	31978	31983		32003	32006	32019	32021	32022	32028	32029	32035	32036		32038	32039	32044	32045	32062	32072	32073
Exon SEQ ID NO:	18928	18936	18936	18947	18947	18949	18957	18968	18982	19002	19006	19020	19028	19031	19042	19044	19045	19051	19051	19055	19055	19058	19058	19058	19062	19063	19076	19088	19088
Probe SEQ ID NO:	6151	6129	6150	. 6170	6170	6172	8180	6189	6207	6228	6232	6246	6264	6257	6529	6271	6272	6278	6278	6282	6282	6283	6285	6285	6280	08Z9	88	8317	6817

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Table 4
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| Top Hit Descriptor | 7K43N05.x1 NCI_CGAP_Ov18 Homo septems cDNA done IMAGE:3478496 3' similer to TR:O14653 O145(| IIIHERI O SALLASAJII H NIJU 1400 97 LI | HILLHE AI A ANAL TO A MILE TANK AT IT TO SECTION CON INA GENERAL TO ANAL TO A MILE TANK AT IT. | AV719444 GLC Home, enters CONA along CI CELLOSS. | 801681150F1 NIH MAC 0 Home section CONA 1 11 ACT 2001 | 601681150F1 NIH MGC 9 Homo sapiens aDNA dama IMAGE:3051301 5 | Homo sapiens low voltage activated T-type calclum channel alpha 1G splice variant CevT.1a (CACNA1G) | Homo saniens transformation/franscription description | aughors agreement and the state of the state | augh08.9.1 Schneider fetal brain 00004 Horno sepiens cDNA clone IMAGE:2784159 5' stimilar to | 20209617 Scares fetal lung NHL19W Homo septens cDNA clone IMAGE:302626 5' similar to SW:2N45 HIMAN 002398 7'NC EINCED DECTEN 45.
 | 2020e06.11 Sceres fetal Jung NbHL19W Homo sepiens cDNA clone IMAGE:302626 5' similar to | SWIZNAS HUMAN QUZZBB ZINC FINGER PROTEIN 45; | NO 130837 IF I NIT MACC / Home eathers CDNA clone IMAGE:3943504 5 | OUT-GNOOKS-LANSIN-STAR-NO REPIERS CONA CIONE IMAGE:3941847 6 | QV1-GN0065-140800-318-h02 GN0065 Home series conv

 | 601512058F1 NIH_MGC_71 Homo septens cDNA clone IMAGE:3013311 5 | 601512058F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3913311 5' | Human antigen CD27 gene, exons 1-2
 | Homo sapiens chromosome 21 segment HS21C004 | Homo septens chromosome 21 segment HS21C004 | From sapers zona peliticida giycoprotein 3A (sperm receptor) (ZP3A), mRNA tt31f111 NCI_CGAP_GC8 Homo sepiens dDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE | HOWEN BENGTO-ONCOGENE PROTEIN PRECURSOR. | without a committee of the lif | 2W3Z0U3.1 Soares_post_reus_Nb2HF8_9W Home sapiens cDNA clone IMAGE:773668 5"
801885317F1 NIH MACC 57 Home septems_DNA_1 His Commissions to the commission
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| Expression
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 | 280 | 108 | 5.81 | 0.56 | 0.58

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 | 1.98 | 4.00 | 4.78 | 1.38 | 4.12 | 0.99
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 | 19289 |
| Probe
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NO: | 6355 | 6388 | 8388 | 8418 | 827 | 9427 | 8430 | 88 | 6440 | 54 | 4
 | 4 | 6459 | 9466 | 6467 | 6467

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 | 28 | 6491 | 484 | 8495 | 9507 | 9320
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| | Exon ORF SEQ Expression (Top) Hit Top Hit Acession No. Signal Value Source | Exon ORF SEQ Expression (Top) Hit Nost Signal Top Hit Acession Top Hit Acession Top Hit Detablese Top Hit Source Top Hit Acession Top Hit Detablese Top Hit Acession Top Hit Acession Detablese Detablese Detablese Acession Detablese Acession Detablese Acession Detablese Acession Detablese Acession Acession | Exan
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Table 4
Single Exon Probes Expressed in Brain

Prabe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6554	19319	32326	1.11	00+30°0	11426758 NT	NT	Homo seplens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
8554	19319	32328	11.1	0.0E+00	11426758 NT	LΝ	Homo sepiens solute cerrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6571	19335	32346	1.6	0.0E+00	0.0E+00 AU125928.1	EST_HUMAN	AU125628 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6573	19337	32348	1.88	0.0E+00	0.0E+00 BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6573	19337	32349	1.88	0.0E+00	0.0E+00 BE701434.1	EST_HUMAN	PM2-NN0174-280700-001-h10 NN0174 Homo seplens cDNA
6594	19357	32371	1.67	0.0E+00	0.0E+00 BE142363.1	EST_HUMAN	CM0-HT0143-270999-062-d08 HT0143 Homo sapiens cDNA
9614	19377	32391	1.44	0.0E+00	0.0E+00 BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
9614	19377	32392	1.44	0.0E+00	0.0E+00 BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
9638	19400	32415	8.38	0.0E+00	0.0E+00 BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
0640		32417	1.93	0.0E+00		EST_HUMAN	ILE-GN0032-180900-145-d07 GN0032 Homo sepiens cDNA
82/8	19595	32833	3.49	0.0E+00	0.0E+00 AA190755.1	EST_HUMAN	zp88e03.r1 Stratagene HeLa cell s3 837216 Homo sepiens cDNA clone IMAGE:627292 6
06890	19607	32647	76.0	0.0E+00	0.0E+00 U39573.1	IN	Human salivary perceddase mRNA, complete cds
							7e49b07x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:092285 Q92285
6683		32649	0.91	0.0E+00	0.0E+00 BE671987.1	EST HUMAN	TEKTIN.;
6703		32660		0.0E+00	0.0E+00 AI940621.1	EST_HUMAN	IL3-ST0024-230799-001-801 ST0024 Homo sepiens cDNA
6703		32861	6.69	0.0E+00	Ai940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
8714	19629	32674	1.91	0.0E+00	11435626 NT	NT	Homo sepiens CD6 entigen (CD6), mRNA
6726	19560	32592	66.0	0.0E+00	0.0E+00 AL042443.1	EST_HUMAN	DKFZp434D2021_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2021 5'
							00/0001.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:1565761 3' stmiler to
67/29		32595		0.0E+00	0.0E+00 AI168270.1	EST HOMAN	IKUZOWZ UZOGZ IEKIIN CI.:
973		32600		0.0E+00			601567370F1 NIH_MGC_21 Hamo septiens cDNA dane IMAGE:3842080 5
6752		30558		0.0E+00		EST_HUMAN	601339977F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:3082267 5'
6761		30565	11.84	0.0E+00	0.0E+00 BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo septens cDNA clane IMAGE:3847897 5
6781	17930	30586	11.84	0.0E+00	0.0E+00 BE867889.1	EST_HUMAN	801443887F1 NIH_MGC_65 Hamo septems aDNA clame IMAGE:3847897 5'
							7b49f03.x1 NCI_CGAP_LI24 Homo sepiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
6796	19510	32535	22	0.0E+00	0.0E+00 BE550162.1	EST_HUMAN	Q08379 GOLGIN-95.;
							7b49f03.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
848		32536		0.0E+00	0.0E+00 BE550162.1	EST_HUMAN	Q08379 GOLGIN-95.;
6790		32562	1.25	0.0E+00		EST HUMAN	CM1-HT0877-060900-397-g11 HT0877 Homo septems cDNA
8228	19540	32568	2.48	0.0E+00	0.0E+00 AA195106.1	EST_HUMAN	z34g03.r1 Soares_NhHMPu_S1 Homo sepiens aDNA dane IMAGE:665332 5
6803	19464		12.37	0.0E+00	11034810 NT	LN	Homo sapiens caterin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA

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					Sir	igle Exon Pro	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession	Top Hit Database Source	Top Hit Descriptor
6805	19468	32487	7	20.00			
6807	_		000	0.04400	0.0E+00 0.0E+00 0.0E+00	LN LOL	Homo septens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
6807	L		0.6		0.0E+00 BE313075 4	EST HUMAN	601150662F1 NIH_MGC_19 Hamo sepiens cDNA clone IMAGE:3503391 5'
6822	19483	32505	2.69		0.0E+00 RE569905 4	EST CINAN	CONTRODUCT NIM MIGG 19 Home sapiens cDNA clone IMAGE:3503391 5
6837	19499		2.32	0.0E+00	0.0E+00 J03060 4	TOWARK TA	UZISSSSZF1 NIH MGC 45 Homo sapiens CDNA ckine IMAGE:4310076 5
6845	19545	32573	3.52	0.0E+00	0.0E+00 AF217289 1	L Z	numen MTCLZ gene, complete cds
8845	10545	32574	3.52	0.0E+00	T	Į.	Lionino saprensi cadinerin 20 (CDHZO) mRNA, complete cds
6846	19546	32575	1.18	0.0E+00		FN	Indino sapiens cacherin 20 (CDH20) mRNA, complete cds
6858	17935	30571	3.2	0.0E+00	420775	LN	i rem i remonitatosis type 1 gene, exch XX
6829	17836	30572	0.74	0.0E+00	0.0E+00 Al419989.1	T HUMAN	tg53c06x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone IMAGE:2112490 3' similar to SW-CXYR HI IMAN Provision over the provision of the provisio
6859		30573	0.74	0.0E+00	0.0E+00 AI419989 1	T	tg53c06x1 Soars NFL T GBC S1 Homo sepiens dDNA done IMAGE:2112490 3' similar to
8883 8883		30576	0.78	0.0E+00	-	Т	ON THE STATE OF TH
6874		30546	0.58	0.0E+00	Ţ	Т	SOLVESTINE INC. 16 Home suplens converse (MAGE:3356330 5:
8884		30514	1.05	0.0E+00		Т	A11148.78 LEMBAR 11.
6887		30518	8.08	0.0E+00	-	Т	200148056 ENLY AND SEPTEMBER CLINA GOVE HEMBA1003679 5
8888		30519	228	0.0E+00 Z37978.1	Ī	Т	Contract I I III TWILE THE HOME SEPTENS CON COME IMAGE: 3501829 5'
8888		30520	2.26	0.0E+00 Z37976,1			H entires month ()
6889		30521	3.28	0.0E+00	-		reseptents ritives for mitter transforming growth factor-beta binding protein (LTBP-2)
6889		30522	3.26	0.0E+00			Homo earliers ciliary de minery origin 9 (DNAH9) mRNA, complete cos
8894	_1	30527	1.06	0.0E+00,			Homo seniens NAI P4 mBNA complete cds
088	19637	32681	1.03	0.0E+00	-	EST HUMAN	QV3-NT0022-140800-223-fn1 NT0032 Hzm.
3	19642	32687	2.37	0.0E+00		Г	60218585751 NIH MGC 45 Home seeking september 1001
8069	19846	32092	4.53	0.0E+00 L01978.1		Т	Human News IV scrifting changes and a constitution of the constitu
6013	19850	32696	0.79	0.0E+00	0.0E+00 AW502362.1	EST HUMAN	11-HF-RRDs etc. 4.0.0.111-4 Nilst Moor of the Control of the Contr
6913	19850	32697	0.79	0.0E+00	-	Т	THE BROG also A to 0.11 a Not 1 and
6922	19658	32704	0.7	0.0E+00		Т	DISTRICT STATES AND STATE OF THE SEPTEMBER STATES AND COME IMAGE: 3076290 5
6922	19658	32705	0.7	0.0E+00	Ī	7	DNEZ-DA 2011 L. 1-44 (syronym: ntess) Home septens cDNA clone DKFZp434D2211 5
6829	19665	32711	5.87	0.0E+00	0.0E+00 BF306096.1	1	601880823F1 NIH MCC 47 Home Control Annie Sapiens cDNA clone DKFZp434D2211 5
9634	19889	37745	233	000000		ľ	Squers CONA GORB IMAGE:4123948 5
6972	19464	32474	1 18	0.0E+00 0413021	T		Human chromosome 16 creatine transporter (SLOGAB) and (CDM) paralogous genes, complete cds
7008	19700	32754	2 6	1001300			Novel human gene mapping to chomosome 13
			2.00	0.0E+00 AB025893.1]	Ŧ	Homo sepiens mRNA for vescular cadherin-2, complete cds

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Table 4

Single Exon Probes Expressed in Brain

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	3283 3049 3049 3049 3287 3281 3291 3291 3291 3291 3291 3291 3291 329

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Table 4
Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	Top Hit Descriptor	DKFZp434B0228_r1 434 (synonym: https3) Homo sepiens cDNA clone DKFZp434B0228 5	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0228 5	601174578F1 NIH_MGC_17 Hamo sepiens cDNA clane IMAGE:3529794 5	Homo sapiens hypothetical protein (FL/20281), mRNA	AU118607 HEMBA1 Homo sepiens cDNA clone HEMBA1003969 5	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds	Homo sepiens ankyrin 1 (ANK1) mRNA, complete ods	Homo sapiens adlicen mRNA, complete ods	H. sapiens DNA for ZNGP2 pseudogene, excn 4	Human P2x1 receptor mRNA, complete cds	Human P2x1 receptor mRNA, complete cds	EST368573 MAGE resequences, MAGD Homo seplens cDNA	7e80h08.x1 NCI_CGAP_GC8 Homo septens cDNA clone IMAGE:3223167 3' similar to gb:M54911_ma11G HEAVY CHAIN PRECURSOR V-II REGION (HUMAN):	EST362586 MAGE resequences, MAGA Hamo septens cDNA	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa 200	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo saplens oDNA clone kappa, 200	AF001543 Human cDNA (Chandrasekharappa, S.C.) Homo sapiens cDNA clone kappa. 200	Human BTF3 protein homologue gene, complete cds	601302679F1 NIH_MGC_21 Hamo septens cDNA clone IMAGE:3637434 5'	UI-HF-BK0-ess-g-07-0-UI-M NIH_MGC_36 Hamo septems cDNA dane IMAGE:3054924 5	ym88h10.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:168051 5'	x839e05.y1 NCI_CGAP_Lu31 Hamo septens cDNA clone IMAGE:2578840 5' similar to TR:Q08050 Q08050 HNF3/FH TRANSCRIPTION FACTOR GENESIS;	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'	Homo sapiens glucegon-like peptide 2 receptor (GLP2R), mRNA	MR0-AN0083-270900-004-f07 AN0083 Homo sepiens cDNA	Homo saplens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds	601889823F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:4123948 5'	601889823F1 N#1_MGC_17 Hamo septens cDNA clane IMAGE:4123948 5'	AU118767 HEMBA1 Homo sepiens CDNA clone HEMBA1004314 5	cn17d05x1 Normal Human Trabecular Bone Cells Homo sapiens cONA clone NHTBC_cn17d05 random
gie Exori Proc	Top Hit Detabese Source	EST_HUMAN	EST_HUMAN	EST HUMAN	1	EST_HUMAN	TN	LN	Ę	LN.	N	N	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN		EST_HUMAN	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Г		EST_HUMAN	\Box	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN
	Top Hit Acession No.	0.0E+00 AL079497.1	0.0E+00 AL079497.1	0.0E+00 BE295499.1	11427965 NT	0.0E+00 AU118607.1	0.0E+00 AF005213.1	0.0E+00 AF005213.1	0.0E+00 AF245505.1	C70172.1		J45448.1	0.0E+00 AW956503.1	0.0E+00 BE672445.1	0.0E+00 AW950516.1	0.0E+00 AF001543.1	-	_		0.0E+00 BE408233.1	0.0E+00 AW402542.1	87430.1	0.0E+00 AW238326.1		11427135 NT	5.1		0.0E+00 BF306696.1	0.0E+00 BF306996.1	0.0E+00 AU118787.1	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X70172.1	0.0E+00 U45448.1	0.0E+00 U45448.1	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00 AF001543.	0.0E+00 AF001543.	0.0E+00 M90354.1	0.0E+00	0.0E+00	0.0E+00[R87430.1	0.0E+00	0.0E+00 AU117553.	0.0E+00	0.0E+00	0.0E+00 L32832.1	0.0E+00	0.0E+00	0.0E+00.	0.0E+00 AI752561.1
	Expression Signal	0.7	0.7	1.09	-	1.42	1.99	1.89	0.87	8.04	8.51	8.51	0.86	0.56	2.52	0.67	29.0	0.57	99'0	0.98	0.6	1.43	1.88	1.31	3.67	0.58	0.67	1.18	1.18	0.92	4.16
	ORF SEQ ID NO:		82828	69628	32970		32973	32974	32984	32289	32991	32892	33007	33009	33010	33033	33034	33035		33053	33064		33083		33101	33125	33133	33154	33155	33166	3323
	SEQ ID NO:		19856	19863	19865	19898	1986	19899	19911	19917	18919	19919	19032	18934	19035	18957	19957	19957	19975	19976	19988	20005	20008	20023	20025	20046	20052	20075	20075	20083	20133
	Probe SEQ ID NO:	7170	7170	7208	7210	7213	7214	7214	7228	7232	7234	7234	7247	7249	7250	7273	7273	7273	7292	7293	7305	7322	7323	7342	7344	7366	7372	7397	7397	7408	7460

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Table 4
Single Exon Probes Evergan

Single Exon Probes Expressed in Brain

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7460	20133	33224	4.16		0.0E+00 AI752581.1	EST HUMAN	Control Styles Trebenies Bose Cale U.
7535	20205	33301	1.83		0.0E+00 AF064205.1	Į Į	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete ods
7535	20205		1.83		0.0E+00 AF064205.1	2	Homo sapiens dynactin 1 (DCTN1) gene, atternatively spliced products, exons 7 through 32 and complete
7543	_ !	33313	1.14		0.0E+00 U74315.1	EST HUMAN	HSU74315 Human chromosome 14 Homo septeme DNA
7557	20227	33330	1.1	0.0E+00	11417342 NT	Į.	Home sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-1Ke), transmembrane domain (TM) and short cytonisemic domain semantic femantic fem
7570	20230	33343	2.28	0.0E+00	0.0E+00 AW672785.1	EST HUMAN	be01e06.y/ NIH_MGC_7 Homo septemblish Joh (SEMASA), mrdvA PHOSPHATIDY INOSTRO 4-KINA SE BEOLI # 17-00-011.
7570	20239	33344	2.28	0.0E+00	0.0E+00 AW672785.1	EST HUMAN	ba01a06.y1 NIH_MGC_7 Home septem signed and live septem signed by the september of the sept
7586	20264	33360	1.97	0.0E+00	0.0E+00 AI825504.1	EST HUMAN	wb17go5x1 NCI_CGAP_GC8 Home septems cDNA done IMAGE:2305976 3' similar to TR:075363 075363
7586		33361	1.97	0.0E+00		HST LE MAN	wb17g05x1 NCI_CGAP_GC8 Homo sapiens cDNA done IMAGE_2305076 3' similar to TR:075363 075363
7594		33370	1.51	0.0E+00	6912735	-1	HOTO sablens franciant renewtor and the life francians
7599	_ l	33373	1.09	0.0E+00	N76126.1	EST HUMAN	2288-605 St Schools finds have allest controlled in the State of Schools finds and the state of
780	20270	33377	5.87	0.0E+00	0.0E+00 BF217905.1	EST HUMAN	601885465F1 NIH MGC 67 Home sentene DNA April 10.00 C 1.00000000000000000000000000000
7813	20279	33387	5.41	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT 2RP2 Hamp september 2NA chare NT 2RP200603 5
7822	25117	33408	0.97	0.0E+00		EST_HUMAN	G42e09.X1 Jis bone marrow stroma Homo sapiens cDNA cione HBMSC G42e00.31
7636	2030	33407	0.97	0.0E+00	0.0E+00 AW069274.1	EST HUMAN	cr42e09.x1 Jie bone marrow strome Homo septens cDNA clone HBMSC cr42e09.3'
7643	20308	33416	4 43	0.05+00	0.0E+00 41/7554674	12	Homo saplens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7645	20309	33417	6.31	0 OF +00	T	EST LINES	AV 73497 BM Homo saplens cDNA clone BMFBGG05 5'
7645	20309	33418	6.31	0.0E+00	T	EST HIMAN	001393158F1 NIH MGC_9 Hamo sepiens cDNA done IMAGE:3947365 5
7646	20310	33419	1.18	0.0E+00	2461	5	Homo septens afrochin 1 Interaction products to the control of the
7646	20310	33420	1.18	0.0E+00	60124R1 NT		Home control of the second of
7647	20311	33421	0.71	0.0E+001		T HIMAN	11100.00 services acutomic interesting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7847	20311	33422	0.71	0.0E+00/	Γ	Т	AU120424 HEMBB1 Home series CNNA clone HEMBB1000655 5
7680	20344	33456	1.81	0.0E+00 [Т	601481713F1 NIH MGC 68 Homo septens cDNA close INAGE-3842555 F
						1	C SCZ 5000 - DOWN BY DO CALCADO CONTRACTOR C

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Exon ORF SEQ Expression (Top) Hit Acession Signal BLAST E No. Source Source	33457 1.81 0.0E+00 BE787610.1 EST_HUMAN	33498 0.63 0.0E+00 W62873.1 EST_HUMAN	33513 0.56 0.0E+00 AW 402332.1 EST_HUMAN	33515 0.76 0.0E+00 AA7606921 EST_HUMAN	O ZE O DELLO AATRORO 1 FST HIMAN	0.64 0.0E+00 AU133187.1 EST_HUMAN	33830 0.82 0.0E+00 BE313013.1 EST_HUMAN	33645 1.13 0.0E+00 AA149791.1 EST_HUMAN	33659 0.84 0.0E+00 BF026628.1 EST_HUMAN	HUMAN	33688 2.31 0.0E+00 BE736046.1 EST_HUMAN	33703 10.46 0.0E+00 M34872.1 NT	33704 10.46 0.0E+00 M34872.1 NT	ACTO AWITAES 1 EST HUMAN	33735 0.74 0.0E+00 AW 674581.1 EST_HUMAN F17K2.26 PROTEIN.;	3.91 0.0E+00 AA397551.1 EST_HUMAN	33742 1.41 0.0E+00 AW387131.1 EST_HUMAN	0.73 0.0E+00 AB020691.1 NT	33744 7.02 0.0E+00 AU142402.1 EST_HUMAN	33748 1.63 0.0E+00 BE388421.1 EST_HUMAN	33749 1.63 0.0E+00 BE388421.1 EST_HUMAN	33764 1.00 0.0E+00 W05278.1 EST_HUMAN	33765 1.09 0.0E+00 W96278.1 EST_HUMAN	6.89 0.0E+00 BF573096.1 EST_HUMAN	0.67 0.0E+00 AU134114.1 EST_HUMAN	33782 0.95 0.0E+00 BF525634.1 EST_HUMAN	EST_HUMAN	33813 1.59 0.0E+00 AL.120124.1 EST_HUMAN	20687 33814 1.69 0.0E+00 AL120124.1 EST_HUMAN DKFZp/61P082_T1 /61 (synonym: hemy2) Homb septems CLNA Grans DKFZp/01F082.5
									ļ			<u> </u>										L			2843				
SEQ ID SEC NO:		77.20				7752 24	<u> </u>	L	L	L		L	_	<u> </u>	8087		1	1_	L	L		L		L		<u></u>	L	Ш	

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Databasa Source	Top Hit Descriptor
8035	20730		1.32		0.0E+00 BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887773 5'
8057	20751	33882	2.48		0.0E+00 AW 500549.1	EST_HUMAN	UI-HF-BNO-akt-01-0-UI.r1 NIH_MGC_50 Homo saplens cDNA clone IMAGE:3077496 5'
8065	20759	33888	18.05		0.0E+00 AW157233.1	EST HUMAN	aus3b08.x1 Schneider fetal brain 00004 Homo septens cDNA clone IMAGE:2783799 3' similar to TR:0e0483 060483 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
8082	20778	33906	0.68	0.0E+00	0.0E+00 AW072395.1	EST HUMAN	xe07d12x1 Soares NFL_T_GBC_S1 Homo septens cDNA done IMAGE:2567639 3' similar to contains element OFR repetitive element;
8089	20783	33924	1.09		. 11421722 NT	LN LN	Homo sapiens centrocanel protein 2 (CEP2), mRNA
8102	20796	33927	1.07	0.0E+00	0.0E+00 W01618.1	EST_HUMAN	za36d05,r1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:294633 5
8104	20798	33929	122	0.0E+00	0.0E+00 BE745597.1	EST_HUMAN	801578195F1 NIH_MGC_9 Hamo septens aDNA dane IMAGE:3926998 5
8104	20798	33830	1.22	0.0E+00	0.0E+00 BE745597.1	EST HUMAN	801578195F1 NIH_MGC_9 Hamo septens aDNA clane IMAGE:3928998 5'
8115	20802	33943	1.46	0.0E+00	0.0E+00 AJ271735.1	·	Homo sapiens Xq pseudoautosomal region; segment 1/2
8154	20848	33080	0.95		0.0E+00 Al367350.1	EST_HUMAN	qv85c12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN.;
8165	20869	33991	2.63	0.0E+00	0.0E+00 BE674157.1	EST_HUMAN	7d78s04.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3278862 3' similar to TR:095783 095783 STAUFEN PROTEIN:
8167	20861	33983	1.19	0.0E+00	0.0E+00 AI885671.1	EST HUMAN	wI80b10.x1 NCI_CGAP_Bm25 Homo eaplens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR;
8180	20874	34009	1.07	0.0E+00		EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888655 57
8180	20874	34010	1.07	0.0E+00	0.0E+00 BE563650.1	EST HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888655 57
8189	20883	34020	1.63	0.0E+00	11427235 NT	N	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8189	20883	34021	1.63	0.0E+00	11427235 NT	TN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8191	20885	34023	3.2	0.0E+00	0.0E+00 AA403192.1	EST_HUMAN	zv68f02.r1 Soares_total_fetus_Nb2HF8_9w Homo saplens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD.;
8191	20885	34024	3.2	0.0E+00	0.0E+00 AA403192.1	EST_HUMAN	zv66102.r1 Sceres_total_fetus_Nb2HF8_9w Hamo seplens cDNA clone IMAGE:758619 5' similer to TR:G1304132 G1304132 TPRD.;
8231	20925		89.4	0.0E+00	0.0E+00 AA398511.1	EST HUMAN	zt73e08.s1 Soeres lestis_NHT Homo sepiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);
8240	20934	34071	0.55	0.0E+00		EST HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sepiens cDNA
8241	20835	34072	1.17	0.0E+00	0.0E+00 AW384874.1	EST HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sepiens cDNA
8241	20935	34073	1.17	0.0E+00	0.0E+00 AW384874.1	EST_HUMAN	QV3-DT0045-221288-04607 DT0045 Homo sapiens cDNA
8260	20954	34092	1.88	0.0E+00	0.0E+00 BE612586.1	EST_HUMAN	801452412F1 NIH_MGC_88 Homo sepiens cDNA clone IMAGE:3858179 5
8260	20954	34083	1.88	0.0E+00		T_HUMAN	601452412F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3856179 5'
8275	20969	34110		0.0E+00			Homo saplens chromosome 21 segment HS21C009
8275	20969	34111	1.52	0.0E+00	0.0E+00 AL163209.2	Z	Homo saplens chromosome 21 segment HS21C009

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	-			Most Similar	Sir	igle Exon Pro	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST.E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
828	3 20980	34120	1.3		0.0E+00 AI884477.1	EST_HUMAN	wm33af1.xf NCI_CGAP_Ut4 Homo septens cDNA clone IMAGE:2437724 3' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
8203		34128	127		0.0E+00 AA502294.1	EST HUMAN	ine26410.s1 NCI_CGAP_CO3 Homo sepiens cDNA clone IMAGE:882259 3' similar to TR:G1136434 G1136434 KIAA0197 PROTEIN
8228	L.		0.59		11416799 NT	L	Homo sacients protocachem beta 3 (PCDLR3) mRNA
8305		34137	1.02		0.0E+00 AI580780.1	EST HUMAN	1804f11x1 Scenes pregnant then is NINED Home services ONLY 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
8308	1		1.84		0.0E+00 BE890797.1	EST HUMAN	601431238F1 NIH MGC 72 Home senions CONA About 114A CE 2048E0 F1
8334			0.72		0.0E+00 AW245765.1	EST HUMAN	2822701.5prime NIH MGC 7 Homo septemb chote IMA CE: 3923744 E1
8334 45			0.72		0.0E+00 AW245785.1	EST HUMAN	2822701.5prime NIH MGC 7 Homo septems CDNA close IMAGE: 3822701.5
8335	╝	34165			4758695 NT	- LN	Homo saplers introcen activated private kinase kinase kinase 42 (ALD 2017)
8335	$_{ m L}$		2.24	0.0E+00	4758695 NT	Į.	Hono saplens mitroen-ectivated process in mace misses 13 (MATS 2015), IMENIA
8839	╝		0.59		0.0E+00 U88084.1	₽	Human zinc finger protein (ZNF165) gene exons 2 and 3
8339			0.59		0.0E+00 U88084.1	Ę	Human zinc finoer protein (ZNE165) nerve arms 2 and 3
8404	⅃	34233	99:0		0.0E+00 AJ251760.1	۲	Homo sapiens NESP55 GNAS (antisense (partier) and Y eleber (partier)
800	_]	34239	2.63	0.0E+00 X98922.1	X98922.1	FN	H. sapiens mRNA for gamma-dutamytransferase
8409	- 1	34240	2.63	0.0E+00 X98922.1		N FN	H-seplens mRNA for gamma-distanchmental H-seplens mRNA for gamma-distanchmental H-seplens mRNA for gamma-distanchmental H-seplens mRNA for gamma-distanchmental H-seplens mRNA for gamma-distanchmental H-seplens mRNA for gamma-distanchmental H-seplens mRNA for gamma-distanchmental H-seplens may be a fine for gamma-distance may be a fine for gamma-distance may be a fine for gamma-distanchmental H-seplens may be a fine for gamma-distance may be a fine for gamma-distance may be a fine for gamma-distance may be a fine for gamma-distance may be a fine for gamma-distance may be
8400		34241	2.63	0.0E+00 X98922.1		NT	H-septens mRNA for commanditions for each
8424	_1	34255	0.68	0.0E+00 U82979.1		NT	Human immunoolobulin-lika transcrint 3 mRNA complete ods
8465	_ i	34300	0.88	0.0E+00,	0.0E+00 AF022655.1	TN	Homo sapiens ceu/50 centrearne esercidad models acceptadad central cen
8465	21157	34301	0.88	0.0E+00,		LN	Home servicers cracy 50 mentiocome according in INVA, complete ds
8468	l	34303	2.28	0.0E+00,	0.0E+00 AU131671.1	EST HUMAN	AU131671 NT2RP3 Hamp servings CONA close NT28D2000006 5
8883	21175	34320	0.65	0.0E+00	11428572 NT		Homo septens immunoglobulin superfamily member 2 /(RSE2) mBNA
8487	21179		1.92	0.0E+00	0.0E+00 AW513513.1	EST_HUMAN	2046e01.x1 NCI_CGAP_Utt Homo sapiens dDNA clone IMAGE:2707032 3' similær to gb:M14123_cds4 RETROVIRUS-RELATED POL POL YPROTEIN HI IMANY
8480	21181	24322	77	100		Г	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02
8520	21212	34358	8 2	0.05-20-00-00-00-0		٦	0
8520	27.24	27380	5 6	0.05		T	601236488F1 NIH_MGC_44 Hamo septens cDNA clane IMAGE:3608709 5
0670	2 26 25	302	8	0.0E+00.			2532e04.r1 Soeres overy tumor NbHOT Homo septiens cDNA done IMAGE:724082 5
970	7777	+	2.91	0.0E+00.E	0.0E+00 BF313946.1	EST HUMAN	601900571F1 NIH_MGC_19 Homo sepiens dDNA clone IMAGE:4129744 5
8535	21227	34369	0.52	0.0E+00	11424387 NT		Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
8540	21232	34374	1.46	0.0E+00	0.0E+00 AW 139673.1	T HUMAN	ULH-BIA - 12-01 - 1 NCI COAD S. 12 U.
8540	21232	34375	1.46	0.0E+00		Т	UI-H-Bit art 4-12 O II et MC COAD 8-4-2 U
							COLUMN COLOR COLOR COLOR DIGINO SEPTEMBER CLAVA CIONO IMAGE: 2717687 3'

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					5	ioi i iova oigi	
Probe SEQ ID 8 NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
8545	21237		0.49	0.0E+00	0.0E+00 AI640190.1	EST_HUMAN	we30b10x1 NCI_CGAP_Kid11 Homo saplens cDNA done IMAGE:2299579 3' similar to TR:015044 015044 KIAA0335.;
8564	21256	34383	0.76	0.0E+00	0.0E+00 BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
8574	21286		0.59	0.0E+00	0.0E+00 AL163301.2	TN	Homo sepiens chromosome 21 segment HS21C101
8580	21272	34410	6.89	0.0E+00	0.0E+00 BE280272.1	EST_HUMAN	601150051F1 NIH_MGC_19 Hamo saplens cDNA clane IMAGE:3502836 5'
8585	21277	34414	2.51	0.0E+00	0.0E+00 BF700165.1	EST_HUMAN	802127664F1 NIH_MGC_66 Homo sapiens cDNA clane IMAGE:4284542 5'
8585	21277	34415		0.0E+00	0.0E+00 BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4284542 5'
8585	21277	34416	2.51	0.0E+00	0.0E+00 BF700165.1	EST_HUMAN	802127684F1 NIH_MGC_56 Homo saplens cDNA clone IMAGE:4284542 5'
8600	21292	34434	0.53	0.0E+00	0.0E+00 AI458722.1	EST_HUMAN	tk13h11,x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:2150949 3'
8626	21318	34460	0.86	0.0E+00	0.0E+00 AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stawrides GS) Homo sapiens cDNA
	242.00	rorre	16. 6	00.50	4 4 0 0 0 0 0 0 0		or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1802194 3' similar to gb:M36072 60S
1200	21322	40440	67.7	0.0=+00	0.0E+00 AA862527.1	ESI HUMAN	INDOSOMAL PROTEIN L'A (FIGNIAN);
à	252	344/2	SO.S	0.05+00	1094/US/ N	Z	TIONS SAPISTS BINGTON 1, GEVENOCYDC (ANN.), USESCIPT VERSETT INCLEA
8637	21320	34473	3.09	0.0E+00	10947037	LN L	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8000	21352	34499	1.3	0.0E+00	0.0E+00 Y11107.3	N	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8662	21354	34501	1.62	0.0E+00	0.0E+00 BE278917.1	EST_HUMAN	801156330F1 NIH_MGC_21 Homo septens dDNA clane IMAGE:3139734 5'
8672	21364		1.91	0.0E+00	0.0E+00 AV718377.1	EST HUMAN	AV718377 FHTB Hama sapiens cDNA clone FHTBAAF11 5
8679	21371	34518	3.33	0.05+00	0.0F±00 AW337277 1	FST H MAN	xw73c07.xt NCL_CGAP_Pan1 Homo saplens cDNA clone IMAGE:2833644 3' similar to gb:X53587 INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN)
8685	21377	34521	1.12	0.0E+00	0.0E+00 AU124051.1	EST HUMAN	AU124051 NT2RM2 Homo septens cDNA clone NT2RM2001575 5'
8761	21453	34601	1.05	0.0E+00	0.0E+00 AU140704.1	EST_HUMAN	AU140704 PLACE4 Homo sepiens cDNA clone PLACE4000089 5
8771	21463	34610	0.86	0.0E+00	0.0E+00 AB007923.1	N FN	Homo septens mRNA for KIAA0454 protein, pertial cds
8778	21468	34614	0.54	0.0E+00	0.0E+00 R17132.1	EST_HUMAN	1g09e09.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674.5'
8776	21468	34815	0.54	0.0E+00	0.0E+00 R17132.1	EST_HUMAN	yg09e09.r1 Soeres Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 5
8780	21472	34617	4.43	0.0E+00	0.0E+00 AW 592233.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Home septems cDNA done IMAGE:2835096 3'
8780	21472	34618	4.43	0.0E+00	0.0E+00 AW 592233.1	EST_HUMAN	Hf48a09.x1 Soares_NFL_T_GBC_S1 Homo septens cDNA done IMAGE:2935098 3'
8815	21507	34862	0.47	0.0E+00	0.0E+00 AU128804.1	EST_HUMAN	AU128804 NT2RP2 Homo sepiens cDNA clone NT2RP2004245 5'
8827	21519	34664	2.5	0.0E+00	0.0E+00 AV714764.1	EST_HUMAN	AV714764 DCB Homo septens cDNA clane DCBAUA06 5
8843	21535	34679	2.79	0.0E+00	0.0E+00 AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: https:3) Homo saplens cDNA clone DKFZp434C1814 3'
8843	21535	34680	2.79	0.0E+00	0.0E+00 AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Hamo saplens cDNA clone DKFZp434C1814 3'
07.00	07570	0.4000	•	200		ŧ	Homo saplens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes,
3 2	200		1.1/	0.01-100		z!	partie cos
8851	21542	١	2.03	0.0E+00		Ż	Home sapiens mitNA for KIAA1512 protein, partial cds
8858	21549	34696	0.65	0.0F+00	0.0E+00 BF675505.1	EST HUMAN	602138483F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274708 5

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Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	Most Similar (Top) Hit Top Hit Acession Database No. Source	0.0E+00 BF058289.1 EST HUMAN S GAG.:	Т	K01241.1	NT NT		EST HUMAN	9838 NT	T HUMAN	ĮN	-7.	EST HUMAN	2.1 EST HUMAN	1 EST HUMAN		.1 EST HUMAN	Г		0.0E+00 A1091395.1 EST HUMAN en29604.x1 Gessler Wilms tumor Homo services CIVIA door 1446.CE-1720205.12		56596 NT	AW958311.1 EST HUMAN	15487 NT	0.0E+00 AU142662.1 EST HUMAN AU142662 Y79AA1 Home serviers ATMA Appropriate Est	5995 NT	T HUMAN	0.0E+00 BF002024 1 EST HI IMAN OOI HAS DYDOTTETTAL AS FOR HOM SACIES STAND OF HIS DYDOTTETTAL AS FOR HOME SACIES STAND OF HIS DYDOTTETTAL AS FOR HIS DYDOTTETTAL	NT	EST HIMAN	į	1 EST HUMAN	1 EST_HUMAN
	Most Simila (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+0	0.0E+0C	0.0E+0C	0.0E+0C	0.0E+0C	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	0.8	3.97	1.19	4.27	4.27	1.79	2.88	0.5	0.73	0.73	0.91	4.57	4.57	0.48	0.48	0.45	3.88	2.03	1.95	4.65	1.42	2.48	1.53	1.78	1.18	8:	1.1	7.72	0.99	0.99	2.93
	ORF SEQ ID NO:			34729		34738	34744	34750		34756	34757		34779	34780	34795	34786		34800	34820	34824	34828	34840	34851	34869	34887		34904	34920	34021	34926	34927	34830
	Ban SEQ ID NO:		[21596			21612	21613	21613	21625	21635	21635	21645	21045	21648	21860	21670	21675	21679	21690	21701	21716	21732	21733	21745	21759	21760	21764	21764	21787
	Probe SEQ ID NO:	8860	8888	888	8005	8905	8910	8916	<u>2</u> 28	88	8	88	8	8	8	8	8957	88	88	8985	8968	000	8017	828	9042	843	9056	0206	9071	9075	9075	8078

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Single Exon Probes Expressed in Brain

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Single Exon Probes Expressed in Brain	Top Hit Descriptor Source	NT AIGF-androgen-Induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt segment 5 of 5]	NT AIGF-androcen-Induced growth factor AIGF frumen placents. General-MBNA AGB at secures 6 of 61	EST HUMAN	EST HUMAN	432 NT		EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	Г	EST_HUMAN 601595558F1 NIH_MGC_9 Homo sepiens cDNA done IMAGE:3949383 5	NT Homo saplens mRNA for KIAA1231 protein, perfeil cies	NT Homo septens mRNA for KIAA1231 protein, partial cds	F	EST_HUMAN DKFZp434L0120_r1 434 (synonym: https:// Homo sapiens.cDNA clare DKFZp4341 0120 5:	EST_HUMAN DKFZp434B2416_r1 434 (synonym: Mes3) Homo septients cDNA clone DKFZp434B2416 5	EST_HUMAN	NT Homo sapiens protocedherin elpha 12 (PCDH-alpha12) mRNA, complete cds	NT Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds	NT Homo saplens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds	EST_HUMAN MR4-TN0114-110900-101-604 TN0114 Homo saptens cDNA	EST_HUMAN 601155227F1 NIH MGC_21 Homo septems cDNA done IMAGE:3138788 5	EST_HUMAN 601286351F1 NIH MGC 44 Homo septents cDNA clone IMAGE:3613/45 57	EST_HUMAN 601286351F1 NIH_MGC_44 Homo septems cDNA clone IMAGE:3613045 5		EST HUMAN	EST HUMAN	EST_HUMAN	\neg	
e Exon Probes Expressed in Brain	Top Hit Detabase Source			T HUMAN	HUMAN			T HUMAN	HUMAN	Г	Т	Г	Г				1		HOMAN					Г	HUMAN	Г		\neg		П		
Sing	Top Hit Acession No.	0.0E+00 S78486.1 N	0.0E+00 S78466.1	0.0E+00 BE563320.1 E		¥32	11424387 NT	0.0E+00 BE206710.1 E		0.0E+00 AU132349.1 E	0.0E+00 AW 500936.1 E		0.0E+00 BE740490.1 E	.1	0.0E+00 AB033057.1 N	7862067 N	0.0E+00 AL042278.1 ES	0.0E+00 AL041084.2 ES	0.0E+00 AU132349.1 ES	1	1	0.0E+00 AF009220.1 NT	.1	ı	_	0.0E+00 BE388700.1 ES			7	-	_	0.0E+00 AU143673.1 ES
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	L	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00/
	Expression Signal	2.23	2.23	2.93	1.9	0.46	0.51	0.54	2.57	2.57	0.77	80.6	9.08	0.48	0.48	1.73	1.59	1.53	2.54	2.37	2.63	2.63	1.81	2.41	0.86	0.86		3.63	1.06	78.0	7.01	7.01
<u></u>	ORF SEQ ID NO:	35469	35500	36505	35521	35537	35538	35548	35568	35569	35581	35586	35587	35588	35580	35603	35623	35629	35636	35637	35664	35865	35678	35704	35710	35711	25747	71/05	32/18	35748	35/69	35760
	Exan SEQ ID NO:	22304	22304			22343	22344			22370	22379	22384	22384	22385	22385	22398	22416	22421	22431	22432	22450	22459	22475	22504	22514	22514	206.00	3000	47C77	22023	7007	22564
	Probe SEQ ID NO:	9662	2986	9655	9674	9692	8663	9702	8719	9719	8228	9733	9733	9734	9734	9747	9765	9770	9780	9781	808	8086	9824	9854	9864	986	04473	2/08	8	400	2 2	9915

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					П	П		T	7	П	٦	7	٦			П	T	7	٦	7	\neg	7	Т	Т	Т	Т	1	7	Т	7	\neg	_		
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo caniane killer rell inhibit successions. VIDA	Homo senieros HIFE II.o Devoir (1951) - Data	Homo septemble file Devote (1557) - Data	A 1139837 DI ACET Home seeing DNA 1155837 DI ACET Home seeing DNA 1155837 DI ACET Home seeing DNA 1155837 DI ACET Home seeing DNA 1155837 DI ACET HOME seeing DNA 1155837 DI ACET HOME SEEING DNA 115583 DNA 1155	ALITABERT PLACE HAIR SERVICE CONTRACTOR PLACE 1004/37 S	Homo sapiens partial RANBD7 news for DeepDate	Homo sapiens partiel RANBP7 cene for RanBP7//mmc/fin7 and martial 7/15/20	AV695712 GKC Home sentens CONA character milipotating and perdell ZNF143 gene	AV695712 GKC Hamp saples chive circle GKChyvaoz E	Hamo septens feller cell inhibition preprint KIRCI anno 2001	ZD97h11.r1 Strategie militarie 93720 Homo content CNA Link Content	23101 of Scarce meaning ideas Mikipi Li	231f01.1 Spares Pregnant them Nicipi II.	Home series KIEA (KIEA) mbNA American Advance of the control of th	1601491565F1 NIH MGC 60 Home services CINA class 184A CE 20022 EE EI	1801570712F1 NIH MGC 21 Homo septembers ANA Alone MARCE 2015/272 F1	601570712F1 NIH MGC 21 Home sections CONA A CONTROLL SECTION OF CO	AU127403 NT2RP2 Home servines CNA Above NT2882000 5	601645134F1 NIH MGC ER Homo enters ANN Alms IN A CE SASSATT E	601645134F1 NIH MGC 56 Home septeme CONA State MA OF COMMENT	801432317F1 NIH MGC 72 Homo seniens of NA Alone 14AGE 28474F2 E1	EST182353 Jurkat T-cells VI Homo sections of DNA 5' and	Homo sapiens neuredn III (NRXN3) mRNA	601432228F1 NIH_MGC_72 Homo saplens cDNA clone IMAGE 3017508 F	Homo sapiens hypothetical C2H2 zinc finger protein FL122504 (FL122504) mRNA	Homo saplens mRNA for actin binding protein ARPR20 complete cole	1801105459F1 NIH MGC 15 Homo services CONA Accountations and	601105459F1 NIH MGC 15 Homo serviens CDNA Apre 1840E-2867918 5	Homo saplens mRNA for estrocen recenter hate complete cuts	Homo sapiens mRNA for estrogen receptor beta, complete ods	219b08.s1 Sogree_fetal_liver_spieen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:450707 3' skriller to	HIMSP FOLS (A CASSESSED)	numan beta 1,4-gatactusy-transferase mRNA, complete cds 802037045F1 NCI_CGAP_Bm64 Homo saplens cDNA close IMAGE:4184030 kt
gle Exon Pro	Top Hit Database Source	Į.	LN	Į.	FST HIMAN	EST HUMAN	ij.	F	EST HUMAN			EST HUMAN	EST HIMAN	EST HUMAN	L	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	L	EST_HUMAN	11	NT	EST HUMAN	EST HUMAN	Į.	NT	TAT LINAM	TOWN	EST_HUMAN
uis l	Top Hit Acession No.	AF072408.1	11421001 NT		0.0E+00 AU138637 1	0.0E+00 AU136637.1							0.0E+00 AA131248.1								0.0E+00 BE958511.1	Γ	0.0E+00 AA311624.1	8827	0.0E+00 BE891113.1	11560151 NT			0.0E+00 BE304522.1					
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 B	0.0E+00	0.0E+00	0.0E+00 B	0.0E+00	0.0E+00 AB006590.1	0.0E+00 AB006590.1	0.0E+00 AA704457 1	0.0E+00 M22921.1	0.0E+00 BF340331.1
	Expression Signal	2.98	2.75	2.75		8	2.08	2.08	1.04	1.04	0.74	3.11	-	-	1.44	0.92	6.22	6.22	76.0	0.87	0.87	0.88	0.67	1.01	0.67	1.13	1.72	0.48	0.46	8.02	6.02	8.	0.74	5.45
-	ORF SEQ ID NO:	35763	35765	35766	35809	35810	35824	35825	35832	35833	35840	35843	35873	35874	35022	35964	35972	35973	35977	35988	32080	36007	36020	38021	38032	36035	36041	36042	36043	36048	36049	36056	38057	38060
	Exan SEQ ID NO:	22587	22569	22569	22604	22604	22620	22620	22625	22625	22631	22633	22659	22659	22704	22749	22760	22760	22765	22775	22775	22792	22802	22803	22814	22817	22827	22828	22828	22835	2835	22841	22843	22845
	Probe SEQ ID NO:	9918	8921	8921	9966	8956	2268	2202	201	2024	88	9888	10011	10011	10056	10101	10112	10112	10117	10127	10127	1014	10154	10155	2010	10103	2 5	1938	10180	10187	10187	10183	10195	10197

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SCD D CREST Expression Top-Hit Accession Top-Hit Descriptor Top-Hit Descriptor SCD D SCO D D.N.C. Signal BLAST E F.A. Notice of Behaviorsh (1.17 ps), He Accession Top-Hit Descriptor Top-Hit Descriptor 10222 ZEXDO SRODI D D.N.C. Signal D.GColl B-SACKST 1.1 SET HAMAN MOREST 14 HILL MAGE 2.1 have neglese a CDM clean MAGE 2024778 F 10222 ZEXDO SROSI D C.D.GCOLL MATERT 1.1 SET HAMAN MOREST 1.1 HILL MAGE 2.2 have neglese a CDM clean MAGE 2020778 F 10222 ZEXDO SRY11 C.D.GCOLL MATERT 1.1 SET HAMAN MOREST 1.1 HILL MAGE 2.2 have a coll with Clean MAGE 2020778 F 10222 ZEXDO SRY11 C.D.GCOLL MATERT 1.1 SET HAMAN MOREST 2.2 have a coll with Clean MAGE 2020778 F 1022 ZEXDO SRY11 C.D.GCOLL MATERT 1.1 SET HAMAN MOREST 2.2 have a coll with Clean MAGE 202078 F 1022 ZEXDO SRY11 D.GCOLL MATERT 2.1 SET HAMAN MOREST 2.2 has a coll with Clean MAGE 202078 F 1022 ZEXDO SRY11 D.GCOLL MATERT 2.2 has a coll w								
22846 36061 5.45 0.0E+00 BF340331.1 EST HUMAN 22870 36082 0.63 0.0E+00 BE897149.1 EST HUMAN 22870 36110 0.55 0.0E+00 BA718271.1 EST HUMAN 22900 36111 0.65 0.0E+00 AV718271.1 EST HUMAN 22900 36141 0.65 0.0E+00 AV718271.1 EST HUMAN 22930 36142 2.36 0.0E+00 AV718271.1 EST HUMAN 22930 36149 2.36 0.0E+00 AV718271.1 EST HUMAN 22946 36190 0.0E+00 AV718271.1 EST HUMAN 22947 36190 0.0E+00 AV718271.1 EST HUMAN 22946 36240 0.0E+00 AV624786.1 EST HUMAN 22947 36190 0.0E+00 BE548218.1 EST HUMAN 22948 36279 0.0E+00 BE743231.1 EST HUMAN 23049 36234 0.75 0.0E+00 BE743231.1 EST HUMA		Exan SEQ ID NO:	o Rg ⊡	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
22870 36082 0.83 0.0E+00 BE897149.1 EST_HUMAN 22800 36110 0.55 0.0E+00 AV716271.1 EST_HUMAN 22800 36111 0.55 0.0E+00 AV716271.1 EST_HUMAN 22800 36114 0.56 0.0E+00 AV716271.1 EST_HUMAN 22800 36144 2.36 0.0E+00 AV716271.1 EST_HUMAN 22818 36149 0.49 0.0E+00 AV716271.1 EST_HUMAN 22810 36190 0.04 0.0E+00 AV716271.1 EST_HUMAN 22810 36190 0.04 0.0E+00 AV716271.1 EST_HUMAN 22810 36190 0.04 0.0E+00 AV64765.1 EST_HUMAN 22810 36234 2.5 0.0E+00 BF432428.1 EST_HUMAN 23040 36236 3.5 0.0E+00 BE742428.1 EST_HUMAN 23041 36236 1.9 0.0E+00 BE742428.1 EST_HUMAN 23041	197	22845		5.45	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184939 6'
22870 36083 0.88 0.0E+00 BE997149.1 EST_HUMAN 22900 36110 0.55 0.0E+00 AV716271.1 EST_HUMAN 22900 36111 0.56 0.0E+00 AV716271.1 EST_HUMAN 22920 36143 2.36 0.0E+00 AI631818.1 EST_HUMAN 22936 36149 0.49 0.0E+00 AI631818.1 EST_HUMAN 22946 36136 0.46 0.0E+00 AI631818.1 EST_HUMAN 22946 36136 0.49 0.0E+00 AI631818.1 EST_HUMAN 22946 36136 0.46 0.0E+00 AI634222.1 EST_HUMAN 22947 36236 0.64 0.0E+00 BE743228.1 EST_HUMAN 23020 36236 8.82 0.0E+00 BE642730.1 EST_HUMAN 23041 36236 1.9 0.0E+00 BE642730.1 EST_HUMAN 23042 36236 1.9 0.0E+00 BE642720.1 EST_HUMAN 23049 <t< td=""><td>Ø</td><td>22870</td><td>36082</td><td>880</td><td>0.0E+00</td><td>BE897149.1</td><td>EST_HUMAN</td><td>601439713F1 NIH_MGC_72 Homo septens cDNA done INAGE:3924578 5'</td></t<>	Ø	22870	36082	880	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo septens cDNA done INAGE:3924578 5'
22900 36110 0.55 0.0E+00 AV716Z71.1 EST_HUMAN 22900 36111 0.65 0.0E+00 AV716Z71.1 EST_HUMAN 22923 36141 2.36 0.0E+00 AR31818.1 EST_HUMAN 22926 36149 0.49 0.0E+00 11545730 NT 22945 36159 1.52 0.0E+00 17545730 NT 22946 36190 0.64 0.0E+00 17545730 NT 22947 36190 0.64 0.0E+00 AU722429.1 EST_HUMAN 22946 36236 0.64 0.0E+00 AV64706.1 EST_HUMAN 22906 36236 0.37 0.0E+00 BE38218.1 EST_HUMAN 23029 36236 0.37 0.0E+00 BE38218.1 EST_HUMAN 23029 36236 0.3 0.0E+00 BE38272.1 EST_HUMAN 23029 36236 0.3 0.0E+00 BE38272.1 EST_HUMAN 23029 36336 0.3	222	22870		0.83	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo saplens cDNA done IMAGE:3924578 5
22960 36111 0.66 0.0E+00 AV716271.1 EST_HUMAN 22930 36143 2.36 0.0E+00 AI631818.1 EST_HUMAN 22936 36144 2.36 0.0E+00 AI63181.1 EST_HUMAN 22945 36159 1.52 0.0E+00 AI722429.1 EST_HUMAN 22976 36190 0.64 0.0E+00 AU722429.1 EST_HUMAN 22976 36190 0.64 0.0E+00 AU722429.1 EST_HUMAN 22976 36234 2.5 0.0E+00 BF436218.1 EST_HUMAN 22905 36234 2.5 0.0E+00 BF436218.1 EST_HUMAN 23020 36236 8.82 0.0E+00 BE64272.1 EST_HUMAN 23020 36237 1.9 0.0E+00 BE64272.1 EST_HUMAN 23028 36251 1.9 0.0E+00 BE64272.1 EST_HUMAN 23029 36306 1.9 0.0E+00 BE64272.1 EST_HUMAN 23029 36307<	252	22900		0.55		AV716271.1	EST_HUMAN	AV716271 DCB Hamo septens cDNA clane DCBBDC09 5'
22930 36143 2.36 0.0E+00 Al631818.1 EST_HUMAN 22930 36144 2.36 0.0E+00 Al631818.1 EST_HUMAN 22936 36144 2.36 0.0E+00 T1545730 NT 22946 36159 1.62 0.0E+00 T1545730 NT 22947 36196 0.46 0.0E+00 AU122421.1 EST_HUMAN 22946 36196 0.46 0.0E+00 AU122421.1 EST_HUMAN 22946 36214 2.5 0.0E+00 AU64786.1 EST_HUMAN 22966 36214 2.5 0.0E+00 BC43786.1 EST_HUMAN 23020 36236 8.82 0.0E+00 BE546273.1 EST_HUMAN 23040 36236 1.9 0.0E+00 BE64273.1 EST_HUMAN 23041 2.5 0.0E+00 BE64273.1 EST_HUMAN 23050 36236 1.9 0.0E+00 BE64273.1 EST_HUMAN 23040 36331 1.3 0.0	Š	22900	36111	99.0		AV716271.1	EST_HUMAN	AV716271 DCB Homo septens cDNA clone DCBBDC09 5"
22830 36144 2.36 0.0E+00 AI631818.1 EST HUMAN 22846 36149 0.49 0.0E+00 T03078.1 EST HUMAN 22946 36159 1.52 0.0E+00 T03078.1 EST HUMAN 22976 36190 0.64 0.0E+00 BF486218.1 EST HUMAN 22966 36234 2.5 0.0E+00 BF486218.1 EST HUMAN 22968 36234 2.75 0.0E+00 BF486218.1 EST HUMAN 23020 36236 8.82 0.0E+00 BF486218.1 EST HUMAN 23021 36236 0.37 0.0E+00 BE546278.1 EST HUMAN 23020 36236 1.9 0.0E+00 BE64278.1 EST HUMAN 23040 36236 1.9 0.0E+00 BE64273.1 EST HUMAN 23041 36326 0.9 0.0E+00 BE64273.1 EST HUMAN 23040 36331 1.3 0.0E+00 BE64268.0 EST HUMAN 23105 36332 <td>82</td> <td>22830</td> <td>36143</td> <td></td> <td>0.0E+00</td> <td>Al631818.1</td> <td>EST_HUMAN</td> <td>ws36603.x1 NCI_CGAP_Kid11 Homo sapiens dDNA clone IMAGE:2300188 3' similar to TR:061204 Q01204 NOTCH2-LIKE;</td>	82	22830	36143		0.0E+00	Al631818.1	EST_HUMAN	ws36603.x1 NCI_CGAP_Kid11 Homo sapiens dDNA clone IMAGE:2300188 3' similar to TR:061204 Q01204 NOTCH2-LIKE;
22936 36149 0.049 0.0E+00 11545730 NT 22945 36159 1.62 0.0E+00 T03078.1 EST_HUMAN 22976 36190 0.046 0.0E+00 AU122429.1 EST_HUMAN 22996 36214 2.5 0.0E+00 BF438218.1 EST_HUMAN 22996 36231 2.75 0.0E+00 BF438218.1 EST_HUMAN 23020 36236 8.82 0.0E+00 BF438218.1 EST_HUMAN 23021 36236 8.82 0.0E+00 BE546213.1 EST_HUMAN 23040 36236 1.9 0.0E+00 BE546213.1 EST_HUMAN 23041 2.75 0.0E+00 BE646213.1 EST_HUMAN 23050 36237 1.9 0.0E+00 BE646213.1 EST_HUMAN 23081 36306 1.9 0.0E+00 BE646213.1 EST_HUMAN 23081 36316 0.0E+00 BE646212.1 EST_HUMAN 23100 36331 1.33 0.0E+00 </td <td>382</td> <td>22830</td> <td>36144</td> <td>2.36</td> <td>0.0E+00</td> <td>A1631818.1</td> <td>EST HUMAN</td> <td>wa38e03.x1 NCI_CGAP_Kid11 Homo septens dDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2LIKE;</td>	382	22830	36144	2.36	0.0E+00	A1631818.1	EST HUMAN	wa38e03.x1 NCI_CGAP_Kid11 Homo septens dDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2LIKE;
22945 36159 1.62 0.0E+00 T03078.1 EST HUMAN 22976 36190 0.64 0.0E+00 AU122429.1 EST HUMAN 22976 36196 0.46 0.0E+00 BF438218.1 EST HUMAN 22986 36214 2.5 0.0E+00 BF438218.1 EST HUMAN 22907 36236 36231 0.0F+00 BF438218.1 EST HUMAN 23020 36236 36251 0.0F+00 BF4064786.1 EST HUMAN 23020 36236 8.82 0.0E+00 BE546213.1 EST HUMAN 23040 36237 0.75 0.0E+00 BE546213.1 EST HUMAN 23041 2.79 0.0E+00 BE646213.1 EST HUMAN 23042 36307 1.9 0.0E+00 BE082720.1 EST HUMAN 23041 36336 0.0E+00 BE042720.1 EST HUMAN 23100 36331 1.33 0.0E+00 BE0436215.1 EST HUMAN 23106 36332 0.0E+00	巖	22936		0.49	0.0E+00	LZ.	Z	Homo sapiens Gigaxonin (GAN), mRNA
22976 36190 0.64 0.0E+00 AU122429.1 EST HUMAN 22976 36196 0.46 0.0E+00 6005921 NT 22986 36214 2.5 0.0E+00 BF438218.1 EST HUMAN 22907 36236 36231 0.0F+00 AV654766.1 EST HUMAN 23020 36236 8.82 0.0E+00 BE546213.1 EST HUMAN 23035 36251 0.75 0.0E+00 BE546213.1 EST HUMAN 23040 36236 8.82 0.0E+00 BE546213.1 EST HUMAN 23040 36251 0.75 0.0E+00 BE646213.1 EST HUMAN 23040 36251 0.75 0.0E+00 BE646213.1 EST HUMAN 23041 36307 1.9 0.0E+00 BE082720.1 EST HUMAN 23081 36316 0.06 0.0E+00 BE042720.1 EST HUMAN 23100 36331 1.33 0.0E+00 BE0473215.1 EST HUMAN 23104 36332<	8	22945			0.0E+00	T03078.1	EST_HUMAN	FB23A4 Fetal brain, Stratagene Homo sapiens cDNA clone FB23A4 3'end
22976 36196 0.46 0.0E+00 6005921 NT 22986 36214 2.5 0.0E+00 BF438218.1 EST_HUMAN 22986 0.97 0.0E+00 AV654766.1 EST_HUMAN 23020 36231 2.75 0.0E+00 BE546213.1 EST_HUMAN 23020 36251 0.75 0.0E+00 BE546213.1 EST_HUMAN 23040 36251 0.75 0.0E+00 BE546213.1 EST_HUMAN 23060 36279 0.75 0.0E+00 BE546213.1 EST_HUMAN 23081 36307 1.9 0.0E+00 BE646213.1 EST_HUMAN 23081 36306 1.9 0.0E+00 BE082720.1 EST_HUMAN 23081 36316 0.06 0.0E+00 BE042720.1 EST_HUMAN 23100 36331 1.33 0.0E+00 BE047665.1 EST_HUMAN 23100 36332 0.08 0.0E+00 BE047665.1 EST_HUMAN 23101 36332 0.33	23	22970			0.0E+00	AU122429.1	1. 4	AU122429 MAMIMA1 Homo saplens cDNA clone MAMIMA1002358 5
22966 36214 2.5 0.0E+00 BF438218.1 EST_HUMAN 22986 0.97 0.0E+00 AV654766.1 EST_HUMAN 23020 36231 2.75 0.0E+00 BE540213.1 EST_HUMAN 23020 36236 8.82 0.0E+00 BE540213.1 EST_HUMAN 23020 36251 0.75 0.0E+00 BE540213.1 EST_HUMAN 23081 36279 2.79 0.0E+00 BE781742.1 EST_HUMAN 23081 36307 1.9 0.0E+00 BE082720.1 EST_HUMAN 23084 36316 0.0E+00 BE082720.1 EST_HUMAN 23094 36325 0.0B 0.0E+00 BC082720.1 EST_HUMAN 23100 36331 1.33 0.0E+00 BE743215.1 EST_HUMAN 23100 36332 1.33 0.0E+00 BE617865.1 EST_HUMAN 2310 36335 2.49 0.0E+00 BE617865.1 EST_HUMAN 2315 36385 0.57	83	22976			0.0E+00	5921	ᅜ	Homo seplens triple functional domain (PTPRF interacting) (TRIO), mRNA
23916 0.87 0.0E+00 AV664766.1 EST HUMAN 23015 36231 2.75 0.0E+00 BE540213.1 EST HUMAN 23020 36236 8.82 0.0E+00 BE540213.1 EST HUMAN 23035 36251 0.75 0.0E+00 BE540213.1 EST HUMAN 23040 36279 0.75 0.0E+00 BE740213.1 EST HUMAN 23081 36307 1.9 0.0E+00 BE082720.1 EST HUMAN 23081 36306 1.9 0.0E+00 BE082720.1 EST HUMAN 23084 36316 0.0E+00 BE082720.1 EST HUMAN 23100 36331 1.33 0.0E+00 BE042720.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE043215.1 EST HUMAN 23100 36333 1.33 0.0E+00 BE047655.1 EST HUMAN 2310 36335 2.49 0.0E+00 BE047655.1 EST HUMAN 2315 36336 0.45	84	22805	36214			BF436218.1	EST_HUMAN	Inab45e12.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sepiens cDNA done IMAGE:3265271 37
23015 36231 2.75 0.0E+00 AW517960.1 EST_HUMAN 23020 36236 8.82 0.0E+00 BE546213.1 EST_HUMAN 23035 36251 0.75 0.0E+00 BE546213.1 EST_HUMAN 23060 36279 0.75 0.0E+00 BE742213.1 EST_HUMAN 23081 36307 1.9 0.0E+00 BE082720.1 EST_HUMAN 23084 36306 1.9 0.0E+00 BE082720.1 EST_HUMAN 23094 36326 0.86 0.0E+00 BE082720.1 EST_HUMAN 23100 36331 1.33 0.0E+00 BE042720.1 EST_HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST_HUMAN 23100 36335 2.49 0.0E+00 BE617655.1 EST_HUMAN 23107 36336 2.49 0.0E+00 BE617655.1 EST_HUMAN 2316 36336 0.57 0.0E+00 BE617655.1 EST_HUMAN 23165 <td< td=""><td>49</td><td>22996</td><td></td><td>78.0</td><td>0.0E+00</td><td>AV654786.1</td><td>EST_HUMAN</td><td>AV654765 GLC Hamo sepiens aDNA clane GLCDZC07 3'</td></td<>	49	22996		78.0	0.0E+00	AV654786.1	EST_HUMAN	AV654765 GLC Hamo sepiens aDNA clane GLCDZC07 3'
23020 36236 8.82 0.0E+00 BE540213.1 EST HUMAN 23035 36251 0.75 0.0E+00 11436005 NT 23060 36279 2.79 0.0E+00 BE781742.1 EST HUMAN 23081 36307 1.9 0.0E+00 BE082720.1 EST HUMAN 23084 36336 0.86 0.0E+00 BE082720.1 EST HUMAN 23094 36331 0.86 0.0E+00 BE082720.1 EST HUMAN 23100 36331 1.33 0.0E+00 BE742215.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE717655.1 EST HUMAN 23106 36336 2.49 0.0E+00 BE617655.1 EST HUMAN 23107 36336 2.49 0.0E+00 BE617655.1 EST HUMAN 2316 36336 0.57 0.0E+00 BE617655.1 EST HUMAN 2316 36336 0.05 0.0E+00 BE617655.1 EST HUMAN 2316 36382 <td>8</td> <td>23015</td> <td>36231</td> <td>2.75</td> <td></td> <td>AW517960.1</td> <td>EST HUMAN</td> <td>xu74b01x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M89086 MOESIN (HUMAN);</td>	8	23015	36231	2.75		AW517960.1	EST HUMAN	xu74b01x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M89086 MOESIN (HUMAN);
23035 36251 0.75 0.0E+00 11436005 NT 23060 36279 2.79 0.0E+00 BE781742.1 EST HUMAN 23081 36307 1.9 0.0E+00 BE082720.1 EST HUMAN 23083 36316 0.66 0.0E+00 BE082720.1 EST HUMAN 23094 36326 0.86 0.0E+00 VD8032.1 NT 23100 36331 1.33 0.0E+00 BE743215.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST HUMAN 2310 36335 2.49 0.0E+00 BE617655.1 EST HUMAN 23107 36335 2.49 0.0E+00 BE617655.1 EST HUMAN 23127 36336 0.57 0.0E+00 BE617655.1 EST HUMAN 2316 36336 0.45 0.0E+00 BE172254.1 EST HUMAN 23165 36336	74	23020	36236	8.82		BE540213.1	EST_HUMAN	801078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5
23060 36279 2.79 0.0E+00 BE781742.1 EST HUMAN 23081 36307 1.9 0.0E+00 BE082720.1 EST HUMAN 23088 36308 1.9 0.0E+00 BE082720.1 EST HUMAN 23084 36326 0.86 0.0E+00 V08032.1 NT 23100 36331 1.33 0.0E+00 BE743215.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST HUMAN 23100 36335 2.49 0.0E+00 BE617855.1 EST HUMAN 23107 36336 0.57 0.0E+00 BE617855.1 EST HUMAN 23127 36335 0.57 0.0E+00 BE617855.1 EST HUMAN 23156 36336 0.45 0.0E+00 BE717855.1 NT 23166 36332 0.057 0.0E+00 BE72254.1 EST HUMAN 23165 36336	88	23035	36251	0.75		11436005	۲	Homo sapiens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
23081 36307 1.9 0.0E+00 BE082720.1 EST_HUMAN 23083 36308 1.9 0.0E+00 BE082720.1 EST_HUMAN 23084 36326 0.66 0.0E+00 YOB032.1 NT 23094 36325 0.86 0.0E+00 YOB032.1 NT 23100 36331 1.33 0.0E+00 BE743215.1 EST_HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST_HUMAN 23105 36335 2.49 0.0E+00 BE617655.1 EST_HUMAN 23127 36335 0.57 0.0E+00 BE617655.1 EST_HUMAN 23127 36335 0.57 0.0E+00 BE617655.1 EST_HUMAN 23156 36335 0.45 0.0E+00 BE617655.1 INT 23165 36336 0.45 0.0E+00 BE172254.1 EST_HUMAN 23165 36332 0.045 0.0E+00 BE172254.1 EST_HUMAN 23165 36332 <t< td=""><td>114</td><td>23060</td><td>36279</td><td>2.79</td><td></td><td>BE781742.1</td><td>EST_HUMAN</td><td>601467419F1 NIH_MGC_67 Hamo saplens cDNA clane IMAGE:3870700 5</td></t<>	114	23060	36279	2.79		BE781742.1	EST_HUMAN	601467419F1 NIH_MGC_67 Hamo saplens cDNA clane IMAGE:3870700 5
23081 36308 1.9 0.0E+00 BE082720.1 EST HUMAN 23088 36316 0.66 0.0E+00 Y08032.1 NT 23094 36325 0.86 0.0E+00 Y08032.1 NT 23100 36331 1.33 0.0E+00 BE743215.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST HUMAN 23105 36335 2.49 0.0E+00 BE617655.1 EST HUMAN 23127 36355 0.57 0.0E+00 BE617655.1 EST HUMAN 23146 36380 1.01 0.0E+00 BE617655.1 EST HUMAN 23157 36355 0.57 0.0E+00 BE617655.1 EST HUMAN 23164 36382 0.45 0.0E+00 B617655.1 NT 23165 36382 0.45 0.0E+00 B6172254.1 EST HUMAN 23165 36382 1.02 0.0E+00 B6172254.1 EST HUMAN 23262 36383	135	23081	36307	1.9	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-dt3 BT0642 Homo saplens cDNA
23088 36316 0.66 0.0E+00 Y080321 NT 23094 36326 0.86 0.0E+00 AI656890.1 EST HUMAN 23100 36331 1.33 0.0E+00 BE743215.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST HUMAN 23105 36336 2.49 0.0E+00 BE617655.1 EST HUMAN 23127 36355 0.57 0.0E+00 BE617655.1 EST HUMAN 23154 36380 1.01 0.0E+00 BF617655.1 EST HUMAN 23157 36355 0.57 0.0E+00 BF617655.1 INT 23156 36382 0.45 0.0E+00 BF617655.1 INT 23165 36382 0.45 0.0E+00 BF172254.1 EST HUMAN 23165 36382 0.05 0.0E+00 BF172254.1 EST HUMAN 23265 36382 0.05 0.0E+00 BF172254.1 EST HUMAN 232629 36463	35	23081	36308	1.9	0.0E+00	BE082720.1	EST HUMAN	RC2-BT0842-150200-012-d03 BT0642 Homo saplens cDNA
23094 36326 0.86 0.0E+00 AI656800.1 EST HUMAN 23100 36331 1.33 0.0E+00 BE743215.1 EST HUMAN 23100 36332 1.33 0.0E+00 BE743215.1 EST HUMAN 23105 36336 2.49 0.0E+00 BE617655.1 EST HUMAN 23127 36355 0.57 0.0E+00 BE617655.1 EST HUMAN 23154 36380 1.01 0.0E+00 BE617655.1 EST HUMAN 23157 36355 0.57 0.0E+00 BE617655.1 EST HUMAN 23156 36382 0.45 0.0E+00 B7675.1 NT 23165 36382 0.45 0.0E+00 B7675.1 NT 23165 36382 1.02 0.0E+00 B7675.1 NT 23166 36382 1.02 0.0E+00 B6172254.1 EST HUMAN 23229 36463 2.76 0.0E+00 B6172254.1 EST HUMAN	7	23088	36316	99.0	0.0E+00	Y08032.1	٦	Human endogenous retrovirus-K, LTR U5 and gag gene
23100 36331 1,33 0.0E+00 BE743215.1 EST_HUMAN 23100 36332 1,33 0.0E+00 BE743215.1 EST_HUMAN 23105 36336 2,49 0.0E+00 BE617655.1 EST_HUMAN 23127 36355 0.57 0.0E+00 BE617655.1 EST_HUMAN 23154 36380 1.01 0.0E+00 BF617655.1 EST_HUMAN 23154 36382 0.57 0.0E+00 BF617655.1 EST_HUMAN 23156 36382 0.45 0.0E+00 BF6775.1 NT 23165 36392 1.02 0.0E+00 BF17254.1 EST_HUMAN 23165 36392 1.02 0.0E+00 BF172254.1 EST_HUMAN 23229 36463 2.76 0.0E+00 AV711075.1 EST_HUMAN	2	23094		0.86	0.0E+00	AI656890.1	EST_HUMAN	H54e07.x1 NCI_CGAP_GC8 Hamo septens cDNA dane IMAGE:22446123'
23100 36332 1.33 0.0E+00 BE743215.1 EST_HUMAN 23106 36336 2.49 0.0E+00 BE617655.1 EST_HUMAN 23107 36356 0.57 0.0E+00 BE617655.1 EST_HUMAN 23157 36356 0.57 0.0E+00 B7675.1 NT 23156 36382 0.45 0.0E+00 B7675.1 NT 23165 36392 0.045 0.0E+00 B772254.1 EST_HUMAN 23165 36392 1.02 0.0E+00 B6172254.1 EST_HUMAN 23166 36393 1.02 0.0E+00 B6172254.1 EST_HUMAN 23229 36463 2.76 0.0E+00 AV711075.1 EST_HUMAN	Š	23100		1.33	0.0E+00	BE743215.1	EST HUMAN	1601573895F1 NIH_MGC_9 Hamo saplens cDNA clone IMAGE:3835188 51
23106 36336 2.49 0.0E+00 BE617655.1 EST_HUMAN 23107 36336 2.49 0.0E+00 BE617655.1 EST_HUMAN 23127 36355 0.57 0.0E+00 H3605.1 EST_HUMAN 23154 36380 1.01 0.0E+00 H875.1 NT 23165 36382 0.45 0.0E+00 H675.1 NT 23165 36392 1.02 0.0E+00 H6172554.1 EST_HUMAN 23165 36393 1.02 0.0E+00 BE172254.1 EST_HUMAN 23229 36463 2.76 0.0E+00 AV711075.1 EST_HUMAN	54	23100	36332	1.33	0.0E+00	BE743215.1	EST_HUMAN	1801573895F1 NIH_MGC_9 Hamo septens cDNA clone IMAGE:3835198 67
23105 36336 2.49 0.0E+00 BE617655.1 EST HUMAN 23127 36355 0.57 0.0E+00 H3605.1 EST HUMAN 23154 36380 1.01 0.0E+00 B7675.1 NT 23156 36382 0.45 0.0E+00 B7675.1 NT 23165 36392 1.02 0.0E+00 BF172254.1 EST HUMAN 23165 36393 1.02 0.0E+00 BE172254.1 EST HUMAN 23229 36463 2.76 0.0E+00 AV711075.1 EST HUMAN	8	23106		2.49	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Hamo saplens cDNA clone IMAGE:3845856 3'
23127 36355 0.57 0.0E+00 H39905.1 EST HUMAN 22164 36380 1.01 0.0E+00 D87675.1 NT 25156 36382 0.45 0.0E+00 AF081364.1 NT 23165 36382 1.02 0.0E+00 BE172254.1 EST HUMAN 23166 36383 1.02 0.0E+00 BE172254.1 EST HUMAN 23229 36463 2.76 0.0E+00 AV711075.1 EST HUMAN	85	23105		2.49	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo septens cDNA clone IMAGE:3845956 3'
23154 36380 1.01 0.0E+00 D87675.1 NT 23156 36382 0.45 0.0E+00 AF081384.1 NT 23165 36382 1.02 0.0E+00 BE172254.1 EST_HUMAN 23166 36383 1.02 0.0E+00 BE172254.1 EST_HUMAN 23229 36463 2.76 0.0E+00 AV711075.1 EST_HUMAN	181	23127	36355	0.57	0.0E+00		EST_HUMAN	yp01a10.r1 Soures breast 3NbHBst Homo sepiens cDNA clone IMAGE:186138 5
23156 36382 0.45 0.0E+00 AF081384.1 NT 23165 36382 1.02 0.0E+00 BE172254.1 EST_HUMAN 23165 36383 1.02 0.0E+00 BE172254.1 EST_HUMAN 23229 36463 2.76 0.0E+00 AV711075.1 EST_HUMAN	308	23154	36380	1.01	0.0E+00		N	Homo sapiens DNA for annyloid precursor protein, complete cds
23165 36392 1.02 0.0E+00 BE172254.1 EST_HUMAN 23166 36383 1.02 0.0E+00 BE172254.1 EST_HUMAN 23229 38463 2.76 0.0E+00 AV711075.1 EST_HUMAN	10510	23156	36382	0.45	0.0E+00	AF081364.1	LN	Synthetic construct CD30 ligand-excitation A fusion protein (CD30L-ETA fusion) mRNA, partial cds
23165 36393 1.02 0.0E+00 BE172254.1 EST_HUMAN 23229 39463 2.76 0.0E+00 AV711075.1 EST_HUMAN	519	23165	36392	1.02	0.0E+00	BE172254.1	EST_HUMAN	MR0-HT0559-270300-006-e12 HT0559 Homo sapiens cDNA
23229 38463 2.76 0.0E+00 AV711075.1 EST_HUMAN	<u>ē</u>	23165	36363	1.02	0.0E+00	BE172254.1	EST_HUMAN	MR0-HT0559-270300-008-e12 HT0559 Homo saplens cDNA
	332	23228	38463	2.76	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Ou Homo sapiens cDNA clone CuAAKG05 6

Page 527 of 536 Table 4 Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Detabase Source	Top Hit Descriptor
10532	23220	36464	2.76	0.0E+00	0.0E+00 AV711075.1	EST_HUMAN	AV711075 Gu Homo sapiens cDNA done GuAAKG05 51
10534	23231		2.13	0.0E+00	.	EST_HUMAN	RC3-ST0197-120200-015-e03 ST0197 Homo septems cDNA
10542	23238	36472	7.02	0.0E+00	0.0E+00 AW963563.1	EST_HUMAN	EST376636 MAGE resequencee, MAGH Hamo sepiens cDNA
10555	23251	36487	3.19	0.0E+00	11431124 NT	LN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10555	23251	36488	3.19	0.0E+00	11431124 NT	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10559	23255	36492	2.09	0.0E+00	0.0E+00 AW057821.1	EST_HUMAN	wy61f09.x1 Soeres_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:2553065 3' similar to TR:0e0568 Qe0566 VDX;
10567	23262	36480	8.	0.0E+00	0.0E+00 BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemta cell (FAB M1) Baylor-HGSC project=TCAA Homo seplens cDNA clone TCAAP0917
10568	23263	36500	2.85	0.0E+00	0.0E+00 AI652239.1	EST_HUMAN	wb28a12x1 NC_CGAP_GC8 Homo sepiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
10508	23,263	36501	2.85	0.0F+00	0.0F+00 AI852239.1	EST HUMAN	wb28a12x1 NCL_CGAP_GC8 Home septems cDNA clone IMAGE:2306974 3' similar to contains element MSR1 repetitive element:
10673	23268	36506	1.52	0.0E+00		EST HUMAN	601888704F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:4122649 5
10580	23275		5.08	0.0E+00	45911	NT.	Homo sapiens NOD2 protein (NOD2), mRNA
10580	23275		5.06	0.0E+00	11545911 NT	LN	Homo sapiens NOD2 protein (NOD2), mRNA
10598	23290	36528	1.98	0.0E+00	0.0E+00 AW 404795.1	EST_HUMAN	UI-HF-BLO-acm-d-04-0-UI.r1 NIH_MGC_37 Hamo septens aDNA dane IMAGE:3059383 5'
10800	23294	36533	3.17	0.0E+00	11424829 NT	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
10801	23295		7.47	0.0E+00		LN.	Homo sapiens 5-hydroxydryptamine (serotonin) receptor 1E (HTR1E) mRNA
10601	23205		7.47	0.0E+00		TN	Homo sapiens 5-hydroxytryptemine (serotonin) receptor 1E (HTR1E) mRNA
10602	23296		3.68	0.0E+00		EST_HUMAN	wu32b08x1 Soares_Dieckgraefe_colon_NHCD Homo sepiens cDNA clone IMAGE:2521715 3
10805	23299	36540	4.48	0.0E+00	0.0E+00 BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5
10609	23303	36542	8.24	0.0E+00	0.0E+00 BE891630.1	EST_HUMAN	801434522F1 NIH_MGC_72 Homo sapiens aDNA dane IMAGE:3919636 5
10612	23306	36544	1.68	0.0E+00	8923939 NT	NT	Homo sepiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10612	23306	36545	1.00	0.0E+00	8923939 NT	TN	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10619	23312	36551	1.4	0.0E+00		NT	Homo sapiens mRNA for KIAA0708 protein, pertial ods
10619	23312	36552	1.4	0.0E+00		ᅜ	Homo sepiens mRNA for KIAA0708 protein, perital cds
10628	23321	36559	1.31	0.0E+00	0.0E+00 BE903304.1	EST HUMAN	601674332F1 NIH_MGC_21 Homo sepiens cDNA dane IMAGE:3957343 5
10631	18484	31403	1.65	0.0E+00	0.0E+00 AA195905.1	EST HUMAN	zp95b11.r1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:627633 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10652	23343	36581	5.53	0.0E+00	0.0E+00 BE793498.1	EST_HUMAN	601588829F1 NIH_MGC_7 Homo sepiens cDNA clone IMAGE:3943015 57
10860	23351	36588	1.79	0.0E+00	0.0E+00 BE729706.1	EST_HUMAN	801562864F1 NIH_MGC_20 Hamo explens cDNA clane IMAGE:3832575 5
10660	23351	36589	1.79	0.0E+00		EST_HUMAN	601562864F1 NIH_MGC_20 Hamo septens cDNA clone IMAGE:3832575 5
10661	23352	36590	33.99	0.0E+00	0.0E+00 AV727362.1	EST_HUMAN	AV727362 HTC Homo sepiens cDNA clone HTCAQH06 5'

. Page 528 of 536 Table 4

		52226 3' similar to gb:\M60854 40S		475 3' similar to contains	53' similar to contains	3' similar to contains						(17115 IG MU															
	AV727362 HTC Homo saplens cDNA clone HTCAQH06 5'	304910.x1 NCI_CGAP_Lym12 Homo sepiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S48 (1918AN)	AU135741 PLACE1 Homo sepiens cDNA clone Pl ACE1002794 F	hg13d02xt Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element	hg13d02.xt Scares_NFL_T_GBC_S1 Homo sapiens cDNA done IMAGE:2945475.3' similar to contains element MSR1 recently a element	hg13d02xt Sceree_NFL_T_GBC_S1 Home septens cDNA clone IMAGE:2845475 3' similar to contains	H saplans mRNA for H1 Neternion	HSCSIC031 normalized infant brain cDNA Homo serviens cONA signal and	Homo sapiens RGH1 nene metmetris-like alemani	Homo saplens EdyA7 (EPHA7) mRNA	Homo sepiens EphA7 (EPHA7) mRNA	XW6901.X1 NCI_CGAP_Part1 Homo septens oDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION OF INANY.	ULH-BIS-ghe-01-01 II of NO. COAD Sine Low	ULH-Bi3-alh-e-01-0-1 is 1 NC COAP Subs Home series CANA cone IMAGE:2736649 3	Homo sepiens ribosomal purifici. 134 (RPI s41 mBNA	Homo sepiens mRNA for KIAA0867 brokein partial cyle	801119248F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:3020219 5	Homo sapiens mRNA for KIAA0545 protein, partial cds	AU124108 NT2RM2 Homo sepiens cDNA clone NT2RM2001675 5'	Homo sapiens mRNA for KIAA1117 protein, partial cds	domo sepiens mRNA for KJAA117 protein, partial ods	601582048F1 NIH MGC_7 Hamo sepiens aDNA clane IMAGE:3836539 5	202141402F1 NIH MGC_48 Homo sepiens cDNA clone IMAGE:4302432 5	AUT18386 HEMBAT Home septemble CUNA Clone IMAGE:3544259 6	143c03.x1 Source healts NHT Homo services and a line 144 or 1755-175	9743003.x1 Sostes tesds NHT Homo septems cDNA clare INACE:1752/72.3	QV4-ST0234-121199-032-b06 ST0234 Homo septens cDNA
	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	FST HEIMAN	LN LN	EST HUMAN	Ł	N.	77	EST HUMAN	ST HUMAN	ST HUMAN	5	F	ST HUMAN	- 1	⊢'I.	<u> </u>	11	Т	T	Т	Т	Г	П
	AV727362.1	AW 516055.1	AU135741.1	4W59333.1	1W593333.1					4758281	4768281		Γ		00032										Γ		
Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 B	0.0E+00A	0.0E+00 A	0.0E+00 A	0.00=+00.0	00-100 00-100	0.0E+00 Bi	0.0E+00 A(0.0E+00 AI	0.0E+00 AI	0.0E+00 AW391937
	33.99	9.30	3.18	3.41	3.41	3.41	8	297	1.79	1.33	1.33	2.13	4.62	4.62	11.67	2.63	88.	204	5,	1.40 1.40 1.40 1.40 1.40 1.40 1.40 1.40	2 2	50 14	13	5.8	6.53	6.53	3.04
				36617	36678	36619	36820	36621	36629	36634	38635	36648	36649	36650		36652	38670	30083	2,000,0	36808	36702		36703	36708	36710	36711	36712
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70007	10661	10674	10680	10686	10686	10686	10688	10689	10700	10708	10706	10718	10719	10719	10721	10723	10/38	10783	10777	107771	10778	107777	10778	10781	10788	10786	10787
		00 AV727362.1 EST_HUMAN	23352 36591 33.99 0.0E+00 AV727362.1 EST HUMAN 8.39 0.0E+00 AW516055.1 EST HUMAN	23352 36591 33.99 0.0E+00 AV727362.1 EST_HUMAN 23365 36508 8.59 0.0E+00 AW518055.1 EST_HUMAN 23371 36813 3.18 0.0E+00 AU135741.1 EST_HUMAN	23352 36591 33.99 0.0E+00 AV727362.1 EST_HUMAN 23371 36613 3.18 0.0E+00 AV15055.1 EST_HUMAN 23377 39613 3.41 0.0E+00 AV159333.1 EST_HUMAN	23352 36591 33.99 0.0E+00 AV727362.1 EST HUMAN 23365 36608 9.59 0.0E+00 AV727362.1 EST HUMAN 23371 36613 3.41 0.0E+00 AW59333.1 EST HUMAN 23377 36618 3.41 0.0E+00 AW59333.1 EST HUMAN	23365 36591 33.99 0.0E+00 AV727362.1 EST HUMAN 23371 36618 8.59 0.0E+00 AW593333.1 EST HUMAN 23377 36618 3.41 0.0E+00 AW593333.1 EST HUMAN 3.41 0.0E+00 AW593333.1 EST HUMAN 3.41 0.0E+00 AW593333.1 EST HUMAN 3.41 0.0E+00 AW593333.1 EST HUMAN 3.41 0.0E+00 AW593333.1 EST HUMAN 3.41 0.0E+00 AW593333.1 EST HUMAN 3.41 0.0E+00 AW593333.1 EST HUMAN	23365 36591 33.99 0.0E+00 AV727362.1 EST HUMAN 23377 36618 3.41 0.0E+00 AW593333.1 EST 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36649 4.62 0.0E+00 AV51230.1 EST_HUMAN 23408 36650 4.62 0.0E+00 AV51230.1 EST_HUMAN	23362 36591 33.99 0.0E+00 AV727362.1 EST HUMAN 23377 36619 3.41 0.0E+00 AV618055.1 EST HUMAN EST HUMAN 23377 36619 3.41 0.0E+00 AV68333.1 EST HUMAN 23377 36619 3.41 0.0E+00 AV68333.1 EST HUMAN 23377 36619 3.41 0.0E+00 AV68333.1 EST HUMAN 23370 36620 1.89 0.0E+00 AV68333.1 EST HUMAN 23380 36620 1.89 0.0E+00 E+00 E+00 E+00 ET HUMAN 23380 36620 1.79 0.0E+00 E+00 E+00 ET HUMAN 23380 36620 1.79 0.0E+00 AV58333.1 EST HUMAN 23380 36620 1.73 0.0E+00 AV58333.1 EST HUMAN 23380 36620 1.73 0.0E+00 AV758291 NT EST HUMAN 23380 36650 4.62 0.0E+00 AV758230.1 EST HUMAN 23408 36650 4.62 0.0E+00 AV75130.1 EST HUMAN 133 0.0E+00 AV75130.1 EST HUMAN 133 0.0E+00 AV75120.1 EST HUMAN 133 0.0E+00 AV75120.1 EST HUMAN 133 0.0E+00 AV75120.1 EST HUMAN 133021 NT EST HUMAN 145021 EST HUMAN 145021 NT EST HUM	23365 36591 33.99 0.0E+00 AV727362.1 EST HUMAN 23377 36619 3.41 0.0E+00 AW518055.1 EST HUMAN 23377 36619 3.41 0.0E+00 AW59333.1 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36634 1.33 0.0E+00 AV563333.1 EST_HUMAN 23407 36648 2.13 0.0E+00 AV563333.1 EST_HUMAN 23408 36650 4.62 0.0E+00 AV563333.1 EST_HUMAN 23418 36650 4.62 0.0E+00 AV563333.1 EST_HUMAN 23447 36650 4.62 0.0E+00 AV563333.1 EST_HUMAN 23447 36650 4.62 0.0E+00 AV563201 EST_HUMAN 23448 2.43 0.0E+00 AV563201 EST_HUMAN 23447 36693 1.45 0.0E+00 AV5632040.1 IT 23464 36703 1.31 0.0E+00 AV5632040.1 IT 23464 36703 1.31 0.0E+00 AV5632040.1 IT 23469 36710 6.53 0.0E+00 AV148900.1 EST_HUMAN 23460 36710 6.53 0.0E+00 AV148900.1 EST_HUMAN 23460 36710 6.53 0.0E+00 AV148900.1 EST_HUMAN 23460 36710 6.53 0.0E+00 AV148000.1	

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Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	St Shriter Top Hit Acession LAST E No. Source	0.0E+00 AF223391.1 NT spliced home saplens calclum channel alpha1E subunit (CACNA1E) gene, excris 7-49, and partial cds, alternatively spliced	0.0E+00 AF223391.1 NT soliced	424726 NT	T HUMAN	EST_HUMAN	1 EST_HUMAN	1 EST HUMAN	0.0F-t00 AB0029040.1 NT Home sapiens mRNA for KIAA1117 protein, partiel ods	- LA	1.5	.1 EST HUMAN	0.0E+00 W21826.1 EST HUMAN 57E10 Human refine CDNA Tsr509H-deawed stripters Human content cont	0.0E+00 AA7407821 FST HIMAN MSR1 requestions services control models of the services of the	EST HIMAN	Į.	EST HUMAN	0.0E+00 AA748375.1 EST_HUMAN los56h01.r1 NCI CGAP GCB1 Home sentens characteristics for the control of the cont	1.1 EST_HUMAN	EST_HUMAN	EST_HUMAN	1 EST HUMAN	1 EST_HUMAN	1 EST_HUMAN	EST_HUMAN	₩.	LN L	T	EST HIMAN	
Single E		4.	•	424726			1					-		_	\ <u>.</u>			-	1			1	1	_			LN .	EST		1
	Most Similar (Top) Hit BLAST E Value			0.0E+00				0.0E+00B	0.05+00	00+400	0.0E+00 B	0.0E+00 BE	0.0E+00 W	0.0E+00 AA	0.0E+00 AV	0.0E+00 AF	0.0E+00 CC	0.0E+00 AA	0.0E+00 AA	0.0E+00 M7	0.0E+00 M7	0.0E+00 AL	0.0E+00 AU	0.0E+00 AV	0.0E+00 BF	0.0E+00 AB	0.0E+00 AB	0.0E+00 BE	0.0E+00 AV	
	Expression Signal	4.39	4.39	9.57	1.42			52.94	1.69	3.47	1.55	1.55	1.47	136.01	2.05	2.91	7.34	2.31	2.31	3.74	3.74	9.82	5.81	1.64	238	273	2.73	2.04	4.	12
	ORF SEQ ID NO:	38721	36722	Ц	36733			36738					36762	36770	36783	36790									30862	31311	31312	36888		00000
	SEQ ID NO:	23481	23481		23497			23500	1	23510	23514		23520	23534	23537				\perp	235/5	235/5	235/8	23590	4000	71007	10283	ASSO -	23636	23637	22000
	Probe SEQ ID NO:	10798	10798	10807	10814	10814	10815	1087	10824	10828	10832	10832	10838	10854	10857	10863	10879	10886	10886	10807				10824	10932	10800	1000	10960	10961	40000

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			Τ			Τ	Т	Τ			Г		Γ	Т	Τ	Т	Т	Т	Т		ТМ	٦,	_	Т	T	_	Т-		
Single Exon Probes Expressed in Brain	Top Hit Descriptor	III HE BNO also also also also also also also also	ILLHE BNO. 45.4 02.0 11.4 MILL MODE & Home sapiens cDNA done IMAGE:3077019 6'	by the case of the control of the co	protein (MOUSE);	COLALASSI / I'LI NCI CICAP BIN67 Homo sepiens cDNA clone IMAGE:4181083 5	MONAGE THE INCLUDE OF BIRDY Hamp sepiens CDNA clane IMAGE:4181083 5	MIRA STANDO AND AND AND AND AND AND AND AND AND AND	MRA STOATS OATON AT STOATS HOME SEPTENCE CONA	Home septemble ENA 7 (EDLAY) - DATA	CONTACTOR LATER TO THE CONTACTOR TO THE	BOSRO14 of SAMILY MOST / A HOME SEPTEMBER CLINA CIONE IMAGE:3925403 5	ASSECTATION OF THE PROPERTY OF	INKETARAM 0120 of 424 /	Low State 120 1 454 (syndrym): 19853) Homo saplens cDNA clone DKFZp434 0120 5	Lower Supporting (G-TH), mrt/A	FACETOWNS NOTICED III (NEXNS) THENA	Out of version with Middle 19 Home septems cDNA clone IMAGE:4101433 5'	Hamperstrange-House, NC, CGAP_Sub4 Home sapiens cDNA clone IMAGE:2724312.3'	Homo series mRNA for KIA A7217	be04407.17 NIH_MGC_T han septens cDNA done IMAGE:2823373 5 similar to TR:076022 076022 E1B.	be04d07.y1 NIH_MGC_7 Home septems cDNA done IMAGE.2823373 5 smiler to TR:076022 OZE022 E1R.	63KDA-ASSOCIATED PROTEIN.;	Hamo sapiens KIAA0428 gene product (KIAA0428), mRNA	Homo saplens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA	Hamo septens zinc finger hameodamein protein (ATBF1-A) mRNA, complete cds	ROS-LTROSS CARES 446 LTROSS Hamo sapiens cDNA	beddown y NIH MGC_10 Home septems cDNA done IMAGE:2900367 5' similer to TR:060275 C60275	ba54408.y3 NIH_MGC_10 Homo sepiens cDNA done IMAGE.2900367 5 similar to TR: 080275 060275 KIAA0522 PROTEIN;
igle Exon Pro	Top Hit Databese Source	EST HIMAN	EST HIMAN		EST HUMAN	EST CHIMAIN	EST LINAN	EST HIMAN	EST HIMAN	.1	EST HIMAN	EST HUMAN	FST HIMAN	FST HIMAN	-1.	1	EST LIMAN	EST LINAN	NT TOWN	LZ	EST HIMAN		HOMAN			Т	LI IMAN		
Si	Top Hit Acession No.	0.0E+00 AW 500307.1	0.0E+00 AW 500307.1	0 0F+00 RE048202 4	0.0E+00 BE528007.4	0.0E+00 BF528907 4	0.0E+00 BF528807 1	0.0E+00 AW387788 1	Ī	1281	0.0E+00 BE897953.1			-	880082	4758827 NT	0.0F+00 BF208581 1						76790	11000408	1024/11	7			-
	Most Similar (Top) Hit BLAST E ·	0.0€+00	0.0	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.00.	0.05+00	0.0E+00	0.0	0.05+00	0.05+00	0.0E+00/	0.0E+00/	0.0E+00 BE206846	000000000000000000000000000000000000000	0	201	0.0E+00 (22822 4	0.0E+00 BE148078	0.0E+00 BE148076	0.0E+00 AW673489	0.0E+00 AW673469.
	Expression Signal	1.85	1.85	2.39	1.77	1.7	1.77	1.27	1.27	1.53	8.73	1.89	1.89	2.78	1.61	3.98	2.67	12.22	423	4.23	2.68	2 80	9	1.52	15	3.84	3.84	-7 -28	1.96
	ORF SEQ ID NO:	36919	36920	36923	36949	39960	36951	36964	36965	36973	36974	36977	36978	36882	37028	37031	37032	37038	37040	37041	37043	37044	37065	37069	33133	37074	37075	37101	37102
	Exen SEQ ID NO:	23683	23663	23600	23688	23688	23688	25133	26133	23705	23706	23708	23708	23721	23763	23755	23756	23761	23766	23706	23788	23768	23780	23783	20052	23780	23789	23821	23821
	Probe SEQ ID NO:	10989	10989	10992	11016	11016	11018	11028	11028	11034	11035	11037	11037	11051	11083	11085	11086	11091	11096	11096	11098	11098	11110	11124	11127	11131	11131	11164	11154
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Probe SEQ ID 8 NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11176	23843	37128	6.21	0.0E.+00	0.0E.+00 BF507876.1	EST_HUMAN	UI-H-BI4-eck-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sepiens cDNA clone IMAGE:3086028 3'
11176	23843	37129	621	0.0E+00	0.0E+00 BF507876.1	EST_HUMAN	UFH-BI4-eck-b-10-0-UI.s1 NCI_CGAP_Sub8 Hamo septems cDNA dane IMAGE:3085028 3'
11185	23850	37136	1.57	0.0E+00	0.0E+00 AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sepiens cDNA clone PLACE1001381 5'
11189	23854	37140	1.82	0.0E+00	0.0E+00 BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sepiens cDNA done IMAGE:4271630 5
11189	23854	37141	1.82	0.0E+00	0.0E+00 BF576138.1	EST_HUMAN	802132459F1 NIH_MGC_81 Homo sepiens cDNA clone IMAGE:4271630 5'
11190	23855	37142	1.67	0.0E+00	0.0E+00 BF086811.1	EST_HUMAN	RC3-GN0089-190900-011-06 GN0089 Homo sepiens cDNA
11192	23857	37143	5.5	0.0E+00	0.0E+00 BE878401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo septems cDNA done IMAGE:3899207 57
11192	23857	37144	5.5	0.0E+00	0.0E+00 BE878401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Hamo sepiens cDNA done IMAGE:3899207 5'
11199	23864	37150	1.94	0.0E+00 D87682.1		LN PI	Human mRNA for KIAA0241 gene, partial cds
11204	23868		5.95	0.0E+00	0.0E+00 BF240538.1	EST_HUMAN	601875630F1 NIH_MGC_55 Hamo septems cDNA done IMAGE:4099710 5
11218	23881	37166	2.04	0.0E+00	0.0E+00 AB037737.1	NT	Homo saplens mRNA for KIAA1316 protein, pertiel cds
11218	23881	37187	2.04	0.0E+00	0.0E+00 AB037737.1	LN	Homo sepiens mRNA for KIAA1316 protein, partial cds
11222	23885	37170	4.17	0.0E+00	11430868 NT	Z	Homo saplens retinchlastoma-like 2 (p130) (RBL2), mRNA
11222	23885	37171	4.17	0.0E+00	11430868 NT	Z.	Homo sepiens retinoblestome-like 2 (p130) (RBL2), mRNA
11230	23893	37179	1.8	0.0E+00	0.0E+00 AA772837.1	EST_HUMAN	8674g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969942 3'
11241	23903	37192	1.62	0.0E+00	0.0E+00 AF223391.1	¥	Homo seplens caldum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11241	23903	37193	1.62	0.0E+00	0.0E+00 AF223391.1	Ę	Homo septens caldium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spitoed
11244	23906	37198	8.18	0.0E+00	503544	Z	Homo saplens eukanyotic translation initiation factor 5A (EIF5A) mRNA
11251	23913	37205	1.36	0.0E+00	0.0E+00 BF578267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Hamo septens cDNA clane IMAGE:4289502 5
11254	23916	37.209	5.84	0.0E+00	.1	EST_HUMAN	dr04g05.xt NIH_MGC_3 Hamo septens aDNA done IMAGE:2847177 5
11258	23920		71.88	0.0E+00		TN	Human gamma actin-like pseudogene, complete cds
11264	23926	37216		0.0E+00	0.0E+00 BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:4123948 5
11264	23926	37217	283	0.0E+00	0.0E+00 BF300995.1	EST HUMAN	601889823F1 NIH_MGC_17 Hamo sepiens cDNA clans IMAGE:4123948 5'
11271	23832	37225	105.67	0.0E+00	2.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sepiens cDNA
11291	23952	37249	2.34	0.0E+00 U36284.1		NT	Human beta-prime-adeptin (BAMZ2) gene, expn 16
11291	23952	37250	234	0.0E+00 U36264.1		NT	Human beta-prime-adaptin (BAM22) gene, expn 16
11295	23966		3.03	0.0E+00	0.0E+00 BE897051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo septens cDNA clone IMAGE:3924577 5
11286	23957		1.73	0.0E+00	4503786 NT	NT	Homo sapiens fyn-related kinase (FRK) mRNA
	23969	37271	3.55	0.0E+00	23698	. 1	Homo sepiens golgin-like protein (GLP), mRNA
	23072		2.69	0.0E+00		EST_HUMAN	601861947F1 NIH_MGC_53 Homo septens cDNA clone IMAGE:4081715 5
11314	23973		2.03	0.0E+00	0.0E+00 BE257744.1	EST_HUMAN	601116705F1 NIH_MGC_18 Hamo sepiens cDNA clane IMAGE:3357384 5

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Chiga character and a second in Diani	Most Smiler (Top) Hit Acession Detabase BLASTE No. Source	2 0.0E+00 11418318 NT Homo septions G-2 and S-phase expressed 1 (GTSE1), mRNA	0.0E+00 AL048544.1 EST_HUMAN	0.0E+00 A1903497.1 EST_HUMAN	0.0E+00 N5484.1 EST HUMAN	0.0E+00 AF108656.1 NT	0.0E+00 4507500 NT	0.0E+00 4507500 NT	0.0E+00 10092587 NT	0.0E+00 AF003528.1 NT	10.0E+00 AW 500082.1 EST HUMAN Inspetitive element contains element of the second respective elemen	0.0E+00 BE090210.1 EST HUMAN	0.0E+00 AF068757.1 NT	0.0E+00 9635487 NT	0.0E+00 A1204914.1 EST_HUMAN	0.0E+00 Al904646.1 EST_HUMAN	1 0.0E+00 6912457 NT Homo septens calcineurin binding protein 1 (KIAA0330), mRNA	0.0E+00 6912457 NT	0.0E+00 AF036351 NT	yo59e08.r1 Soeres breast 3NbHBst Homo saplens cDNA clone IMAGE:182246 6' shrillar to gb:M64089 0.0E+00 H30132.1 EST_HUMAN GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	0.0E+00 H30132.1 EST HUMAN	0.0E+00 D50659.1 NT	0.0E+00 11418189 NT	0.0E+00 11418189 NT	0.0E+00 4758489 NT	0.0E+00 AW 884898.1 EST_HUMAN	0.0E+00 8922593 NT Homo sapiens hypothetic	0.0E+00 11528291 NT	6 0.0E+00 4895312 NT Homo saplens G protein-coupled receptor 24 (GPR24), mRNA
}		0.0E+00	0.0E+00 A	0.0E+00 A	0.0E+00 N	0.0E+00 A	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00 A	0.0E+00 BI	0.0E+00 A	0.0E+00	0.0E+00 Ai	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI	0.0E+00 H	0.0E+00 H;	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A\	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	3.12	3.91	1.68	1.52	5.88	3.39	3.39	2.21	2.04	2.63	18.	4.43	3.36	2.41	1.68	1.51	1.51	2.08	2.78	2.78	10.68	2.51	2.51	1.53	1.5	2.09	1.88	4.24
	ORF SEQ ID NO:						28282	26263			30814						27436	27437	31039	27119	27120		31020	31021	27549		26817		28718
	Exam SEQ ID NO:			25281	25390	24594	13503	13593	25264	13318	26198	25248	25258	24732	25252	24778	14718	14718	24799	14424	14424	24816	24818	24818	14817	24856	13953	24884	16069
ſ	Probe SEQ ID NO:	12015	12023	12037	12076	12089	12092	12092	12100	12129	12218	12229	12273	12308	12351	12383	12405	12405	12423	12435	12435	12446	12448	12448	12464	12502	12538	12544	12288

Page 536 of 536 Table 4 Single Exon Probes Expressed in Brain

Chigo Expressed III brain	Top Hit Descriptor	One sarians but dans the three dates and the contract of the c	Home september CST ages for construction of UCKP2), mKNA	Homo sanians cleavane and not action and surface of the sanians cleavane and not have surface of the sanians cleavane and not have surface of the sanians cleavane and not have surface of the sanians cleavane and not have surface of the sanians cleavane and not surface of the sanians cleavane and not surface of the sanians cleavane and the sania	Homo sentens chromosome 21 and 1900 page 11 100 to 100 page 11 mRNA	The supporter four dansels are supported to the control of the con	Homo eachers colored to the time of time of the time of time of the time of the time of time of the time of time of time of time of time of time of time of time o	Homo septems DKF2n434P31 and DKF2D240244 - DKIA	wu83-07.xf NCI_CGAP_KIGS Home septems aDNA clare IMAGE-2527596 3' similar to TR:012844 Q12844	Home series (Los) EX REGION PRO LEIN Jointains 1 ART Beetiffive element;	Homo sapiens difficultionardities recentive sinks 2 m throw (C120RF3), mRNA	Supplied to the supplied of th
100 - 100 of	Top Hit Database Source								TAN E	AIV.		
	Top Hit Acession No.	5806918INT	0.0E+00 AB029000 1	9558724 NT	0.0E+00 AL163246.2	6806918 NT	114178R2 NT	7657020 NT	0.0E+00 AW025032 1	86844	0.0E+00 AF083824.1	
	Most Simfar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00/	
	Expression Signer	3.05	2.12	206	2.08	2.77	1.5	4	1.76	1.37	1.30	
	ORF SEQ ID NO:	30592		31009		26021	30972		30967	28550		
	Probe Exan SEQ ID SEQ ID NO: NO:	17905	24905	24927	25410	13390	24999	25004	25042	13890	25251	
	Probe SEQ ID NO:	12576	12582	12622	12648	12654	12729	12735	12790	12808	12818	

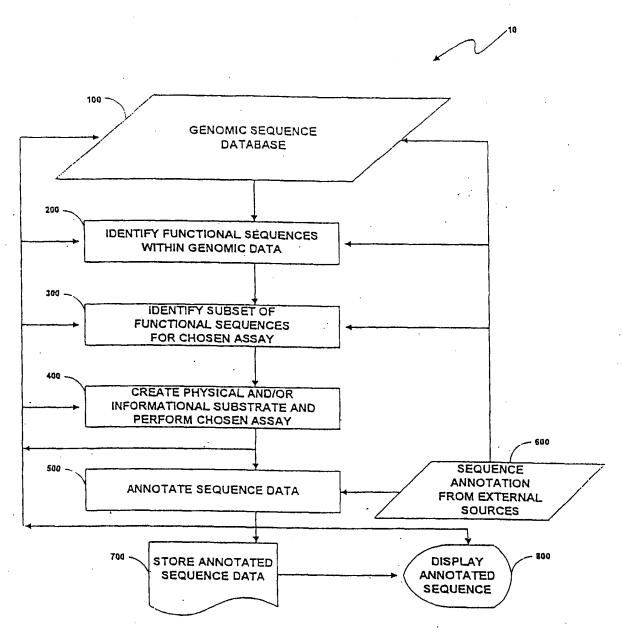


Fig. 1

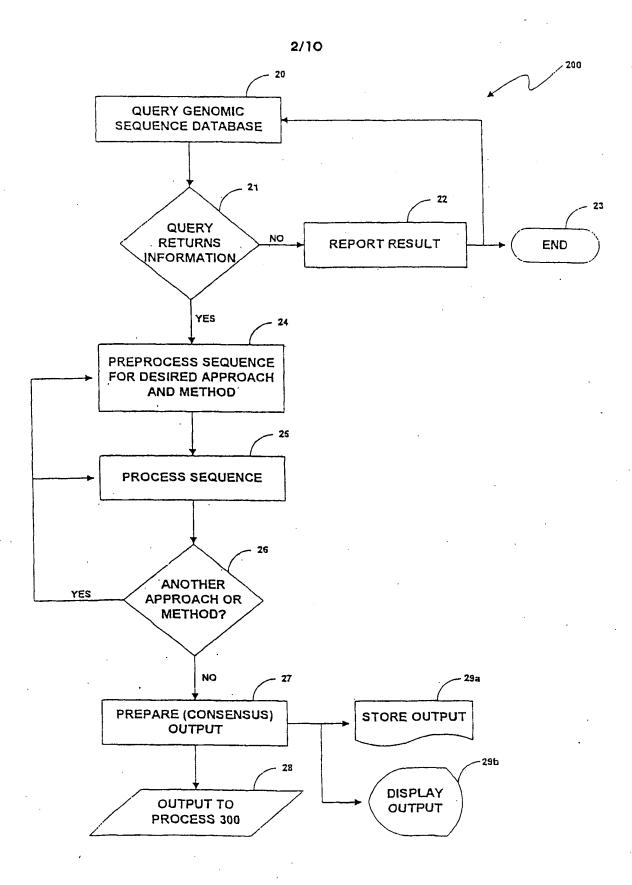


Fig. 2

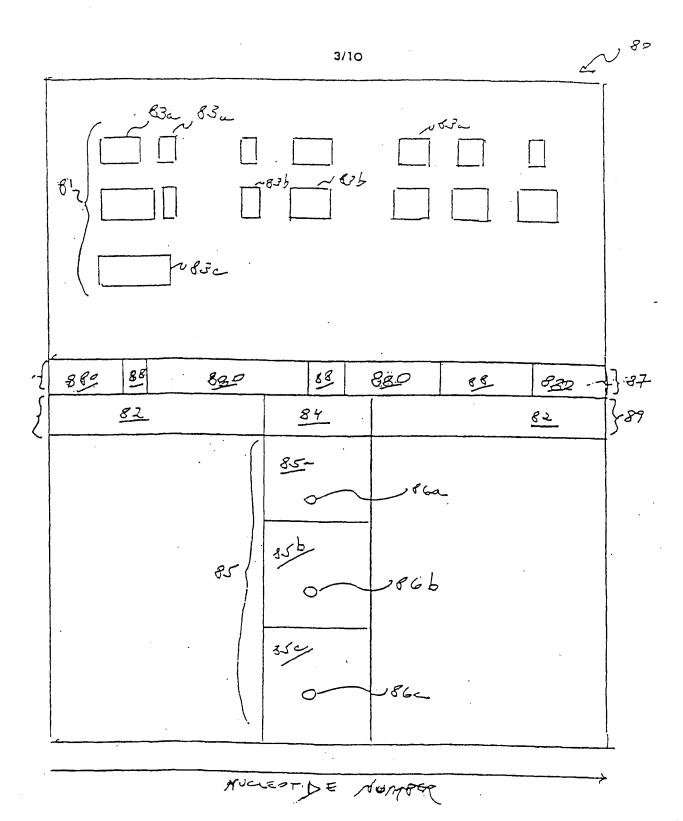


Fig. 3

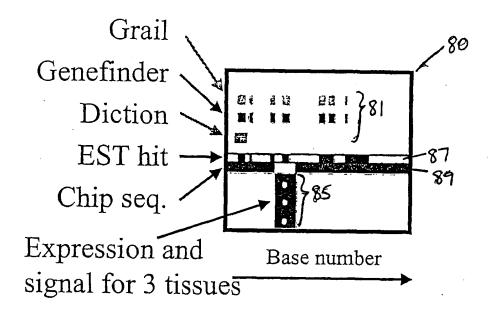


Fig. 4

5/10

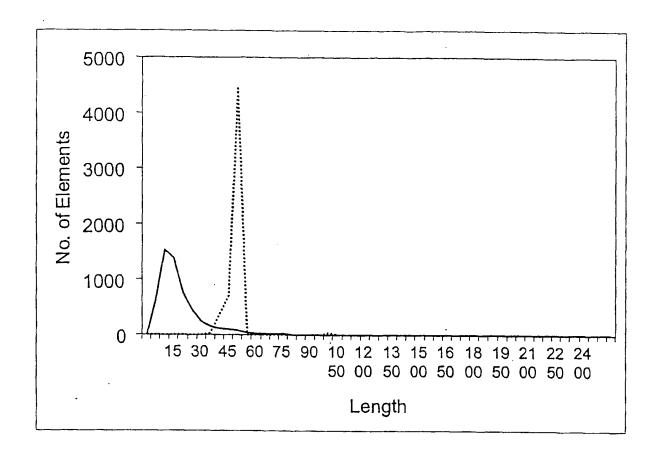


Fig. 5

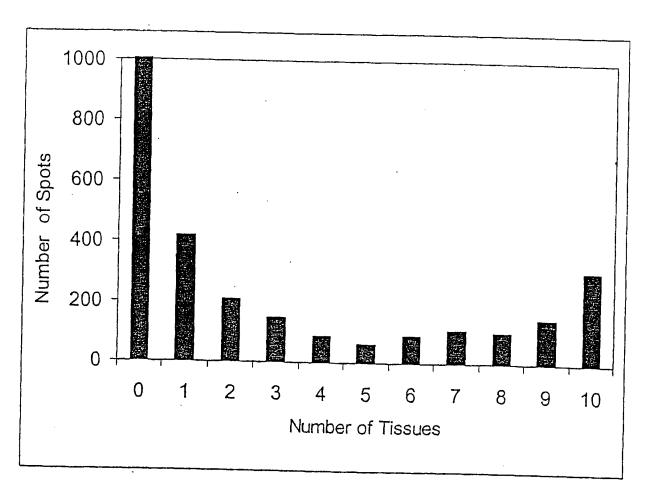
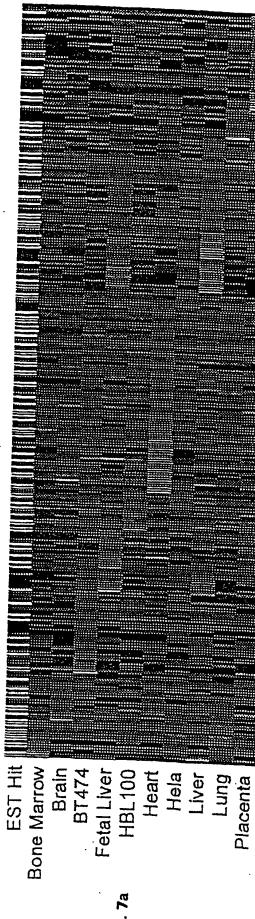


Fig. 6



ratio legend

Q α γ ο α 4 α α +

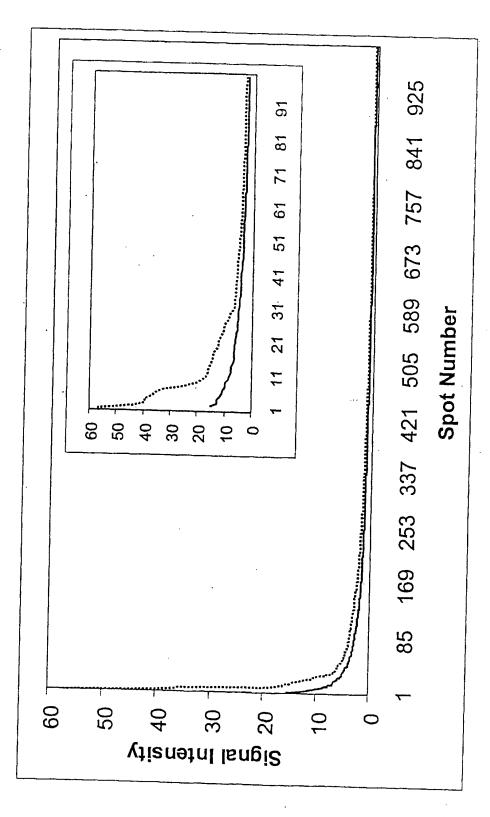


Fig. 8

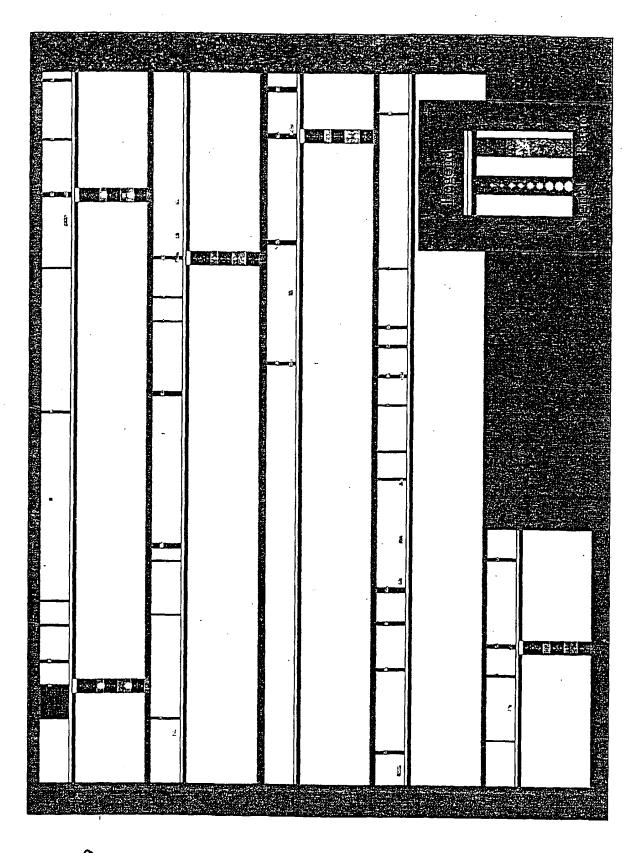
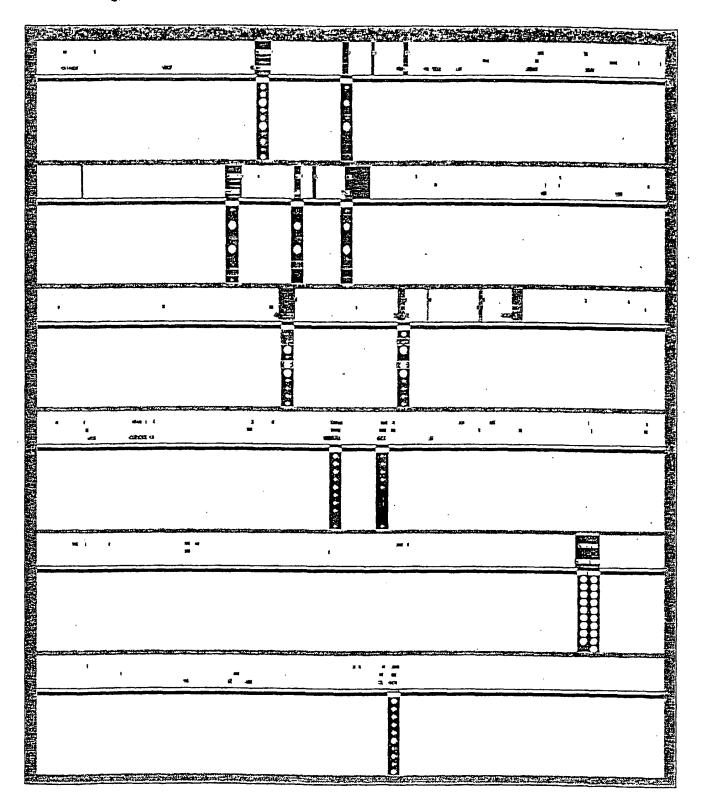


Fig. S

Fig. 10



(19) World Intellectual Property Organization International Bureau





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09/608,408	30 June 2000 (30.06.2000)	US
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60/234,687	21 September 2000 (21.09.2000)	US
60/236,359	27 September 2000 (27.09.2000)	US
0024263.6	4 October 2000 (04.10.2000)	GB

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(72) Inventors; and

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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see PCT Gazette No. 42/2002 of 17 October 2002, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE **EXPRESSION IN HUMAN BRAIN**

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the brain and their use in methods for detecting gene expression.

A. CLASS	SIFICATION OF SUBJECT MATTER		717 00007
IPC 7	C1201/68 G06F19/00 C07	K14/47	
	to International Patent Classification (IPC) or to both national	classification and IPC	
	SSEARCHED		
Minimum of IPC 7	documentation searched (classification system followed by cla C12Q C07K	assification symbols)	
_	ation searched other than minimum documentation to the exte		
Electronic	data base consulted during the international search (name of	data base and, where practical, search terms us	ed)
	nternal, WPI Data, PAJ, MEDLINE,	EMBASE, CHEM ABS Data, EM	BL, BIOSIS, INSPEC
	IENTS CONSIDERED TO BE RELEVANT		
Category °	Citation of document, with indication, where appropriate, or	f the relevant passages	Relevant to claim No.
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Y	iodothyronine deiodinase (DIÖ XP002186078 abstract	2) gene"	1-12, 22-24, 26,27
X	DATABASE EMBL 'Online! ID:CNS0000F, 11 May 1999 (199) HEILIG ET AL.: "Sequencing of chromosome 14" XP002186079	9-05-11) the human	13-21,25
Y	abstract 	-/	1-12, 22-24, 26,27
X Furth	er documents are listed in the continuation of box C.	X Patent family members are listed	in annex.
'A' documer consider earlier de filling de vinch is citation O' documer other m	nt which may throw doubts on priority claim(s) or s cited to establish the publication date of another or other special reason (as specified) nt referring to an oral disclosure, use, exhibition or	"T' later document published after the Interest or priority date and not in conflict with cited to understand the principle or the invention "X" document of particular relevance; the considered novel or cannot involve an inventive step when the document of particular relevance; the considered to involve an inventive step when the document is combined with one or moments, such combination being obvious in the art. "&" document member of the same patent if	mational filing date the application but sory underlying the laimed invention be considered to cument is taken alone aimed invention rentive step when the re other such docu- is to a person skilled
Date of the a	ctual completion of the international search	Date of mailing of the international sea	
26	September 2002	08 10.1	
lame and ma	ailing address of the ISA European Patent Office, P.B. 5818 Patentiaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,	Authorized officer	
m PCT/ISAM1	rax: (+31-70) 340-3016	Hagenmaier, S	
17107721	v (second sheet) (July 1892)		

PCT/US 01/00667

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abstract 	1-12, 22-24, 26,27		
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CHURCH D M ET AL: "ISOLATION OF GENES FROM COMPLEX SOURCES OF MAMMALIAN GENOMIC DNA USING EXON AMPLIFICATION" NATURE GENETICS, NEW YORK, NY, US, vol. 6, 1994, pages 98-105, XP000608940 ISSN: 1061-4036 the whole document	1-12, 22-24, 26,27		
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C.(Continu	nation) DOCUMENTS CONSIDERED TO BE RELEVANT	PCT/US 01	/00667
Category °	Citation of document, with indication, where appropriate, of the relevant passages		
	appropriate, of the relevant passages		Relevant to claim No.
Y	YASOJIMA K ET AL: "TANGLED AREAS OF ALZHEIMER BRAIN HAVE UPREGULATED LEVELS OF EXON 10 CONTAINING TAU MRNA" BRAIN RESEARCH, AMSTERDAM, NL, vol. 831, no. 1/2, 1999, pages 301-305, XP000929899 ISSN: 0006-8993 the whole document		1-12, 22-24
	the whole document ERMAK G ET AL: "RESTRICTED PATTERNS OF CD44 VARIANT EXON EXPRESSION IN HUMAN PAPILLARY THYROID CARCINOMA" CANCER RESEARCH, AMERICAN ASSOCIATION FOR CANCER RESEARCH, BALTIMORE, MD, US, vol. 56, no. 1, 1 March 1996 (1996-03-01), pages 1037-1042, XP002063388 ISSN: 0008-5472 the whole document		1-12, 22-24

INTERNATIONAL SEARCH REPORT

PCT/US 01/00667

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. X Claims Nos.: 1-24,26 (partially) because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful international Search can be carried out, specifically: See FURTHER INFORMATION sheet PCT/ISA/210
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
see additional sheet
As all required additional search fees were timely paid by the applicant, this international Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.: 1-27 (all partially)
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Remark on Protest The additional search fees were accompanied by the applicant's protest. X No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-24,26 (partially)

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first invention in form 206 PCT. If additional fees are paid for the (one or more) as yet unsearched inventions, similar statements about incomplete searches could be issued.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq.Id. 1 or 2 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising Seq. Id. 1 or 2 has been limited to the Seq. Id as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 25443. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 12830).

Likewise, claim 26, which refers to peptides encoded by Seq. Ids. 1 or 2 and 12830, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide disclosed, identified by Seq. Id. 25443.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

PC	705	017	00667

Patent document cited in search report		Publication date		Patent family member(s)		Publication date
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WO 9967422	Α	29-12-1999	CA EP JP WO	2330731 1090144 2002518064 9967422	A1 T	29-12-1999 11-04-2001 25-06-2002 29-12-1999